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GenCore version 5.1.6
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protein search, using sw model OM protein -

December 30, 2005, 13:02:01; Search time 142.194 Seconds (without alignments) 49.440 Million cell updates/sec Run on:

US-10-735-916A-2

Title: Perfect score:

1 RSSQSIVHSNGNTYLQ 16 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 Total number of hits satisfying chosen parameters: 2443163 segs, 439378781 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_21:* 1: geneseqp1980s:* Database :

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2001s:* geneseqp2004s:* geneseqp2005s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMMETER

	Description	683	_	-	Adj76899 Anti-IGF-	Adj76895 Anti-IGF-	Adz67058 Murine im	Adz67069 Human ant	Adz67065 Human ant	Aeb21358 Mouse ant		Adj76883 Anti-IGF-			Adj76897 Anti-IGF-	Adz67071 Human ant	Adz67067 Human ant	Aaw14937 Murine an	Aaw14942 3F4 Human	Aay53587 Anti-HPV1	1 VL	Abp52343 Fv region	[0]	Add94147 Mouse HUI	Adh61992 Mouse ant
SUMMAKIES	8	ADJ76836	ADZ67006	ADJ76888	ADJ76899	ADJ76895	ADZ67058	ADZ67069	ADZ67065	AEB21358	AEB31116	ADJ76883	ADZ67053	ADJ76901	ADJ76897	ADZ67071	ADZ67067	AAW14937	AAW14942	AAY53587	AAR70451	ABP52343	ADC03151	ADD94147	ADH61992
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Ad127487 CDR from Adm78123 Human SJB Adm78129 Human SJB Adm78081 Human SJB Adp84865 Complemen Adr19270 Glycosyla Ad887339 Humanised Aar27009 Hypercalc Aae06963 Mouse ger Aae06963 Mouse ger Add89248 Mouse imm Add89250 Mouse imm Add81447 House mou Aeb09521 Murine ge Aeb09521 Murine ge Aeb09523 Murine ge Abp25310 Fy region Abp25310 Fy region Abg74916 Murine MA	
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ALIGNMENTS

ADJ76836 standard; peptide; 16 ADJ76836; RESULT 1 ADJ76836

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(first entry) 06-MAY-2004 CDR sequence for anti-IGF-1R antibody.

insulin-like growth factor. Inscriptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. cytostatic; antipsoriatic; antibody;

Mus musculus.

WO2003059951-A2.

24-JUL-2003.

20-JAN-2003; 2003WO-FR000178.

18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753.

(FABR) FABRE MEDICAMENT SA PIERRE.

Leger O; Corvaia N, Goetsch L,

WPI; 2003-569653/53. N-PSDB; ADJ76835.

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Claim 1; SEQ ID NO 2; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with

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             these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF1R and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
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hyperactivity of signal transduction pathways mediated by interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:2.
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                                                                                                                                                                  100.0%; Score 81; DB 7; Length 16; 100.0%; Pred. No. 4.8e-07; Live 0; Mismatches 0; Indels
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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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Matches 16; Conservative
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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ADZ67006
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of

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comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary controlled and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment coff at liness connected with an antibody of the invention or treatment coff an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or connected with a cativation of the ransduction pathway of the signal mediated by the interaction of IGF or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin contractor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of not HERZ/neu-dependent and/or EGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent calls. (I) is useful in the preparation of a medicament calls. (I) is useful in the preparation of a medicament intended for prevention or for the preparation of a medicament intended for prevention or for the preparation of a medicament intended for prevention or for the preparation of a medicament intended for prevention or for the preparation of a medicament intended for the specific targeting of an endicament intended for the specific targeting of a medicament intended for the specific targeting or a biologically active compound to the standfor EGF readment of provided semple in which the abnormal presence, of IGF-IR and/or IGF-IR and/or IGF-IR and/or EGF reaceptor is suspected, which involves concaring th
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18-JAN-2002; 2002FR-0000654.
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit craneformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and passiste, lung, breast, and one to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
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                                                                                 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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100.0%; Pred. No. 5e-06;
iive 0; Mismatches 0;
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                  Corvaia N,
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nes 16; Conserv
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                  Goetsch L,
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                                           The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (II) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transition of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating portaging. Ab are also used to diagnose diseases caused also for treating portaging. Ab are also used to diagnose diseases caused also man also on the contraging and also entomed the property.
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                                                                                                                                                                                                                                                                                              by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
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                                                                                                                                                                                                                                                                                                                   protein sequence used to generate the Ab of the invention.
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               Disclosure; SEQ ID NO 65; 164pp; French
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hes 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003059951-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ76895;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
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treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Sepecially they inhibit transformation of normal calls to tumor calls, inhibit growth and/or proliferation of tumor calls, so are useful against cancers of the proliferation of tumor calls, so are useful against cancers of the also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
tinase activity of IGF-1R. Ab and its fragments are used to prevent or
8888888888888888888
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Sequence 112 AA;

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Gaps
                                 ö
100.0%; Score 81; DB 7; Length 112;
100.0%; Pred. No. 5e-06;
iive 0; Mismatches 0; Indels
                              16; Conservative
               Best Local Similarity
 Query Match
                                Matches
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ADZ67058 standard; protein; 112 AA.

ADZ67058;

30-JUN-2005 (first entry)

neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immune disorder; Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:54 Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;

Mus musculus,

US2005084906-A1.

21-APR-2005.

16-DEC-2003; 2003US-00735916

2002FR-00000653 18-JAN-2002;

18-JAN-2002; 2002FR-00000554. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. 11-JUL-2003; 2003FR-00006538.

GOETSCH L. CORVAIA N. LEGER O. DUFLOS A. HAEUW J. GOET/) LEGE/)

BECK A. (DUFL/) 1 (HAEU/) 1 (BECK/) 1

Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, WPI; 2005-321968/33.

Beck A;

Duflos A, Haeuw J,

Leger O,

Corvaia N,

Goetsch L,

Example 12; SEQ ID NO 54; 125pp; English.

useful for treating cancer.

The invention relates to a novel isolated anti-insulin-like grow'n ractor or peable of states to a novel isolated anti-insulin-like grow'n ractor capable of binding to human IGF-IR and, if necessary, capable of apable of specifically inhibiting to human igF-IR and, if necessary, capable of apable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary cardeterming region (CDR) consisting of one of two fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the prevention or treatment of an edicament intended for the prevention of the IGF-IR and/or connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGF, and/or connected with a cativation of the IGF-IR and/or EGF, and/or connected with cativation of the IGF-IR and/or EGF, with IGF-IR and/or of EGF with EGF, where the administration of the medicament does not induce or only slightly induces accondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to IGF-IR and/or IREZ/reu-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IREZ/reu-dependent and/or IREZ/reu-dependent calls. (I) is useful in the preparation of a medicament intended for prevention or two the treatment of cancer, where cand-or the specifies and prostate cancer, osteosarcoma, lung cancer, che cancer; endometrial cancer or colon cancer. (I) is useful in preparation of a medicament intended for the prevention of a medicament intended for prevention or two the present or preparation of a medicament intended for the presention of a medicament intended for the specified and/or EGF receptor. (I) is useful in the expensing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful in which the abnormal presence of IGF-IR and/or EGFR receptor is useful in the exemplification of the invention. (E biological sam invention relates to a novel isolated anti-insulin-like growth factor

Sequence 112 AA;

Gaps ö Length 112; 100.0%; Score 81; DB 9; Length 11 100.0%; Pred. No. 5e-06; n. Mismatches 0; Indels 16; Conservative Similarity Query Match Local Matches

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16 24 RSSQSIVHSNGNTYLQ 39 1 RSSOSIVHSNGNTYLO ઠ 셤

RESULT 7

ADZ67069

ADZ67069 standard; protein; 112 AA. 30-JUN-2005 (first entry) ADZ67069;

Human antibody 7C10 2 light chain variable region SEQ ID NO:65.

neoplasm; prostate tumor; andrology; genttourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obsterrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region. Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;

Homo sapiens.

US2005084906-A1.

21-APR-2005.

16-DEC-2003; 2003US-00735916.

ADZ67065 standard; protein; 112 AA

(first entry)

30-JUN-2005

Beck A;

Haeuw J,

Duflos A,

ADZ67065;

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invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the
                                                                                                                                Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ological sample with (I), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is used in the exemplification of the invention.
                                                                                                                                                                        Example 12; SEQ ID NO 65; 125pp; English.
                                                                                                  Leger O,
     18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003FR-PR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                          useful for treating cancer.
                                                                                                   Corvaia N,
                                                                                                                   WPI; 2005-321968/33.
                                           GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 112 AA;
                                                                                    BECK A.
18-JAN-2002;
                                                                                                    Soetsch L,
                                                                                    (BECK/)
                                             (GOET/)
                                                                     DUFL/)
                                                            LEGE/)
                                                                            (HAEU/)
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Score 81; DB 9; Length 112; Pred. No. 5e-06; .; 0 100.0%; 16 24 RSSQSIVHSNGNTYLQ 39 1 RSSOSIVHSNGNTYLO 16; Conservative Query Match Best Local Similarity Matches

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Gaps

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0; Indels

Mismatches

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neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obsterrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
                                                          nsulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                          Human antibody 7C10 1 light chain variable region SEQ ID NO:61
                                                                                                                                      Location/Qualifiers
                                                                                                                                                          .61
- "CDR2"
                                                                                                                                                     "CDR1"
                                                                                                                                                                                    /note= "CDR3"
                                                                                                                                                                                                                                                18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-0000554.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                  16-DEC-2003; 2003US-00735916
                                                                                                                                                                           .102
                                                                                                                                                                     /note=
94. .10
                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                               GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
                                                                                                                                                                                                                                                                                                                              HAEUW J.
                                                                                                                                                                                                    US2005084906-A1.
                                                                                                                                                                                                                                                                                                                                       BECK A.
                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                (GOET/)
                                                                                                                                                                                                                                                                                                              (LEGE/)
                                                                                                                                                                                                                                                                                                                             (HAEU/)
                                                                                                                                                                                                                                                                                                                                       (BECK/)
                                                                                                                                               Region
                                                                                                                                                               Region
                                                                                                                                                                              Region
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Beck A; Haeuw J, Duflos A, Leger O, Corvaia N, Goetsch L,

WPI; 2005-321968/33. N-PSDB; ADZ67066 Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer

Example 12; SEQ ID NO 61; 125pp; English.

The invention relates to a novel isolated anti-insulin-like growth factor
I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
specifically inhibiting tyrosine kinses activity of the receptor,
comprising a light or heavy chain having at least one complementary
determining region (CDR) consisting of one of two fully defined 16 amino
acids (ADE5/006 and AD55/016). An antibody of the invention is useful in
the preparation of a medicament intended for the prevention or treatment
of an illness connected with an overexpression and/or an abnormal
cof an illness connected with an overexpression and/or an abnormal
cof activation of the IGF-IR and/or EGFR, and/or connected with a
the administration of the medicament does not induce or only alightly
induces secondary effects connected with inhibition of the insulin
receptor. The antibody is useful for preparation of a medicament intended
to inhibit the transformation of normal cells into cells with tumoral

us-10-735-916a-2.rag

character, preferably IGF-dependent, especially IGF1 and/or IGF2dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
useful for preparation of a medicament intended to inhibit the growth
and/or the proliferation of tumor cells, preferably IGF-dependent,
especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent cells. (I) is useful in the preparation of a
medicament intended for provention or for the treatment of cancer, where
the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
breast cancer, endometrial cancer or colon cancer. (I) is useful in the
treatment of psoriasis. (I) is useful in preparation of a medicament
intended for the specific targeting of a biologically active compound to
cells expressing or overexpressing the IGF-IR and/or EGFR receptor.
Coverexpression or an underexpression of illnesses induced by an
overexpression or an underexpression of the IGF-IR and/or EGFR receptor
starting from a biological sample in which the abnormal presence, of IGFIR and/or EGFR receptor is suspected, which involves contacting the
biological sample with (I), which is optionally labeled. The present \$

Sequence 112 AA;

Gaps . 100.0%; Score 81; DB 9; Length 112; 100.0%; Pred. No. 5e-06; ive 0; Mismatches 0; Indels 100.0%; Preu. 16; Conservative Best Local Similarity Query Match Matches

1 RSSQSIVHSNGNTYLQ 16

24 RSSQSIVHSNGNTYLQ 39

RESULT 9

AEB21358 standard; protein; 114 AA.

AEB21358;

22-SEP-2005 (first entry)

Mouse anti-IL-13 antibody 227-26 light chain variable region (VK)

Interleukin-13; IL-13; antibody engineering; humanized antibody; Antiasthmatic; Antiinflammatory; Dermatological; Antiallergic; Respiratory-Gen.; Antiulcer; Gastrointestinal-Gen.; Ophthalmological; Osteopathic; Virucide; asthma; allergic rhinitis; atopic dermatitis; allergic conjunctivitis; eczema; urticaria; allergy; chronic obstructive pulmonary disease; ulcerative colitis; respiratory syncytial virus infection; uvefitis; ecleroderma; osteoporosis; monoclonal antibody; light chain variable region. AEB21358

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 AEB2
 AEB

Mus sp

WO2005062967-A2.

14-JUL-2005.

23-DEC-2004; 2004WO-US043501.

23-DEC-2003; 2003US-0532130P

(TANO-) TANOX INC.

New antibody or its antigen-binding fragment that binds specifically and with high affinity to glycosylated and non-glycosylated human interleukin -13 (IL-13), useful for treating IL-13-mediated disorders, such as asthma WPI; 2005-506603/51. Fung SC, Moyle M,

Lu M, Yan C, Singh S, Huang D;

Claim 10; SEQ ID NO 7; 129pp; English.

mouse anti-IL-13 monoclonal antibody.

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Sequence 114 AA;

Gaps ö Length 114; 0; Indels 100.0%; Score 81; DB 9; L 100.0%; Pred. No. 5.1e-06; iive 0; Mismatches 0; 16; Conservative Query Match Best Local Similarity Matches 16; Conserva

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ð 셤 RESULT 10 **AEB31116** AEB31116;

AEB31116 standard; protein; 114 AA.

Antibody 227-26/227-26.1 variable light chain. 22-SEP-2005 (first entry)

cytostatic; antibody therapy; neoplasm; interleukin 13; IL-13; cancer; diagnosis; tumor; humanized antibody; cell proliferation; Hodgkins disease; cytotoxin; chemotherapy; lymphoma; skin tumor; stomach tumor; oolon tumor; breast tumor; pancreatic tumor; lung tumor; head and neck tumor; renal tumor; squamous cell carcinoma; brain tumor; Raposis carcinoma; solid tumor; monoclonal antibody; 227-26; 227-26-1; light chain variable region.

```
Treating a neoplasm, e.g. Hodgkin's disease, that expresses and/or binds interleukin-13 (IL-13) comprises administering an anti-IL-13 antibody or its binding fragment that binds to both glycosylated and non-glycosylated human IL-13.
                                                                                                                    Claim 13; SEQ ID NO 7; 98pp; English.
                                               33-DEC-2003; 2003US-0532130P
                                   23-DEC-2004; 2004WO-US043541
                                                                              WPI; 2005-506604/51.
                                                                     Fung SC, Moyle M;
                                                         (TANO-) TANOX INC.
               WO2005062972-A2.
                          14-JUL-2005.
Mus sp.
Synthetic.
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This invention describes a novel method for treating a neoplasm that expresses and/or binds interleukin-13 (IL-13). The method comprises administering an anti-IL-13 antibody or its binding fragment that binds of peotifically and with high affinity to both glycosylated and non-gpeotifically and with high affinity to both glycosylated and non-gproximate molar ratio of 1:2 (MAD:IL-13). The method also describes 1) a method for treating Hodgxin's disease comprising administering a numbit of the biological activity of binding fragment to a patient; also decrease activity of IL-13 and 3) disagnosing a cancer or tumor overexpressing IL-13 comprising the use of the anti-IL-13 antibody to detect overexpressing IL-13 comprising the use of the anti-IL-13 antibody to detect overexpressing of IL-13 in the biological sample taken from a patient suspected of having the cancer or tumor. The antibods used in patient suspected of having the cancer or tumor. The antibody to the invention are 2288/C produced by the hybridoma designated PTA-5657, 228A-4 and produced by the hybridoma designated PTA-5655. The antibody is a human antibody, a chimeric antibody, a single domain antibody or a humanized antibody, a chimeric antibody, a single domain antibody or a humanized antibody in the antibody further comprises a physiologically acceptable carrier, diluent, excipient, or stabilizer. The antibody mediates killing carrier, diluent, excipient, or stabilizer. The antibody mediates within region comprises at least a variable; FRL1-chain region comprises a constant region. The variable ight or heavy chain region further comprises at least a variable; from an igd antibody. The natibody is an igd; igd; igd; or an igd antibody is an igd; antibody with a cycloxic agent. Energies the heavy of chain and igd antibody is an igd antibody with a cycloxic agency and a region further comprises a constant region. The variable is a red of the constant region is a red of seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated with a cytotoxic agent, such as a radioisotope or a chemotherapeutic agent. The methods and antibodies are useful for treating neoplasms such as Hodgkin's lymphoma, skin cancer, stomach cancer, colon cancer, prostate cancer, parameter, parameter, cancer, lung cancer, head-and-neck cancer, renal call cancer, squamous cell carcinoma, AIDS-associated Kaposi's carcinoma and brain cancer. This sequence represents the humanized mouse monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227-26 and 227-26-1 variable light chain
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                                                  Gaps
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                       100.0%; Score 81; DB 9; Length 114; 100.0%; Pred. No. 5.1e-06;
                                                 Indels
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                                                    Mismatches
                                                    ö
                                     Best Local Similarity 100.
Matches 16; Conservative
Sequence 114 AA;
                          Query Match
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; antipsoriatic; antibody; (FABR) FABRE MEDICAMENT SA PIERRE. ADJ76883 standard; protein; 122 AA. Goetsch L, Corvaia N, Leger O; Anti-IGF-1R related protein #3. 18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178 (first entry) WPI; 2003-569653/53. WO2003059951-A2 Mus musculus. 06-MAY-2004 cytostatic; 24-JUL-2003 ADJ76883; ADJ76883

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 49; 164pp; French

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells, so are useful against cancers of the proliferation of tumor cells, on are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteessarcoma, and also for treating psoriagis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.

Sequence 122 AA;

Gaps ; Indels 100.0%; Score 81; DB 7; I 100.0%; Pred. No. 5.6e-06; tive 0; Mismatches 0; 100.08; Conservative Query Match Best Local Similarity Matches · 16;

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A SECTION OF THE SECT 34 RSSQSIVHSNGNTYLQ 49

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ADZ67053 standard; protein; 122 AA. ADZ67053; RESULT 12 ADZ67053

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US2005084906-A1
           GOET/)
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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor;
Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:49
                                                                                                                                                                                                                                                                                                                       endometroid carcinomi, gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; light chain variable region.
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Mus musculus.

1. .10
/note= "leader peptide" Location/Qualifiers "CDR1" 55. .71 /note= "CDR2" 104. .111 /note= "CDR3" 34. .49 /note= Peptide Region Region Region

21-APR-2005

18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR001178. 11-JUL-2003; 2003FR-00008538. 16-DEC-2003; 2003US-00735916

GOETSCH L. CORVAIA N. LEGER O. DUFLOS A. HAEUW J. BECK A. (DUFL/) (HAEU/) (BECK/) LEGE/)

Beck A; Leger O, Duflos A, Haeuw J, Goetsch L, Corvaia N,

WPI; 2005-321968/33. N-PSDB; ADZ67052 Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.

Example 8; SEQ ID NO 49; 125pp; English.

The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal caturaction of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells with tumoral to inhibit the transformation or norman cerse character, preferably IGF-dependent, especially IGF1 and/or IGF2.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGP-IR) and optionally; (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

(FABR) FABRE MEDICAMENT SA PIERRE.

18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753.

20-JAN-2003; 2003WO-FR000178 18-JAN-2002; 2002FR-00000653

WO2003059951-A2. Homo sapiens.

24-JUL-2003

Goetsch L, Corvaia N, Leger O

WPI; 2003-569653/53.

Disclosure; SEQ ID NO 67; 164pp; French

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useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent and/or the proliferation of tumor cells, preferably IGF-dependent, and/or the proliferation of tumor cells, preferably IGF-dependent and/or respecially IGF-and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-and/or IGF2-dependent and/or EGF-dependent and/or EGF concer. (I) is useful in the preparation of a medicament intended for prevention or for the preparation of a medicament intended for the prevention or for the preparation of a medicament intended for the prevention or for the creatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention or for the contemporation of a medicament concerns intended for the specific targeting of a biologically active compound to colls expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor is suspected, which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present contacting the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 81; DB 9; I
100.0%; Pred. No. 5.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ76901 standard, protein, 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-IGF-1R related protein #15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 122 AA;
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kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells, to use cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. Jung, breast, endometrium and colon, also osteosarcom, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                          100.0%; Score 81; DB 7; Length 131; 100.0%; Pred. No. 6.1e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                  protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 63; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ76897 standard; protein; 131 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-IGF-1R related protein #13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2002; 2002FR-0000654.
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hes 16; Conservative
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                                                                                                                                                                                                                       Sequence 131 AA;
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prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriates. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                            Gaps
                                                                                                             ö
                                                                                                                                                                                                                                                                                                   Human antibody 7C10 2 light chain variable region SEQ ID NO:67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beck A;
                                                                                    Length 131;
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                                                                                                  6.1e-06;
                                                                                   ; Score 81; DB 7;
; Pred. No. 6.1e-06
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                   100.0%;
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113. .121
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18-JAN-2002; 2002FR-00000554.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WD-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-2003; 2003US-00735916.
                                                                                                                                      16
                                                                                                                                                   RSSQSIVHSNGNTYLQ
                                                                                                                                      1 RSSOSIVHSNGNTYLO
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                                                                                                             16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
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N-PSDB; ADZ67070.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                Local Similarity
                                                              Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2005084906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Matches
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useful for treating cancer.

Example 12; SEQ ID NO 67; 125pp; English.

The invention relates to a novel isolated anti-insulin-like growth factor

The invention relates to a novel isolated and initialin-like growin ractor or receptor (IGP-IR) antibody (I) or its functional fragment, being growin capable of capable of binding to human IGF-IR and, if necessary, capable of apable of binding to human IGF-IR and, if necessary, capable of opecifically inhibiting tytosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary capable of determining region (CDR) consisting of one of two fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a culture or only slightly interaction of IGF or IR and/or EGFR, and/or connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the growth and/or EGF dependent and/or EGF dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent calls. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer is chosen from prostate cancer, osteosarcoma, lung cancer, because andomeral andomerappearation of a medicament intended for prevention or for the preparation of a medicament intended for prevention or colon cancer. (I) is useful in the preparation of a medicament intended for the preparation of a medicament intended for the prevention or colon cancer. (I) is useful in the cancer is chosen from prostate cancer, osteosarcoma, lung cancer. Colon cancer intended for the specific targeting the IGF-IR and/or EGFR receptor. It and/or EGFR receptor is useful in whi

Sequence 131 AA;

Gaps ö 100.0%; Score 81; DB 9; Length 131; 100.0%; Pred. No. 6.1e-06; 0; Indels 0; Mismatches Local Similarity 100. Query Match Matches

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Search completed: December 30, 2005, 13:23:55 Job time : 144.194 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                   Copyright
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sw model using protein search, protein ξõ

December 30, 2005, 13:11:41; Search time 22.7097 Seconds (without alignments) 67.789 Million cell updates/sec Run on:

US-10-735-916A-2 81 score: Title: Perfect

1 RSSQSIVHSNGNTYLQ 16 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:* Database :

1: Pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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131	112	118	219	100	103	103	103	103
96.3	93.8 92.6	92.6	92.6	91.4	91.4 91.4	91.4 91.4	91.4	91.4 91.4
78	76	75	75	4.	4.4	74	74	74
30	33 33 33	4. E	36	8 6	40	4. 4. 1. 2.	43	44 45

ALIGNMENTS

C29380

Ig kappa chain precursor V region (BC-1004) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Species: Musculus (house mouse)

C;Species: Musculus (house mouse)

C;Species: Musculus (house mouse)

C;Species: Musculus (house mouse)

S;Chen, H.T.; Kabat, B.A.; Lundblad, A.; Ratcliffe, R.M.

J. Biol. Chem. 262, 13579-13583, 1987

A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable A;Reference number: A92612; MUID:88007582; PMID:3115981

A;Reference number: A92612; MUID:88007582; PMID:3115981

A;Residues: 1-130 cCHB>

A;Residues: 1-130 cCHB>

A;Residues: 1-130 cCHB>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heteroterramer; immunoglobulin homology <INM>

F;34-113/Domain: immunoglobulin homology <INM>

Gaps ö Length 130; 0; Indels 97.5%; Score 79; DB 2; I 93.8%; Pred. No. 3.4e-06; tive 1; Mismatches 0; 15; Conservative Local Similarity Query Match Best Loca Matches

; 0

1 RSSQSIVHSNGNTYLO 16

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D29380

Ig kappa chain precursor V region (B003 46/2D7) - mouse (fragment)

Ig kappa chain precursor V region (B003 46/2D7) - mouse (fragment)

C;Species Mus musculus (house mouse)

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C;Accession: D29380

C;Accession: D29380

A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable A;Reference number: A92612; MUID:88007582; PMID:3115981

A;Accession: D29380

A;Accession: D29380

A;Reference number: A92612; MUID:88007582; PMID:3115981

A;Residues: 1-131 <CHE>

A;Cross-references: UNIPROT:Q8VCI6; UNIPARC:UPI000017678A C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-113/Domain: immunoglobulin homology <IMM>

Gaps ; 0 Length 131; 97.5%; Score 79; DB 2; Length 131 93.8%; Pred. No. 3.5e-06; Artive 1; Mismatches 0; Indels Query Match Best Local Similarity 93.8 Matches 15; Conservative

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1 RSSQSIVHSNGNTYLO 16

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42 RSSQSLVHSNGNTYLQ 57

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Grappa chain V region (clone NQ2-45.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus-1997 #sequence_revision 23-Aug-1997 #text_change 23-Aug-1997
C;Accession: S11126
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1993
A;Fitle: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone A;Reference number: S07331; MUID:83271467; PMID:6877353
                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S24504
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Cispecies: Mus musculus (house mouse)
Cibate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
Cibates: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
Cibate: Sation S24501
Rikaartinen, M.
Submitted to the EMBL Data Library, October 1991
A;Reference number: 824490
                                                                               Gaps
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C;Superfanily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;I6-95/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;I6-95/Domain: immunoglobulin homology <IMM>
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96.3%; Score 78; DB 2; Length 93; 93.8%; Pred. No. 3.5e-06; ive 1; Mismatches 0; Indels
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93.8%; Pred. No. 3.8e-06;
tive 1; Mismatches 0;
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                                                                                                                                                          1 RSSOSIVHSNGNTYLQ 16
                                                                                                                                                                                                      18 RSSQSIVHSNGNTYLE 33
                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V region - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 93.8
Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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nes 15; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-99 < KAA>
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Best Local S:
Matches 15
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Best Local S:
Matches 15,
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                                                                       RESULT 3
S07456
Ig kappa chain V region (hybridoma G8 Ad 3.8) - mouse
Ig kappa chain V region (hybridoma G8 Ad 3.8) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-May-1997
C;Date: 07-Sep-1990 #text_change 09-May-1990
C;Date: 07-Sep-1990
C;Date: 07-Sep-1990 #text_change 09-May-1990
C;Date: 07-Sep-1990

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325463
Ig kappa chain V region - mouse
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Datession: S25463
C;Accession: S25463
C;Accession: S25463
C;Accession: M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
A;Description: Structure and binding properties of monoclonal antibodies to core histone
A;Reference number: S25174
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A;Residues: 1-91 <MON>
A;Cross-rences: U-91 <MON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S24502
R;Kaartinen, M.
Rubmitted to the EMBL Data Library, October 1991
A;Reference number: S24490
A;Reference number: S24490
A;Reference number: S24450
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;10-89/Domain: immunoglobulin homology <IMM>
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A;Molecule type: protein
A;Residues: 1-46 <ROC>
A;Cross-references: UNIPARC:UPI0000176DBD
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 93.8%;
Matches 15; Conservative 1
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A, Status: preliminary
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Cjacession FF1043 "Determine_reverse." John Prof. T.N.
Rrillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
Arritles Both Ign and IgG anti-DNA antibodies are the products of clonally selective B c A; Reference number: PH0971; MUID:92381444; PMID:1512540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: $26335
R;Stark, S.B.; Caton, A.J.
J. Exp. Ned. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: $26309; MUID:91341421; PMID:1908510
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A;Residues: 1-112 <CAT>
A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176A19
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
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C;Species: Mus musculus (house mouse)
C;Decies: Hs-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: F27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 157-1587, 1986
A.Title: Structural and functional implications of a restricted antibody response to A;Reference number: A91043; MUD:86300658; PMID:2427335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
               Ig light chain V region (clone 111.68) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                            A)Status: nucleic acid sequence not shown A;Molecule type: mRWA A;Residues: 1-103 <TIL>
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Best Local Similarity
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A Molecule type: mRNA
A;Residues: 1-110 <STA>
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Iglight chain V region (clone 202.838) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J; Exp. Med. 176, 761-779, 1992

A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B C A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1042

A;Status: nucleic acid sequence not shown

A;Residues: 1-103 < rIL.

A;Cross-references: UNIPROT:Q99M37; UNIPARC:UP10000176AA4

A;Cross-references: UNIPROT:Q99M37; UNIPARC:UP100000176AA4
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A;Status: preliminary
A;Nolecule type: mRD:
A;Residues: 1-102 <CHE>
A;Residues: 1-102 <CHE>
A;CCOSS-references: UNIPARC:UPI0000115F40; EMBL:X58662; NID:952927; PIDN:CAA41519.1; PID
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: 814590, 814589
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
Rschen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH A;Reference number: 814484
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                                   A;Molecule type: mRNA
A;Residues: 1-101 <NAT>
A;Cross-references: UNIPARC:UPI0000176E8F
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 4e-06;
                                                                                                                                                                                                                     Length 101;
                                                                                                                                                                                                             96.3%; Score 78; DB 2; Length 101
93.8%; Pred. No. 3.9e-06;
ive 1; Mismatches 0; Indels
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Best Local Similarity 93.8%;
Matches 15; Conservative
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RESULT 11

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anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Was musculus (house mouse)
C.Accession: P0203
R.Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A.Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N A; Reference number: P10198; MUID:90309768; PMID:2114528
A.Accession: P10203
A.Molecule type: mawa
A.Residues: 1-113 <8ML>
A.Residues: 1-113 <8ML>
A.Cross-references: UNIPPARC:UPI0000113786; GB:X53643; NID:g50196; PIDN:CAA37694.1; PID:g C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 16-95/Domain: immunoglobulin homology A:MM>
F; 24-39/Region: complementarity-determining 1
F; 55-61/Region: complementarity-determining 3
F; 101-113/Region: D region
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A31807

Ig Asapa chain V region (PAC1) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 09-Jul-2004
C;Accession: A31807
R;Taub, R.; Gould, R.J.; Garsky, V.W.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt A; Taub, R.; Gould, R.J.; Species and July Species and July Species and July Species and July Species A;Reference number: A1807; MUD:89079661; PMID:2909518
A;Accession: A31807
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroterramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                    Query Match 96.3%; Score 78; DB 2; Length 112; Best Local Similarity 93.8%; Pred. No. 4.3e-06; Matches 15; Conservative 1; Mismatches 0; Indels
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A,Molecule type: mRNA
A,Residues: 1-112 <TAU>
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                                                                                                       December 30, 2005, 13:11:26 ; Search time 144 Seconds (without alignments) 78.392 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                               2166443 seqs, 705528306 residues
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Q5527_9 WULI

Q65207_9 WULI

Q65207_9 WULI

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G518EMB WÜUSE

Q518EMB WÜUSE

Q518EMB WÜUSE

Q51EMB WÜUSE

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Q51EMB WÜUSE

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C72B HÜMAN

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G51EMB WÜUSE

KV2E MÜMBN

KV2E HÜMAN

G61EMB WÜUSE

KV2E MÜMBN

KV2E MÜMBN

KV2E MÜNGE

KV2E MÜUSE

KV2E MÜNGE

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KV2E MÜNGE

KV2E MÜNGE

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Q54VMS ÜLGÜL

Q54VMS ÜLGÜL

Q54VMS ÜLGÜL

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2: uniprot_trembl:*
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44 54.3 448 2 Q8A7N7_BACTN Q8a7n7_bacteroides 34 45.3 2399 2 Q92KS9_HELPU Q92k89 helicobacte 35 44 54.3 2392 2 Q92KS9_HELPU Q92k89 helicobacte 36 43.5 53.7 647 2 Q68S95_CHLEL Q08529 helicobacte 37 43 53.1 218 2 Q08S95_CHLEL Q08922 mouse musculu Q86HQ2 shewanella 43 53.1 218 2 Q6V4Z7_SCHMA Q6V4Z7 SCHISCHOOMA Q6V4Z7 S	ALIGNME MOUSE KVZG_MOUSE STANDARD; PRT; 1 P01.611, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence up	Charles Charle	, PubMed=6404298; Olles M.N.; ence of the light chain variable region fron ridoma antibody."; 1153-1158(1983). S. This chain was isolated from an IgG2a hy; binds digoxin.	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use as long as its content is in no way modified and this statement is no removed.	PIR; A01914; KVMS26.
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Query Match 91.4%; Score 74; DB 1; Length 113; Best Local Similarity 93.3%; Pred. No. 5.2e-05; Matches 14; Conservative 1; Mismatches 0; Indels

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InterPro; IPR003599; IG.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003596; IG_v.
SMART; SM04409; IG; 2.
SMART; SM04466; IGv, 2.
PROSITE; PS50835; IG_LIKE; 2.
NON TER 248 248
SEQUENCE 248 AA; 26634 MW;
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nes 14; Conservative
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Q65ZCO;
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Brlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
Witudies of the interactions between the anticytokeratin 8 monoclonal antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";
J. Mol. Recognit. 16:157-163(2003).
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10095;
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MUCLEOTIDE SEQUENCE.

Brinkmann U., Pail L.H., FitzGerald D.J., Willingham M., Pastan I.;

Brinkmann U., Pail L.H., FitzGerald D.J., Willingham M., Pastan I.;

Brinkmann U., Pail L.H., FitzGerald D.J., Willingham M., Pastan I.;

"BJ (FV)-PEBBKDEL, a single-chain immunotoxin that causes complete regression of a human carcinoma in mice.";

regression of a human carcinoma in mice.";

FORTI ACAG SCI. U.S.A. 88:8616-8620(1991).

EMBL; SS7990; AAB19971.2; -; mRNA.

SNR; Q65ZQ7; 4-247.
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AJSB4575; CAI56337.1; -; mRNA.
R InterPro; IPR003599; 19.
R InterPro; IPR003599; 19.
R InterPro; IPR003596; 19.
R Ffam; PP07686; V. Set; 1.
R Ffam; PR07686; V. Set; 1.
R SWART; SM00409; IG; 1.
R SWART; SM00406; IGv; 1.
R PROSITE; PS50835; IG_LIKE; 1.
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115 AA; 12560 MW; B4D3BF3D63E88007 CRC64;
                                                                                                                                                                                                                           10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Kappa light chain variable region (Fragment).
Names1gg1 anti-T61 VL;
Mus musculus (Mouse).
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25-0CT-2004 (TrEMBLrel. 28, La
25-0CT-2004 (TrEMBLrel. 28, La
B3 (FV) - PE40 (Fragment).
                                 24 RSSQSLVHSNGNTYL 38
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     RSSQSIVHSNGNTYL 15
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NCBi_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Balb/c; TISSUE-Spleen;
MEDLINE=96319505; PubMed=8768802;
Kipp B., Schlaak M., Becker W.M.,
"Cloning and expression of a recombinant mouse Fab-fragment
recognizing a defined linear epitope of Chironomus thummi thummi major
allergen Chi t I.";
Int. Arch. Allergy Immunol. 110:348-353(1996).
EMBL; Z37499; CAA85724.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Kappa light chain C_region (Fragment).
Mus musculus (Mouse).
Elwaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                      88.9%; Score 72; DB 2; Length 248; 87.5%; Pred. No. 0.0003; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.7%; Score 71; DB 2; Length 219
86.7%; Pred. No. 0.00039;
.ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;
248 AA; 26634 MW; 7A3759B43E570950 CRC64;
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QEP491;
QEP401;
GEJUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                219 AA
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PIR; A01913; KVMS7S.
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NCBI_TaxID=10090;
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          removed.
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                                                                                PROTEIN
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        SO THE FIFT FITTER DRAW DRAW BY THE FITTER BY THE BY THE FITTER BY THE BY THE FITTER BY THE B
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Warner M.B., Toshiyuki S., Carning L.,
Stopleton M.J., Oddin T.B., Toshiyuki S., Carning P., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carning P., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
F. and mouse Chuk serviences "...
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                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhin; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Pred. No. 0.0015;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC63599; AAH63599.1; -; mRNA.
HSSP; P01837; 1KCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A. 99:16899-16903(2002)
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ilg kappa chain V-II region 7534.1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA.
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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InterPro; IPR003109; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PP07654; C1-8et; I.
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80.0%;
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44 RSSESLLHSNGNTYL 58
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SMART; SM00406; IGV; 1.
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            Hypothetical protein.
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Best Local Similarity
Matches 12; Conserva
                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMR; Q6P491; 21-237
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                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA
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P01630;
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            SO COCOCOS RESERVADES 
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
MEDLINE=83256427; PubMed=6409088; Chang J.-Y., Herbst H., Aebersold R., Braun D.G.; Chang J.-Y., Herbst H., Aebersold R., Braun D.G.; A new isotype sequence (V kappa 27) of the variable region of kappa-light chains from a mouse hybridoma-derived anti-(streptococcal group A polysaccharide) antibody containing an additional cysteine residue. Application of the dimethylaminoazobenzene isothiocyanate technique for the isolation of peptides."; Biochem. J. 211:173-180(1933).

I. MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal antibody against the streptococcal group A polysaccharide.
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TISSUE-Hodgkin lymphoma;
Tinguelly M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers I Tinguelly M., Rosenquist A.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ564426, CAD92033.1; -; Genomic_DNA.
HSSP; PO1625; IEEQ.
SWR; Q723Y5; 1-80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
SMART; SMO0406; IGv; 1.
PROSTIR; PS50835; IG LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Framework-2.
Complementarity-determining-2.
Framework-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
12496 MW; 42C019D10ADA3C91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Rearranged VKA17 V gene segment (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.7%; Score 67; DB 1; 1
80.0%; Pred. No. 0.00092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Q99M37; 1191.
SMR; P01630; 1-113.
Ensembl; ENSMUSG0000061260; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Framework-1
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Q7z3YS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSSQSIVHSNGNTYL
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54
61
102
112
93
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Name=Igk-C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V-II region RPMI 6410.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%; Score 63; DB 1; Length 133; 80.0%; Pred. No. 0.0057; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-3
                                                                                                                                                       Score 63; DB 2; Length 86;
Pred. No. 0.0034;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003596; Ig_v.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14707 MW; 513CCAF3673009EB CRC64;
                                                                                                                    D198FC04FE0C78FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           01-07N-1988 (Rel. 06, Created)
01-07N-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
18 Kappa chain V-II region RPMI 6410 precursor.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 200020; CAA77315.1; -; Genomic_DNA.
PIR; A01890; KZHURP.
HSSP; Q99M37; 1191.
SWR; P06310; 21-133.
Ensembl; ENSG0000173758; Homo sapiens.
G0; G0:000556; C:extracellular region; NAS.
G0; G0:0003823; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SWART; SW04406; IGV; 1
                                                                                                                                                                                                                                                                                                                                                                          133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 13:6499-6513(1985).
                                                                                                                                                                                                                                                                                                                                                                          PRT;
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig.v.
SWART; SW00406; IGv; 1.
PR0SITE; PS50815; IG LIKE; 1.
                                                                                                                                                         77.8%;
80.0%;
                                                                                                                  86 AA; 9764 MW;
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                                                                                                                                                                                                                                                         3 RSSQSLVYSDGNTYL 17
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                           Local Similarity 80.0
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
59
74
81
113
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123
43
133
133 AA;
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NON TER
SEQUENCE
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SEQUENCE
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KV2F HUMAN
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                                                                                                                                                                                                 Matches
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RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.;

Expression driven by an MMTV-LTR enhancer.;

RA MEDINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Fedingold B.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeberg B., Buercow K.H., Schaefer C.F., Bhar N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.L., Wang J., Heish F.,

RA Altechul S.F., Jordan H., Moore T., Max S.L., Wang J., Heish F.,

RA Altechul S.F., Jordan H., Moore T., Max S.L., Wang J., Heish F.,

RA Altechul S.F., Jordan H., Moore T., Max S.L., Wang J., Heish F.,

RA Altechul S.F., Jordan H., Moore T., Gravinci P., Prange C.,

RA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RAChards S., Mochey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Nadan A., Young A.C., Grimutz J., Myacs R.M.,

RH Raders W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RH Green R.D., Smein J.E., Jones S.J.M., Marra M.A.,

RH Green R.D., Smein J.E., Jones S.J.M., Marra M.A.,

RH Green R.D., Smein J.E., Shenter R.D., Boutfard C.D., Raden R.D., Butterfield R.S., Sanchez R.D., Marra M.A.,

RH Generation and initial analysis of more than 15,000 full-length human and mounce conversed R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.5%; Score 62; DB 2; Length 239; Best Local Similarity 73.3%; Pred. No. 0.017; Matches 11; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC091750; AAH91750.1; -; mRNA.

SNR; QSBEUB; 21-239.

CO; GO: 0003823; F:antigen binding; IEA.

InterPro; IPR003109; Ig-like.

InterPro; IPR0031006; Ig-like.

InterPro; IPR003599; Ig-
InterPro; IPR003506; Ig-MFC.

InterPro; IPR003506; Ig-MFC.

InterPro; IPR003566; Ig-WHC.

InterPro; IPR004099; IG; 2.

SNART; SN00409; IG; 2.

SNART; SN00409; IG; 1.

SNART; SN00406; IGV; 1.

SNART; SNO0406; IGW; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
RSSQSIVHSNGNTYL 15
                                                44 RSSQSLVYSDGNTYL 58
                                                                                                                                                                                                                                                                                                                  QSBEUB MOUSE PRELIMINARY,
QSBEUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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NUCLEOTIDE SEQUENCE.
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S40374; S40374.
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PIR; S40324; S40324
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                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1598223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=1551402;
                                                                                                                                                                                                                                                                                                                             and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Lung;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hateh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonando M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=22267451; PubMed=12379368; DOI=10.1016/S0022-1759(02)00242-9; Hifumi E., Mitsuda Y., Ohara K., Uda T.; "Targeted destruction of the HIV-1 coat protein gp41 by a catalytic antibody light chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.3%; Score 61; DB 2; Length 112; 73.3%; Pred. No. 0.011; cive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 112
112 AA; 12443 MW; BAD3E14B90BCF122 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                  112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Immunol. Methods 269;283-298(2002)
EMBL; D85104; BAD00151.1; -; mRNA.
HSSP; P01820; 1A70.
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMR; Q6LEMB; 1-112.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
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PROSITE; PS50835; IG_LIKE; 1.
Hypothetical protein.
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TISSUE=Lung;
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Suther R.W., Schein J.S., Wyers R.M., Schein J.S., Jones S.J.M., Marza R.M., Schein J.E., Jones S.J.M., Marza M.A.; Gener I.S., Jones S.J.M., Marza M.A.;
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Klein K. Jaenhen R., Zachau H.G.;
"Expressed human immunoglobulin kappa genes and their hypermutation.";
Eur. J. Immunol. 23:3248-3262(1993).
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"V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 239 AA; 26235 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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EMBL; BC022362; AAH22362.1; -; mRNA.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_VHC.
Pfam; PF07664; Cl-8et; I.
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PIR, S42267; S42267.
PIR, S42268; S42268.
HSSP; P01834; 1172.
SMR; Q8TCD0; 21-237.
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QQULBO HUMAN PRELIMINARY;
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SMR; P03976; 1-113
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MEDILINE-8613012; PubMed=3937730;
MEDILINE-8613012; PubMed=3937730;
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antibodies in the GAT system.";
EMBO J. 4:3681-3688[1985].
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 AA; 12266 MW; C844B7881A89C18A CRC64;
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Last annotation update)
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23-OCT-1986 (Rel. 02, Last sequence update)
10-VMY-2005 (Rel. 47, Last annotation update)
1G kappa chain V-II region 17529.1.
                                                                             112 AA
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                                                                         Q53VP8 MOUSE PRELIMINARY;
Q53VP8;
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HSSP; Q99M37; 1191.
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Huber C., Klobeck H.G., Zachau H.G.;
"Ongoing V kappa-J kappa recombination after formation of a productive
V kappa-J kappa coding join: ";
Eur. J. Immunol. 22:1561-1565(1992).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
Gaskin F., Fu S.M.;
"A rheumatoid factor from a normal individual encoded by VH2 and V
kappa II gene segments.";
Arthritis Rheum. 35:900-904(1992).
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Wapper S.D., Luzzatto L.;
"V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                 SMART; SM00406; IGv; 1.—
PROSTIE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin domain;
Immunoglobulin V region.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
Ensembl; ENSMUSG00000055315; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-84191506; PubMed-6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain V-II region GM607.
Framework-1.
Complementarity-determining-1.
Framework-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-3.
                                                                                                                                                                                                         Query Match 71.6%; Score 58; DB 2; Length 114; Best Local Similarity 80.0%; Pred. No. 0.037; Matches 12; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig kappa chain V-II region GM607 precursor (Fragment).
                                                                                                                                                                   114 114 114 11775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z00009; -; NOT ANNOTATED CDS; Genomic_DNA. PIR; A01889; K2HUGM.
HSSP; Q99M37; 1191.
SMR; P06309; 5-117.
GO; GO:0003825; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR0037110; Ig-like.
InterPro; IPR003566; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                    117 AA
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By similarity.
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EMBL; AF035034; AAD56270.1; -; mRNA.
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           PIR, B49002; B49002.
PIR, S24538; S23538.
PIR, S34094; S34094.
PIR, S34095; S34094.
HSSP; PO1625; 11VB.
SMR; Q9ULB0; 1-114.
InterPro; IPR007110; Ig-like.
                                                                                                                                       PROSITE, PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                   1 RSSOSIVHSNGNTYL 15
                                                                                                                                                                                                                                                                                  24 RSSQSPVYSDGNTYL 38
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Nature 309:73-76(1984).
                                                                                                                          SMART; SM00406; IGV; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                     Query Match 71.6%; Score 58; DB 1; Length 117; Best Local Similarity 73.3%; Pred. No. 0.038; Matches 11; Conservative 2; Mismatches 2; Indels
   1 11
117 117
117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
                                                                                                                                                  1 RSSOSIVHSNGNTYL 15
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30, Appl
29, Appl
4, Appli
20, Appl
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3, Appli
3, Appli
3, Appli
68, Appli
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                                                                    December 30, 2005, 14:15:20 ; Search time 31.5 Seconds (without alignments) 41.994 Million cell updates/sec
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Sequence 28,
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Sequence 29,
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( /cgm2_6/ptodata/1/iaa/5_COMB.pep:*
): /cgm2_6/ptodata/1/iaa/6_COMB.pep:*
): /cgm2_6/ptodata/1/iaa/H_COMB.pep:*
): /cgm2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
): /cgm2_6/ptodata/1/iaa/RE_COMB.pep:*
): /cgm2_6/ptodata/1/iaa/RE_COMB.pep:*
           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-129-930B-30
US-08-134-346A-17
US-08-134-346A-17
US-08-947-88A-30
US-09-947-88B-30
US-09-947-88B-30
US-09-947-88B-30
US-09-947-88B-30
US-09-947-88B-30
US-09-947-88B-30
US-09-947-88B-30
US-09-947-88B-30
US-09-947-88B-88
US-09-947-88B-68
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US-09-947-88B-68
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5.09-406-532-18
5.09-563-222C-8
5.08-672-345C-43
5.09-214-095D-43
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US-08-672-345C-25
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Maximum Match 100%
Listing first 45 summaries
                                                   model
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Gapop 10.0 , Gapext 0.5
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Match Length
                                                   protein search,
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Perfect score:
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complementarity-determining region (CDR1)
BR55-1 antibody light chain"
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COMPUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTONENY/AGENT INPORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 11823-54-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAKE (415) 326-2400
TELEPRAKE (415) 326-2400
TELEPRAKE (415) 326-2400
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            US-09-214-095D-25
US-09-940-727B-22
US-09-940-727B-25
US-08-672-345C-12
US-08-672-345C-28
US-09-214-095D-19
US-09-214-095D-19
US-09-940-727B-19
US-09-940-727B-28
US-09-940-727B-28
US-09-214-095D-79
US-09-214-095D-79
US-09-214-095D-79
US-09-214-095D-79
US-09-214-095D-79
US-09-214-095D-79
US-09-214-095D-79
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US-09-214-180C-4
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Lobbner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Khouri
                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO PERMINE
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OTHER INFORMATION:
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OTHER INFORMATION:
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CORRESPONDENCE ADDRESS:
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                               US-07-977-696C-30

### Sequence 30, Application US/07977696C

### Sequence 30, Application US/07977696C

### Sequence 30, Application US/07977696C

### Sequence 30, Application US. 5792852

### Sequence 30, Application:

### Applicant INFORMATION:

### APPLICANT: Ceriani Dr., Roberto L.

### APPLICANT: Ceriani Dr., Jery A.

### APPLICANT: Ceriani Dr., Jery A.

### APPLICANT: Ceriani Dr., Schardo A.

### TITLE OF INVENTION: Analogue Peptides with Specificity

### TITLE OF INVENTION: and Therapeutic Methods.

### TITLE OF INVENTION: and Therapeutic Methods.

### TITLE OF INVENTION: and Therapeutic Methods.

### CORRESPONDENCE ADDRESS:

### ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI

### STATE: California

### COUNTRY: USA

### ZIP: 90071

COMPINED: 20071
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; Patent No. 3604167
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Peterson Dr., Roberto L.
APPLICANT: Padlan Dr., Eduardo A.
ITILE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Analogue Peptides, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.3%; Score 78; DB 1; Length 16; 93.8%; Pred. No. 4e-06; 1; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
ATONREY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET WUMBER: 966 38227
TELEPRAK: (510) 748-6688
RSSOSIVHSNGNTYLO 16
                          1 RSSQSIVHSNGNTYLE 16
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TYPE: amino acid
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 93.8
Then 15; Conservative
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                                                                                                            RESULT 2
US-07-977-696C-30
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US-08-129-930B-30
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US-08-134-34-346-17, Application US/08134346A

Beant No. 6281335

GENERAL INPROMATION:

APPLICANT:
APPLICANT:
APPLICANT:
Coriani, R.L.C.
APPLICANT:
APPLICANTION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANTION:
APPLICANT:
ATORNEY/AGENT:
APPLICANT:
APPLICA
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                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: Viviana
RATORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REFERENCE DOCKET NUMBER: 30,930
REFERENCE CLASSIFICATION NUMBER: 30,930
REFERENCE CLASSIFICATION NUMBER: 30,930
TELLEPHONE: (510) 521-3541
TELLEY: n.a.
TELLEX: n.a.
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
CHARACTERI
ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
3Y: linear
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Matches 15, Conserva
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HART, MARY KATE
APPLICANT: HART, MARY KATE
APPLICANT: WILSON, UTLIE
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
FILE REFERENCE: ARMY 166
CURRENT APPLICATION NUMBER: US/10/226,795
CURRENT APPLICATION NUMBER: US/10/226,795
CURRENT PILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 16
TYPE: PRT
CREANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Action and Therapeutic Methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic light OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
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Query Match

96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels
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COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

SOFTWARE: PACHONIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.3%; Score 78; DB 2; ilarity 93.8%; Pred. No. 4e-06; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/09947839B; Patent No. 6936706; GENEAL INFORMATION: APPLICANT: do Couto, Fernando J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. Amzel & Assoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,930
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                         Sequence 28, Application US/10226795
Patent No. 6875433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O.Box 159
CITY: Gladwyne
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSSQSIVHSNGNTYLQ 16
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                                                                                                    1 RSSOSIVHSNGNTYLQ 16
                                                                                                                                 1 RSSQSIVHSNGNTYLE 16
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Best Local Similarity
Matches 15; Conserva
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Patent No. 6315997

GENERAL INPORMATION:

APPLICANT: Ceriani Dr., Fernando J.R.

APPLICANT: Peterson Dr., Jerry A.

APPLICANT: Peterson Dr., Jerry A.

APPLICANT: Peterson Dr., Bduardo A.

TITLE OF INVENTION: Analogue Peptides With Broad

TITLE OF INVENTION: Diagnostic Vaccination and

TITLE OF INVENTION: Therapeutic Methods

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: Petetry, Schroeder & Poplawski

STREET: 444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                           DB 2; Length 16;
                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: IBM PC compatible
SECTION: APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
FILING DATE: September 30, 1993
FILING DATE: No. 6315997ember 16, 1992
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
APPLICATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
RELERBAX: (213) 622-7700
TELEFPAN: (213) 489-4210
                                                                                                                                                                                                                                                                                                                 4e-06;
                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                           Score 78;
Pred. No.
            TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-826-6565
TELEFAX: 212-826-5909
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
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TRIERS: n.a.
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                           96.3%;
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-976-288A-30
                                                                                                                                                                                                                                                US-08-134-346A-17
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Gaps

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GENERAL INFORMATION:
APPLICANT: Abdel-Meguid, Sherin
APPLICANT: Ho. Yen Sen
TTLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
TITLE OF INVENTION: Recombinant of IL-18 Mediated Disorders
FILE REFERENCE: P50897
CURRENT APPLICATION NUMBER: US/09/914,695
FILE REPRINGE: P50897
CURRENT FILING DATE: 2001-03-17
PRIOR APPLICATION NUMBER: PCT/US00/07349
FRICH APPLICATION NUMBER: 60/125,299
PRIOR PILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PSECSEC for Windows Version 4.0
SEQ ID NO 20
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74; DB 1; Length 16;
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.4%; Score 74; DB 2; Length 16; 93.3%; Pred. No. 1.8e-05; ive 1; Mismatches 0; Indels
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                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09914695 Patent No. 6706487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.4%;
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Best Local Similarity 93.33
Matches 14; Conservative
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Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-244-626-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT

ORGANISM: Mus musculus
US-09-914-695-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-914-695-20
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US-09-563-222C-29

; Sequence 29, Application US/09563222C

; Patent No. 6696620

; Patent No. 6696620

; APPLICANT: BLICYPE PHARMACEUTICALS, INC.

; APPLICANT: HIATT, ANDREW C.

; APPLICANT: HIATT, ANDREW C.

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

; FILE REFERENCE: 068904-0501

; CURRENT FILING DATE: 2000-05-02

; PRIOR PILING DATE: 2000-05-02

; PRIOR PILING DATE: 2000-05-02

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 182

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 29
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Patent No. 5502167

GENERAL INFORMATION:
APPLICANT: Waldman, Herman
APPLICANT: Crowe, James Scott
APPLICANT: Fight
STREET: S55 Thirteenth Street, N. W.
CTTY: Washington
STATE: D. C.
                                                                                                                                                                                                                                                                                     Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%; Score 76; DB 2; Length 16; 87.5%; Pred. No. 8.4e-06;
                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                   Query Match 96.3%; Score 78; DB 2;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
REFERENCE/DOCKET NUMBER: CRFC-083
                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                TELECOMMUNICATION INFORMATION:
TELEBEHOME: 610-649-0609
TELEFRANCE: 240-359-0299
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                      1 RSSQSIVHSNGNTYLQ 16
                                                                                                                                                                                                                                                                                                                                                                                             1 RSSQSIVHSNGNTYLE 16
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Matches 14; Conservative
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                             US-09-947-839B-30
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US-08-244-626-4
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Gaps

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JOURNALD IN CATALON (1994)

JAPPLICANT: Siggall, Clay

APPLICANT: Wahl, Alan

APPLICANT: Francisco, Joseph

APPLICANT: Fell, H. Perry

TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF

FILE REPRENCES: 962-00.

CURRENT APPLICATION NUMBER: US/09/724,530

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/328,296

PRIOR PRILING DATE: CURRENT FILING DATE: 1999-06-08

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 3

LENGTH: 16 **-
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                                                                                                                Gaps
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APPLICANT: Wahl, Alan
APPLICANT: Wahl, Alan
APPLICANT: Feal, H. Perry
TITLE OF INVERTION RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REPRENCE: 9632-005
CURRENT APPLICATION NUMBER: US/09/724,409
CURRENT FILING DATE: 2000-11-28
PRIOR PPLICATION NUMBER: US/09/328,296
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
LENGTH: 16
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                                                                 Score 73; DB 1; Length 16;
Pred. No. 2.6e-05;
1; Mismatches 0; Indels
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86.4%; Score 70; DB 2; Sebst Local Similarity 86.7%; Pred. No. 7.7e-05; Matches 13; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09724530 Patent No. 6843989 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 RESULT 13
US-09-724-409-3
; Sequence 3, Application US/09724409
; Parent No. 6838261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                      Query Match 90.1%;
Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                                                                                                                          1 RSSONIVHSNGNTYL 15
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Siegall, Clay
APPLICANT: Wahl, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-409-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus US-09-724-530-3
; HYPOTHETICAL:
US-08-560-558E-29
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TITLE OF INVENTION: Humanized and chimeric monoclonal
TITLE OF INVENTION: BGF-R); diagnostic and therapeutic use.
NUMBER OF SEQUENCES: 34
NUMBER OF SEQUENCES: 34
ADDRESSES:
Alber C. Turner, TRASK, BRITT & ROSSA
STREET: P.O. BOX 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                 Sequence 8, Application US/09518737

Patent No. 6709833

GENERAL INFORMATION:
APPLICANT: FUKUI: ASUHISA
APPLICANT: SHIRAL: RYUICHI
APPLICANT: SHIRAL: RYUICHI
APPLICANT: SHIRAL: RYUICHI
APPLICANT: SHIRAL: RYUICHI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: MONOCLONAL
FILE REFERRENCE: 1965449618
CURRENT APPLICATION NUMBER: US/09/518,737
CURRENT FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 1005: 10
SOFTWARE: PATENTIN VOS: 10
SOFTWARE: PATENTIN VOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 16;
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ilarity 93.3%; Pred. No. 1.8e-05
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: WINDOWS95
SOFTWARE: WordPerfect 5.1/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E
FILING DATE: No. 5891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: TUTTOR TALLENCY
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2720US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Salt Lake City
STATE: Utah
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-560-558R-29
; Sequence 29, Application US/08560558E
; Patent No. 5891996
; Patent INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (801) 532-1922
TELEFAX: (801) 531-9168
INFORMATION POR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RSSOSLVHSNGNTYL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-8
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Best Local Similarity
Matches 14; Conserva
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1 RSSQSLVHSNGNTFL 15

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RESULT 15
US-09-328-296-3
i Sequence 3. Application US/09328296
j Setuence 3. Application US/09328296
j GENERAL INFORMATION:
i APPLICANT: Siegall, Clay
i APPLICANT: Francisco, Joseph
j APPLICANT: Francisco, Joseph
j APPLICANT: Francisco, Joseph
j PILE REFERENCE: 9632-005
i CURRENT PILING DATE: 1999-06-08
i CURRENT PILING DATE: 1999-06-08
i CURRENT PILING DATE: 1999-06-08
i NUMBER OF SEQ ID NOS: 15
i SOFTWARE: PATHING SEQ ID NOS: 15
i SEQ ID NO 3
i LENGTH: 16
i TYPE: PRT
i ORGANISM: Mus musculus
i ORGANISM: Muscul
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Search completed: December 30, 2005, 14:26:44 Job time : 32.5 secs

1 RSSQSIVHSNGNTYL 15 |||||||||||||| 1 RSSQSLVHSNGNTFL 15

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                 December 30, 2005, 13:14:26 ; Search time 35.871 Seconds (without alignments) 36.877 Million cell updates/sec
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Sequence 50,
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                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents AA:*
1: /cgn2 6/ptodata/1/iaa/5 COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/HCOMB.pep:*
4: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/RE COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/RB.coMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-07-976-66C-30

US-08-129-930B-30

US-08-129-930B-30

US-08-976-288A-30

US-09-947-839B-30

US-09-947-839B-30

US-09-947-625A-26

US-09-840-459-28

US-09-840-459-28

US-09-840-459-28

US-09-841-15

US-08-053-171-15

US-08-053-171-15

US-08-152-844-15

US-08-152-844-15

US-08-152-844-15

US-08-153-15

US-08-131-39BA-67

US-08-171-5
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US-08-134-346A-50
                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                            572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       using sw model
                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                       1 RSSQSIVHSNGNTYLQ 16
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Maximum DB seq length: 200000000
                                                                                                                                          US-10-735-916A-2
81
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Match Length DB
                                                    protein search,
               Copyright
                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                       OM protein
                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                Searched:
                                                                                    Run on:
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95, Appl 2, Appli 2, Appli 2, Appli 2, Appli 27, Appli 190, Appl 190, Appli 66, Appli 66, Appli 112, Appli 112, Appli 112, Appli 112, Appli 112, Appli 113, Appli 114, Appli 115, Appli 116, Appli 117, Appli 117, Appli 117, Appli		of	Gaps
Sequence Seq		(CDR1)	; 0
28 78 96.3 131 2 US-08-976-288A-95 Se 29 78 96.3 149 1 US-08-752-884-2 Se 29 78 96.3 149 1 US-08-752-884-2 Se 20 78 96.3 149 2 US-08-752-884-2 Se 20 78 96.3 149 2 US-09-192-838B-2 Se 20 78 96.3 149 2 US-09-192-8333-2 Se 20 78 96.3 149 2 US-09-234-131-2 Se 20 78 96.3 149 2 US-09-192-854-1 Se 20 78 96.3 249 2 US-09-192-555-4 Se 20 78 96.3 249 2 US-09-192-555-4 Se 20 78 96.3 249 2 US-09-192-555-4 Se 20 78 96.3 249 2 US-09-192-553-6 Se 20 78 96.3 249 2 US-09-192-553-6 Se 20 78 96.3 249 2 US-09-192-533-6 Se 20 78 96.3 249 2 US-09-293-233-6 Se 20 78 96.3 2 US-09-293-233-6 Se 20 20 20 20 20 20 20 20 20 20 20 20 20	RESULT 1 US-08-053-171-27 US-08-053-171-27 Sequence 27, Application US/08053171 Patent No. 556290 GENERAL INFORMATION: APPLICANT: Co, Lobbner TITLE OF INVENTION: Antibody Derivatives NUMBER OF SEQUENCES: 32 CORRESPONDENCES: 32 CORRESPONDENCES: 32 CONTRY: US ZIRET: 379 Lytton Avenue CITY: Palo Alto STREE: California COUNTRY: US ZIP: 94301 COMPUTER: IBW PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Betenin Release #1.0, Version #1.25 COMPUTER: 18 PETENTION: A24 APPLICATION NUMBER: US/08/053,171 FILING DATE: 22-APP-193 CLASSIFCATION: 424 ATTORNEY/AGRAT INFORMATION: NAME: Smith, Willaim M NAME: Smith, Willaim M NAME: Smith, Willaim M NAME: Smith, Willaim M SEQUENCE CHARACTERISTICS: LENGTH: 16 amino acide TELERAX: (415) 326-2402 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS: LENGTH: 16 amino acide TYPE: amino acide HYPOTHETICAL: NO	; RATURE: ; NAME/KEY: Peptide ; LOCATION: 116 ; OTHER INFORMATION: /note= "First ; OTHER INFORMATION: complementarity-determining region ; OTHER INFORMATION: BRES-1 antibody light chain" US-08-053-171-27	Query Match 96.3%; Score 78; DB 1; Length 16 Best Local Similarity 93.8%; Pred. No. 4e-06; Matches 15; Conservative 1; Mismatches 0; Indels

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US-08-129-930B-30
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| Patent No. 5804187
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Ceriani Dr., Roberto L.
| APPLICANT: Peterson Dr., Jerry A.
| APPLICANT: Padlan Dr., Guardo A.
| TITLE OF INVENTION: Analogue Peptides With Broad
| TITLE OF INVENTION: Diagnostic Vaccination and
| TITLE OF INVENTION: Diagnostic Methods
| TITLE OF INVENTION: Therapeutic Methods
| NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.3%; Score 78; DB 1; Length 16; 93.8%; Pred. No. 4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ameal Ph.D., Viviana
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P66 38227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
TELEFAX: (510) 748-6688
1 RSSOSIVHSNGNTYLO 16
                   1 RSSQSIVHSNGNTYLE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSSQSIVHSNGNTYLQ 16
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Best Local Similarity 93.8
....hes 15; Conservative
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: n.a.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-977-696C-30
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US-08-129-930B-30
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US-08-134-345A-17, Application US/08134346A
| Sequence 17, Application US/0813436A
| Patent No. 6281335
| GENERAL INFORMATION:
| APPLICANT: do Couto, F.J.R.
| APPLICANT: do Couto, F.J.R.
| APPLICANT: Petersen, J.A.
| APPLICANT: Petersen, J.A.
| APPLICANT: PETERSEN: HYBRIDOMA AND ANTI-KC-4 HUMANIZED TITLE OF INVENTION: MONOCICONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS NUMBER OF SEQUENCES: 51
| CORRESONDENCE ADDRESS: ADDRESS: ADDRESSE: DISCONDITER READABLE FORM: STATE: NW YORK STATE: NW YORK STATE: NOW YORK STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                            COMPINITY: USA

ZIP: 94596
COMPUTER READABLE FORM:
MEDIUM TYPE: R10py disk
COMPUTER: IBM PC compatible
SECTION: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: AMRED Ph.D. Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 30,930
TELEEPAN: (510) 521-1333
TELEEPAN: (510) 521-1333
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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SEQUENCE CHARACTERISTICS:
TRNGTH: 16 amino acids
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MOLECULE TYPE: peptide
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Best Local Similarity
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Sequence 30, Application US/09947839B

Patent No. 6936706

GENERAL INPORMATION:
APPLICANT: do Couto, Fernando J.R.
Ceriani Dr., Roberto L.
Peterson Dr., Jerry A.
Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
for Carcinomas and Kit and Diagnostic Vaccination and Therapeutic Methods.
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HART, MARY KATE
APPLICANT: HART, MARY KATE
APPLICANT: WILSON, JULIE
AND AND COMPLEMENTARY: DETERMINING
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
FILE REPRENCE: ARMY 166
CURRENT APPLICATION NUMBER: US/10/226, 795
CURRENT PILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 28
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic light OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
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                                                 Gaps
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    Length 16;
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COMPUTER EACHABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: ISM PC-DOS/MS-DOS 5.0

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839B
Query Match 96.3%; Score 78; DB 2;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%; Score 78; DB 2;
93.8%; Pred. No. 4e-06;
tive 1; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: V. Amzel & Assoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Amzel Viviana
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              US-10-226-795-28
; Sequence 28, Application US/10226795
; Patent No. 6875433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O.Box 159
CITY: Gladwyne
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSSOSIVHSNGNTYLE 16
                                                                                                                        1 RSSQSIVHSNGNTYLE 16
                                                                                              1 RSSQSIVHSNGNTYLQ 16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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Pred. No. 4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Sduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALP: 900.7

CALP: 900.7

CALP: 900.7

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,288A

FILING DATE: No. 6315997ember 21, 1997

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: 08/129,930

FILING DATE: September 30, 1993

PRIOR APPLICATION NUMBER: 07/977,696

RILING DATE: NO. 6315997ember 16, 1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pretty, Schroeder & Poplawski STREET: 444 South Flower St., 19th Floor CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Viviana Amzel Ph.D.
REGISTRATHON NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-976-288A-30
; Sequence 30, Application US/08976288A
; Patent No. 6315997
; GENERL INFORMATION:
APPLICANT: Go Couto Dr., Fernando
APPLICANT: Ceriani Dr., Roberto L
       TELECOMMUNICATION INFORMATION:
TELEPAK: 212-826-5909
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFA..
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                  96.3%;
                                                                                                                                                                                                                                                                                                                                                                            1 RSSQSIVHSNGNTYLQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                      1 RSSOSIVHSNGNTYLE 16
                                                                                                                                                                                                                                                                               Query Match 96.3
Best Local Similarity 93.8
Matches 15, Conservative
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                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90071
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                                                                                                                                                                                                                                       US-08-134-346A-17
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.3%; Score 78; DB 2; Length 100; 93.8%; Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCREMENTOR

APPLICANT: LARGEAG, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Refe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 1855.1052-004

CURRENT PILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 106

SEQ ID NO 26

LENGTH: 100
APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: O9/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1909-07-22
PRIOR APPLICATION NUMBER: 09/3121,781
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR SEQ ID NOS: 107
SEQ ID NO SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09497625A Patent No. 6727349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RSSQSIVHSNGNTYLQ 16
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Best Local Similarity 93.8<sup>1</sup>
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
US-09-497-625A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 15; Conserv
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US-09-497-625A-28
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                                                                                                                                                                                                                                                                                                                                                           Length 16;
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US-09-840-459-26

i Sequence 26. Application US/09840459

i Patent No. 6696550

j GENERAL INFORMATION:

APPLICANT: LaRosa, Gregory J.

APPLICANT: Newman, Walter

APPLICANT: Ones, S. Tarran

APPLICANT: O'Keefe, Theresa

ITILE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

FILE REFERENCE: 1855-1052-012

CURRENT FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-03

PRIOR FILING DATE: 1999-07-23

PRIOR PLICATION NUMBER: 09/11,781

PRIOR PLILING DATE: 1998-07-23

PRIOR PLILING DATE: 1998-07-23

PRIOR PLILING DATE: 1998-07-23
                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                        96.3%; Score 78; DB 2; 93.8%; Pred. No. 4e-06; tive 1; Mismatches
       REFERENCE/DOCKET NUMBER: CRFC-083
                                                                                                                                                                             TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-8398-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 107
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-840-459-28
is Sequence 28, Application US/09840459
jeatent No. 6696550
jeatent No. 6696550
jeatent APPLICANT: LaRosa, Gregory J.
jeatent APPLICANT: Nervath, Christopher
jeatent Newman, Walter
septiCANT: Jones, S. Tarran
                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-649-0609
TELERA: n.a.
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RSSOSIVHSNGNTYLO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSSQSIVHSNGNTYLE 16
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Matches 15; Conservative
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; Sequence 28, Application US/09497625A; Patent No. 6727349

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APPLICANT: HANSEN, HANS J.
APPLICANT: GRIFFITHS, GARY L.
APPLICANT: GRIFFITHS, GARY L.
APPLICANT: MCBRIDS, WILLIAM J.
APPLICANT: LEUNG, SHUI-ON
APPLICANT: LEUNG, SHUI-ON
APPLICANT: US WILLIAM J.
APPLICANT: ON SE WILLIAM J.
APPLICANT: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
TITLE OF INVENTION: USE WITH BI-SPECIFIC ANTIBODIES
FILE REFERENCE: 40923-0074034
CURRENT APPLICATION NUMBER: US/09/823,746
CURRENT PILLING DATE: 1999-06-22
NUMBER: OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 3.3
SEQ ID NO 12
LENGTH: 111
TYPE: PRT
CREATURE:
CRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized; OTHER INFORMATION: Mu-9 amino acid sequence
US-09-823-746-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESULT 14
US-08-053-171-15
i Sequence 15, Application US/08053171
j Patent No. 5562903
i GENERAL INFORMATION:
j TITLE OF INVENTION:
j TITLE OF INVENTION:
j CORRESPONDENCE ADDRESS:
j CORRESPONDENCE ADDRESS:
j ADDRESSES TOWNSEND and Townsend Khourie and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRIT: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMith, Willaim M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 96.3%; Score 78; DB 2; 18est Local Similarity 93.8%; Pred. No. 3.3e-05; Matches 15; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RSSQSIVHSNGNTYLQ 16
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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; Sequence 42, Application US/10114716A
; Patent No. 6855804
; GENERAL INPORMATION:
   APPLICANT: Sudhir Paul
; APPLICANT: Yasuhiro Mishiyama
; TITLE OF INVENTION: Analogs and Methods of Use Thereof
; TITLE OF INVENTION: Analogs and Methods of Use Thereof
; TITLE OF INVENTION: DATE: 2002-04-01
; FILE REFERENCE: UTH001HB
; CURRENT APPLICATION NUMBER: US/10/114,716A
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/046,373
; PRIOR APPLICATION NUMBER: 60/280,624
; PRIOR PILING DATE: 1998-03-23
; PRIOR FILING DATE: 2001-03-31
; NUMBER OF SEQ ID NOS: 57
; SEQ ID NOS: 57
; SEQ ID NOS: 57
; SEQ ID NOS: 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 100;
                  GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Actristopher
APPLICANT: Newan, Walter
APPLICANT: Ones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Horsea
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2
CURRENT FILING DATE: 1855.1052-004
CURRENT FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SEQ ID NO 28
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.3%; Score 78; DB 2; I 93.8%; Pred. No. 2.9e-05; Live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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; ORGANISM: Mus musculus domesticus
US-10-114-716A-42
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
US-09-497-625A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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US-09-823-746-12
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                                                       GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: TREATMENT OF MELANOMA AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE SOFT
STREER: 755 PAGE MILL ROAD
CITY: PALO ALTO
STREET: 755 PAGE MILL ROAD
COUNTY: PALO ALTO
STATE: CA
COUNTYER: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALOMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CHARLOW TOWNER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: Modified-site
; LOCATION: 108
; OTHER INFORMATION: /note= "Residue in the framework
; OTHER INFORMATION: that is replaced with mouse amino acid in the
; OTHER INFORMATION: humanized antibody."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.3%; Score 78; DB 1; Length 112; Best Local Similarity 93.8%; Pred. No. 3.3e-05; Matches 15; Conservative 1; Mismatches 0; Indels
/note= "Sequence of the Light Chain
                                    of Humanized BR55-2 Antibody'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/08752844
Patent No. 5935821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSSQSIVHSNGNTYLQ 16
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OTHER INFORMATION:
                   Patent No. 5562903
OTHER INFORMATION:
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Gaps
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0
                                                                                                                                                                                                                      Length 112;
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93.8%; Pred. No. 3.3e-05;
tive 1; Mismatches 0; Indels
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                                TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               1 RSSOSIVHSNGNTYLO 16
                                                                                                                                                                                                                                                                                                                               24 RSSQSIVHSNGNTYLE 39
(415) 813-5600
                                                                                    LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
                 (415) 494-0792
                                                                                                                                                                                                                                       Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-752-844-15
TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                                        Query Match
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Sequence 54, Application US/10735916A; Publication No. US20050084906A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GOETSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 16;
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                                                         December 30, 2005, 13:33:42; Search time 118.968 Seconds (without alignments) 56.194 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-735-916A-61

US-10-735-916A-61

US-10-735-916A-49

US-10-735-916A-49

US-10-735-916A-63

US-10-735-916A-63

US-10-735-916A-63

US-10-995-529-32

US-09-995-529-32

US-09-995-529-32

US-10-226-795-28

US-10-45-91

US-10-45-92

US-10-45-92

US-10-45-92

US-10-76-610-26

US-10-766-610-26

US-10-766-610-26

US-10-766-610-26

US-10-766-610-26

US-10-766-610-26

US-10-766-610-26
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US-10-729-441-56
US-10-897-406-56
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                                                                                                                                                      1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                         using sw
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Maximum DB seq length: 2000000000
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Match Length DB
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                                           OM protein
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Sequence 2, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GORYSCH, Liliane

APPLICANT: CORYALA, Nathalie

APPLICANT: LEGER, Olivier

APPLICANT: BECK, Alain

APPLICANT: BORY ANII-IGF-IR ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NOVEL ANII-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01773-183

FULS REPERENCE: 0173-183

CURRENT APPLICATION NUMBER: FR 03/08 538

PRIOR FILING DATE: 2003-01-10

PRIOR FILING DATE: 2003-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

SEQ ID NO 2: 156

SEQ ID NO 2: LENGTH: 16

TWOST PRIOR PILING DATE: 2002-01-18

SEQ ID NO 2: LENGTH: 16
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Sequence 4
Sequence 4
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Pred. No. 9.1e-07;
US-09-995-529-10
US-10-153-401-15
US-10-258-728-4
US-10-258-728-25
US-10-258-728-27
US-10-258-728-27
US-10-258-728-27
US-10-735-916A-56
US-10-735-916A-56
US-10-735-916A-56
US-10-735-916A-56
US-10-735-916A-56
US-10-735-916A-59
US-10-739-441-61
US-10-897-406-61
US-11-070-697-36
US-11-070-697-36
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ORGANISM: Mus musculus
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Sequence 49, Application US/10735916A

Sequence 49, Application US/10735916A

Publication No. US2050084906A1

GENERAL INFORMATION:
APPLICANT: GORNSCH, Liliane
APPLICANT: CORVALA, Mathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE REFERENCE: 01775-183
CURRENT APPLICATION NUMBER: US/10/735, 916A
CURRENT APPLICATION NUMBER: US/10/735, 916A
CURRENT APPLICATION NUMBER: FR 03/08 538
FRIOR FILING DATE: 2003-01-11
FRIOR APPLICATION NUMBER: FR 02/06 653
FRIOR APPLICATION NUMBER: FR 02/06 654
FRIOR FILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GORYGLA, Inliane

APPLICANT: CORVAIA, Nathalie

APPLICANT: LEGER, Olivier

APPLICANT: DUFLOS, Alain

APPLICANT: DUFLOS, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT APPLICATION NUMBER: W3/08 538

PRIOR APPLICATION NUMBER: PR 03/08 538

PRIOR PELING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: FR 02/00 653

PRIOR FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR PILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 02/05 654

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-05-07

NUMBER OF SEQ ID NOS: 156

SOFTWARE: PATENTIN VOY: 2.1

TEMOTH: 117
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                                                                                                                                                                      Sequence 65, Application US/10735916A Publication No. US20050084906A1 GENERAL INFORMATION:
24 RSSQSIVHSNGNTYLQ 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSSOSIVHSNGNTYLO 16
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ORGANISM: Homo sapiens
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               APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGP-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGP-IR ANTIBODIES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR PRIOR APPLICATION NUMBER: PR 02/00 653
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 54
LEAST APPLICATION NUMBER: PR 02/05 753
NUMBER OF SEQ ID NOS: 126
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US-10-735-916A-61
i Sequence 61, Application US/10735916A
j Publication No. US20050084906A1
j GENERAL INFORMATION:
j APPLICANT: CORVACH, Liliane
j APPLICANT: CORVACH, Liliane
j APPLICANT: CORVACH, Liliane
j APPLICANT: UBGER, Olivier
j APPLICANT: UBGER, Olivier
j APPLICANT: HAEUW, Jean-Francois
j TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
j TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
j TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
j TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
j TILLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
j FILE REPERENCE: 2003-07-11
j PRIOR APPLICATION NUMBER: PR 03/00 53
j RIOR FILING DATE: 2002-01-20
j PRIOR PLICATION NUMBER: FR 02/00 654
j PRIOR FILING DATE: 2002-01-18
j PRIOR APPLICATION NUMBER: FR 02/05 53
j PRIOR FILING DATE: 2002-01-18
j PRIOR APPLICATION NUMBER: FR 02/05 53
j RRIOR FILING DATE: 2002-01-18
j PRIOR APPLICATION NUMBER: FR 02/05 53
j RRIOR FILING DATE: 2002-05-07
j NUMBER OF SEQ ID NOS: 156
j SOPTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 81; DB 5; Length 112; 100.0%; Pred. No. 8.2e-06; cive 0; Mismatches 0; Indels
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Best Local Similarity 100..
These 16; Conservative
DUFLOS, Alain
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US-10-735-916A-61
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Gaps

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Length 112;

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ÚS-10-735-916A-67
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US-10-/35-9164

Sequence 63, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GORTSCH, Liliane

APPLICANT: CORVAIA, Nathalie

APPLICANT: LEGER, Olivier

APPLICANT: HECK, Alain

APPLICANT: HECK, Alain

APPLICANT: HECK, Alain

APPLICANT: HECK, Alain

APPLICANT: HECK, Olivier

APPLICANT: HECK, Alain

APPLICANT: HECK, Alain

APPLICANT: HAEUW, Jean-Francois

TITLE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735, 916A

CURRENT APPLICATION NUMBER: PR 03/08 538

PRIOR APPLICATION NUMBER: PR 02/00 653

PRIOR FILING DATE: 2003-01-10

PRIOR FILING DATE: 2002-01-18

SEQUENCE OF THE PRIOR PRIOR DATE: 2002-01-18

SEQUENCE OF THE PRIOR DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

SEQUENCE OF THE PRIOR DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

SEQUENCE OF THE PRIOR DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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Spublication No. US20050084906A1

GRNERAL INFORMATION:
APPLICANT: CORVALA. Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INFORMINONEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INFORTION: NOVEL ANTI-IGP-IR ANTIBODIES AND USES THEREOF
TITLE REPERENCE: 017753-183
CURRENT PILING DATE: 2003-12-16
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                                                                                                                                               Length 122;
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                                                                                                                                                  Query Match
100.0%; Score 81; DB 5;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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PRIOR APPLICATION NUMBER: FR 03/08 538
PRIOR FILING DATE: 2003-07-11
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Best Local Similarity 100.0
Matches 16; Conservative
                             ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-49
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ORGANISM: Homo sapiens
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US-10-735-916A-63
LENGTH: 122
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Publication No. US20030138428A1

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.

Ceriani Dr., Roberto L.

Pedierson Dr., Jerry A.

Padlan Dr., Schardo A.

TITLE OF INVENTION: Analogue Peptides With Broad

Diagnostic Vaccination and

Therapeutic Methods
                                                                                                                                                                                                                                                                                                                                                                                         Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 78; DB 3; Length 16; 93.8%; Pred. No. 3e-06; Live 1; Mismatches 0; Indels
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US-09-995-529-32
Sequence 32, Application US/09995529
Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Related Methods
TITLE OF INVENTION: Related Methods
FILE REPREBRENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT APPLICATION NUMBER: 2001-11-26
NUMBER OF FILE 2001-11-26
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NOS: 358
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STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 16; Conservative 0; Mismatches n.
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin Ver. 2.1
FROM TOWN OF 7
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 96.3
Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 28, Application US/1026795
Publication No. US20040053865A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HART, MARY KATE
APPLICANT: WILSON, JULIE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
TITLE OF INVENTION: MONOCLONAL INDING TO EBOLA GLYCOPROTEIN
FILE REFERENCE: ARMY 166
CURRENT APPLICATION NUMBER: US/10/226,795
CURRENT FILING DATE: 202-11-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 28
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic light; OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence US-10-226-795-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Sequence 1, Application US/11070697
Publication No. US20050169926A1
SEQUENCE INFORMATION:
APPLICANT: GU, ZHENGXING
APPLICANT: HANSEN, HANS
APPLICANT: GLEBNBERG, DAVID M.
TITLE OF INVENTION: CHIMBELC, HUMAN AND HUMANIZED ANTI-CSAP MONOCLONAL
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 3e-06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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Publication No. US20040146505A1
GENERAL INFORMATION:
APPLICANT: Scancell Limited
APPLICANT: Durrant, Linda Gillian
APPLICANT: Parsons, Tina
TITLE OF INVENTION: Substances
FILE REFERENCE: P32181WO/NUL
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: US/10/470,045
PRIOR PILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn version 3.1
SENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-10-470-045-53
                         US-10-226-795-28
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                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839

FILING DATE: 06-Sep-2001

CLASSIFICATION NUMBER: 08/976,288

FILING DATE: ADDATA:

APPLICATION NUMBER: 08/976,288

FILING DATE: NO. US20030138428Alember 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel Ph.D.

REGISTRATION NUMBER: 30,930

REGISTRATION NUMBER: 30,930

TELEPRONE: (213) 622-7700

TELEPRONE: (213) 489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.3%; Score 78; DB 3; Length 16; Best Local Similarity 93.8%; Pred. No. 3e-06; Matches 15; Conservative 1; Mismatches 0; Indels
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; Sequence 32, Application US/09995529
; Cabus and Comparation No. US20040091482A9
; Caneral Information:
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Huse, William D.
; APPLICANT: Huse, William D.
; APPLICANT: Huse, William D.
; APPLICANT: Huse, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; TURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT PILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid

TOPOLOGY: linear

MOLECTUE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-839-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ 1D NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RSSQSIVHSNGNTYLQ 16
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STATE: California
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-995-529-32
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LENGTH: 16
TYPE: PRT
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Search completed: December 30, 2005, 14:14:50 Job time : 118.968 secs
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96.3%; Score 78; DB 6; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels
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Sequence 91, Application US/10470045

Publication No. US20040146505A1

GENERAL INFORMATION:
APPLICANT: Scancell Limited
APPLICANT: Durrant, Linda Gillian
APPLICANT: Durrant, Linda Gillian
FILE REFERENCE: P32181WO/NJL
CURRENT APPLICATION: Substances
FILE REFERENCE: P32181WO/NJL
CURRENT APPLICATION NUMBER: US/10/470,045

CURRENT APPLICATION NUMBER: GB 0102145.0

PRIOR APPLICATION NUMBER: GB 0102145.0

PRIOR FILING DATE: 2001-01-26

NUMBER: OF SEQ ID NOS: 101

SEQ ID NO 91

LENGTH: 60

LENGTH: 60
CURRENT APPLICATION NUMBER: US/11/070,697
CURRENT APPLICATION NUMBER: US/11/070,697
PRIOR APPLICATION NUMBER: US/10/116,116
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1998-10-14
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CORGANISM: Mus musculus
US-10-470-045-91
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US-10-470-045-91
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APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED AUTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED AUTI-CCR2 AUTIBODIES AND
CURRENT PELING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: DCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR PELING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR PELING DATE: 1998-07-23
PRIOR PELING DATE: 1998-07-23
PRIOR PELING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FREESEQ for Windows Version 3.0
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CORGANISM: Mus musculus
US-09-840-459-26
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RESULT 2
US-11-012-353-54
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                                                                                                        December 30, 2005, 13:35:07 ; Search time 5.93548 Seconds (without alignments) 20.187 Million cell updates/sec
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4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-932-334-62
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Maximum Match 100%
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seq length: 200000000
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US-11-012-353-2

Sequence 2, Application US/11012353

Publication No. US20060249730A1

GENERAL INFORMATION:
APPLICANT: CORVIAL. NATHALIE
APPLICANT: CORVIAL. NATHALIE
APPLICANT: CORVIAL. NATHALIE
APPLICANT: HAEUW, UEAN-FRANCOIS
APPLICANT: LEGEK, ALAIN
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES
TITLE OF INVENTION: RECEPTORS ANTIBODIES
TITLE OF INVENTION: RECEPTORS ANTIBODIES
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR
Sequence 67, Appl
Sequence 23, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 11, Appl
Sequence 112, Appl
Sequence 112, Appl
Sequence 23, Appli
Sequence 23, Appli
Sequence 118, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 68, Appl
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US-11-0932-334-9
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US-10-932-334-83
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Best Local Similarity 100.
Matches 16; Conservative
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; ORGANISM: Mus musculus
US-11-012-353-2
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Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
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ORGANISM: Homo sapiens
US-11-012-353-65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-11-012-353-49
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US-11-012-353-61

Sequence 61, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GORENCE, LILLANE
APPLICANT: CORVALA, NATHALIE
APPLICANT: CORVALA, NATHALIE
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: BCER, OLIVIER
APPLICANT: BCER, OLIVIER
APPLICANT: BCOVALA, NATHALIE
APPLICANT: BCOVALIAN
TITLE OF INVENTION: NOVERER: US/11/012,353
CURRENT PLING DATE: 2003-12-16
BRIOR FILING DATE: 2003-12-16
BRIOR FILING DATE: 2003-07-11
PRIOR PELICATION NUMBER: FR 020653
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REPERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR PILING DATE: 2003-07-01-20
PRIOR PILING DATE: 2003-07-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-18
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                                      GENERAL INFORMATION:
APPLICANT: GOGESCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: APPLICANT: ALAIN
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    Publication No. US20050249730A1
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ORGANISM: Mus musculus
US-11-012-353-54
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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REPERENCE: 01753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2002-01-18
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DIFLOS, ALAIN
APPLICANT: LIGGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
                                                                         Gaps
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   Length 112;
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                                                                      0; Indels
100.0%; Score 81; DB 7; I 100.0%; Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 65, Application US/11012353;
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HARUW, JEAN-FRANCOIS
APPLICANT: HARUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
                                                                                                                                        1 RSSQSIVHSNGNTYLQ 16
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Sequence 67, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
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                43 RSSQSIVHSNGNTYLQ 58
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-932-334-56
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US-11-012-353-67
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| Sequence 63, Application US/11012353
| Sequence 63, Application No. US20050249730A1
| Publication No. US20050249730A1
| GENERAL INFORMATION:
| APPLICANT: GORYAIA, NATHALIE
| APPLICANT: DUFLOS, ALAINE
| APPLICANT: HAEUN, USAN-FRANCOIS
| APPLICANT: LEGER, OLIVIER
| APPLICANT: BECK, ALAIN
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
| TILLE OF INVENTION: NUMBER: US/11/012,353
| CURRENT APPLICATION NUMBER: 10/735,916
| PRIOR FILING DATE: 2003-12-16
| PRIOR FILING DATE: 2003-07-11
| PRIOR FILING DATE: 2003-07-11
| PRIOR PLILOTION NUMBER: FR 0200553
| PRIOR FILING DATE: 2002-01-18
| PRIOR APPLICATION NUMBER: FR 0200654
| PRIOR FILING DATE: 2002-01-18
| PRIOR FILING DATE: 2002-01-18
| PRIOR PLING DATE: 2002-01-18
| PRIOR FILING DATE: 2002-01-18
| PRIOR PLING DATE: 2002-01-18
| PRIOR FILING DATE: 2002-01-18
| PRIOR PLING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 81; DB 7; Length 122; 100.0%; Pred. No. 1.2e-07; Live 0; Mismatches 0; Indel8
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-13
PRIOR PILING DATE: 2003-07-07
PRIOR PILING DATE: 2002-01-07
PRIOR PILING DATE: 2002-07
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATCHIN Ver: 3.3
SEQ ID NO 49
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CRGANISM: Mus musculus
US-11-012-353-49
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ORGANISM: Homo sapiens
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Best Local Similarity
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| GREEKLA INFOMENTION:
| APPLICANT: GCRATCH, LILLINE
| APPLICANT: GCRATCH, ANTHALIS
| TITLE OF INVERTION: RECEPORS ANTHODISS AND USES THERROF
| FILE OF INVERTION: RECEPORS ANTHODISS AND USES THERROF
| FILE OF INVERTION: RECEPORS ANTHODISS AND USES THERROF
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| FILE OF INVERTION: RECEPORS ANTHODISS AND USES THERROF
| FILE OF INVERTION: RECEPORS ANTHODISS AND USES THERROF
| FRICK PRINKS DATE: 2003-12-146
| FRICK APPLICATION NUMBER: RF 20065-3
| FRICK APPLICATION NUMBER: RF 2006-3-3
| FRICK FILE OF APPLICATION NUMBER: RF 2006-3-3
| FRICK AP
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1 RSSQSIVHSNGNTYLQ 16

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96.3%; Score 78; DB 7; Length 112; 93.8%; Pred. No. 3.6e-07; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; sequence 59, Application US/10932334
; publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.;
; TITLE OF INVENTION: ANTI-IGP-I RECEPTOR ANTIBODY
FILE REFERENCE: A6689
; CURRENT APPLICATION WUMBER: US/10/932,334
; CURRENT APPLICATION WUMBER: US/10/729,441
PRIOR APPLICATION WUMBER: US/10/729,441
; PRIOR APPLICATION WUMBER: 10/10,390
; RIOR APPLICATION WUMBER: 10/10,390
; RIOR APPLICATION WUMBER: 10/170,390
; RIOR APPLICATION WUMBER: 10/170,390
; RIOR PILING DATE: 2002-06-14
; WUMBER OF SEQ ID NOS: 96
; SEQ ID NO 59
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Publication No. US20050249728A1

GENERAL INFORMATION:

APPLICANT: ImmunoGen, Inc.

TITLE OF INVENTION: ANII-IGF-I RECEPTOR ANTIBODY

TILE REFERENCE: A6689

CURRENT APPLICATION NUMBER: US/10/932,334

CURRENT PILING DATE: 2004-09-02

PRIOR APPLICATION NUMBER: US/10/729,441

PRIOR PLING DATE: 2003-12-08

PRIOR PLING DATE: 2003-12-08

PRIOR FILING DATE: 2003-16-08

PRIOR FILING DATE: 2003-16-08

SROID NOS: 96

SOFTWARE PETENT PATENT NOS: 96

SOFTWARE PETENT PATENT NOS: 96

SOFTWARE PETENT NOS: 96
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PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN Ver. 3.3
SEQ ID NO 56
LENGTH: 112
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ORGANISM: Artificial Sequence
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 96.3
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                 trype: PRT CAGANISM: Mus musculus US-11-012-353-56
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US-10-932-334-59
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US-11-02-36

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TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
FILE REFERENCE: 0.17753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CHRENT APPLICATION NUMBER: 10/735,916
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
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Pred. No. 3.6e-07;
1; Mismatches 0; Indels
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US-11-012-353-56
; Sequence 56, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GORTSCH, LILIANB
; APPLICANT: CORTSCH, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: LEGER, OLIVIER
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; APPLICANT: APECK, ALAIN
; APPLICANT: LEGER, OLIVIER
; APPLICANT: LEGER, OLIVIER
; APPLICANT: LEGER, OLIVIER
                                              1 RSSOSIVHSNGNTYLO 16
                                                                                     24 RSSQSIVHSNGNTYLE 39
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Best Local Similarity 93.8%;
Matches 15; Conservative
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US-11-012-353-55
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Sequence 67, Application US/10512184
; Publication No. US2060244901A1
; Publication No. US2060244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: resistance against fungi
rITLE OF INVENTION: resistance against fungi
rITLE OF INVENTION: 2014.10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 67
LENTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: precursor; OTHER INFORMATION: fusion protein comprising AG - linker - scFv VD2.
US-10-512-184-67
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                                                   Length 251;
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                                             Query Match
96.3%; Score 78; DB 6; i
Best Local Similarity 93.8%; Pred. No. 9.1e-07;
Matches 15; Conservative 1; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: December 30, 2005, 14:15:20 Job time : 6.93548 secs
                                                                                                                                                                                                        161 RSSQNIVHSNGNTYLQ 176
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US-10-512-184-30
                                                                                                                                                                                                                                                                                                                      RESULT 15
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Fublication No. US20050250131A1

Fublication No. US20050250131A1

GENERAL INFORMATION:
APPLICANT: USETIN, JEAN-LUC

APPLICANT: USETIN, JEAN-LUC

APPLICANT: USETIN, JEAN-LUC

APPLICANT: WITHER-GUERER, SOPHIE
APPLICANT: WITHOUS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
TITLE OF INVENTION: WATHOUS FOR OBTAINING THE SAME, AND APPLICATION OF THE SAME

TITLE OF INVENTION: WATHOUS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

FILE REFERENCE: 266426USOXCIP
CURRENT FILING DATE: 2005-02-25

PRIOR APPLICATION NUMBER: US 10/787,219

PRIOR APPLICATION NUMBER: US 10/787,219

PRIOR APPLICATION NUMBER: US 10/787,219

PRIOR APPLICATION NUMBER: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patentin version 3.3

LENGTH: 116
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Publication No. US20050244901A1

APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: Antibodies, recombinant

CURRENT FILING DATE: 2004-10-22

NUMBER OF SEQ ID NOS: 72

SOFTWARR: Patentin Ver. 2.1

SEQ ID NOS: 2.2

SEQ ID NOS: 2.2

SEQ ID NOS: 2.2
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OTHER INFORMATION: Description of Artificial Sequence: scFv VD2 with
OTHER INFORMATION: specificity against Verticillium dahliae;
OTHER INFORMATION: originates from Mus musculus.
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                                                                                                                                                                                                  ch 96.3%; Score 78; DB 6; Length 113; I Similarity 93.8%; Pred. No. 3.7e-07; 15; Conservative 1; Mismatches 0; Indels
                                                                                        FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-61
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                    TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-512-184-30
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            LENGTH: 113
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Best Local
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Gaps

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Adz67006 Murine in
Abr52343 Fv requen
Add24147 Mouse HUI
Adh61952 Mouse and
Adh78129 Human SJB
Adm78129 Human SJB
Adm8139 Human SJB
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                                                             ; Search time 132.5 Seconds
(without alignments)
53.057 Million cell updates/sec
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Add94233 1
Adp84888 (
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Aab97198
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                  2443163 segs, 439378781 residues
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                                                               December 30, 2005, 13:37:27
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Maximum Match 100%
Listing first 45 summaries
                                           using sw model
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ADM21487
ADM78123
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ADF8465
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AAR70451
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Gapop 10.0 , Gapext 0.5
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geneseqp20028:*
geneseqp2003a8:*
geneseqp2003b8:*
geneseqp20048:*
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                                         protein search,
           Copyright
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Maximum DB seq length: 16
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Match 1
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Perfect score:
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CDKL1 reg	Aaw31747	AAW31747	N	16	86.4	70	45
Д	Aea45027	AEA45027	σ,	16		17	44
Complemen	Adp84889	ADP84889	œ	16	87.7	11	
Complemen	Adp84866	ADP84866	œ	16	87.7	71	42
Mouse HUI	Add94226	ADD94226	7	16	87.7	71	41
Mouse HUI	Add94229	ADD94229	7	16	87.7	71	40
Murine CD	Aay51154	AAY51154	m	16	87.7	7.1	39
CDR-1 of	Aaw58534	AAW58534	0	16	87.7	71	38
Complemen	Adp84891	ADP84891	8	16	88.9	72	37
Mouse HUI	Add94225	ADD94225	7	16	88.9	72	36
Mouse HUI	Add94261	ADD94261	7	16	88.9	72	35
Humanised	Aar40216	AAR40216	0	16	88.9	72	34
Glycosyla	Adr19287	ADR19287	œ	16	90.1	73	33
Complemen	Adp84886	ADP84886	8	16	90.1	73	32
Complemen	Adp84893	ADP84893	æ	16	90.1	73	31
antibody	Aeb08720	AEB08720	0	16	91.4	74	30
Anti-Nogo	Aeb21685	AEB21685	σ	16	91.4	74	29
Anti-ghre	Ady80084	ADY80084	σ	16	91.4	74	28
Anti-ghre	Ady80101	ADY80101	σ	16	91.4	74	27
Antibody	Ads94307	ADS94307	œ	16	91.4	74	26
Glycosyla	Adr19288	ADR19288	80	16	91.4	74	25

ALIGNMENTS

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. CDR sequence for anti-IGF-1R antibody. ADJ76836 standard; peptide; 16 AA (first entry) 06-MAY-2004 ADJ76836; RESULT

WO2003059951-A2. Mus musculus

24-JUL-2003

20-JAN-2003; 2003WO-FR000178

18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753.

(FABR) FABRE MEDICAMENT SA PIERRE.

Leger 0; Corvaia N, Goetsch L,

WPI; 2003-569653/53. N-PSDB; ADJ76835.

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

claim 1; SEQ ID NO 2; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with

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                          these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of ISPR and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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   hyperactivity of signal transduction pathways mediated by interaction
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                              100.0%; Score 81; DB 7; Length 16; 100.0%; Pred. No. 4.8e-07; Live 0; Mismatches 0; Indels
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
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CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                         Sequence 16 AA;
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comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino actermining region (CDR) consisting of one of two fully defined 16 amino actermining region (CDR) consisting of one of two fully defined 16 amino cated (ADEATOLH). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of activation of the IGP-IR and/or connected with a anbourmal cativation of the IGP-IR and/or of EGF with EGFR, where the administration of the transduction pathway of the signal mediated by the induces secondary effects connected with inhibition of the insulin creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2—

character, preferably IGF-dependent and/or HERZ/neu-dependent and/or EGF-dependent and/or IGF2-dependent in the preparation of a medicament intended for IGF1-and/or IGF2-dependent and/or IGF2-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of portiasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to treatment of portiasis. (I) is useful in preparation of a medicament intended for IN vitro diagnosis of illnesses induced by an expression or an underexpression of the prevention of the prevention of searting from a biological sample in which involves contacting the center is used in the exemplification of the invention.

Is and/or IN vitro d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
specifically inhibiting tyrosine kinase activity of the receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VL sequence of anti-KC-4 monoclonal antibody (kII-Jk2) corresp. complementarity determining region 1 (CDR1).
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100.0%; Pred. No. 4.8e-07;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANC-) CANCER RES FUND CONTRA COSTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR70451 standard, peptide, 16 AA.
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Best Local Similarity
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Local Similarity 93.8
hes 15; Conservative
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                                                                                                                                                                                                                                        Sequence 16 AA;
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                                                                                                       The cDNAs that encode the anti-XC-4 murine immunoglobulin VH and VL were prepared by PCR from polyadenylated RNA isolated from 100 million KC-4 hybridoma calls. All clones were obtd. from independent PCRs. The sequences of the primers are given in AA087519-087526. The PCR products were cloned, without prior purificn., into pCR1000 (Invitrogen) and sequences in both directions. The VL DNA sequence and its derived protein sequences are shown in AA087531 and AAR70449-R70457. The mature VL chain begins at AA D of framework i (FR1). VL is a group II kappa chain. Part of the CDR3 and all of the FR4 are encoded by JK2. There is a an asparagine glycosylation site in the light chain in FR3. The site reads NIS. (Updated on 25-MAR-2003 to correct PM field.) (Updated on 25-MAR-2003 to correct PM field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response; tumour; immune response; cancer; vaccine; antibody.
                                 New humanised anti-KC-4 monoclonal antibody - used for detection of cancer cells, in vivo imaging, ex-vivo purging and treatment of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of polypeptides and nucleic acids encoding the polypeptides, in manufacturing medicament for stimulating a cytotoxic T cell response for preventing or treating cancer, e.g. colorectal, lung, breast or ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                          96.3%; Score 78; DB 2; Length 16; 93.8%; Pred. No. 1.6e-06; ive 1; Mismatches 0; Indels
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                                                                                Example; Table 14, Page 31; 61pp; English
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(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
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Matches 15, Conservative
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   N-PSDB; AAQ87531
                                                                                                                                                                                                                                                                                                                             Sequence 16 AA;
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The present invention describes the use of a polypeptide (I) in the manufacture of a medicament for stimulating a cytotoxic T cell response, where (I) comprises a first portion comprising the part of human Fc that binds to CD64 and a second portion comprising one or more heterologous T.

Example 11; Page 45; 87pp; English.

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cell epitopes. Also described is a method of stimulating a cytotoxic T cell response in a patient such as a mammal, preferably human, by administering (1) to the patient. (1) has cytostatic activity and can be used in vaccine production. (1) and the nucleic acid encoding (1) are useful in the manufacture of a medicament for stimulating cytotoxic T cell response. The medicament is useful for preventing and/or treating endicament eigencest, e.g. colorectal, lung, breast, gastric or ovarian cancer. The medicament stimulates cytotoxic and helper T cell responses. The antibodies are useful as vaccines to stimulate helper and cytotoxic T cell responses. The polypeptides and nucleic acids are useful in optimising immunisation schedules for enhancing a protective immune response against cancer. The present sequence represents an Fv region SC100 antibody CDR-L1 amino acid sequence which is used in an example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a multivalent, multispecific antibody or its fragment comprising one more antigen binding sites having affinity towards colon specific antigen-p mucin (CSAp) target antigen and one or more hapten binding sites having affinity towards hapten molecules. The antibody is useful for screening a targetable conjugate. A therapeutic immunoconjugate comprising the antibody is useful for detecting closerange lesion. The antibody or immunoconjugate are also useful for delivering a diagnostic/detection or therapeutic agent, or their
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combination, to a target. The antibody or a targetable conjugate are useful for detecting or treating tumours expressing CSAp in a mammal, for imaging malignant tissue or normal tissue or calls in a mammal expressing CSAp, where the normal tissue is from ovary, thymus, parathyroid or spleen, for intraoperatively identifying/disclosing the diseased tissues expressing CSAp in a subject, and for endoscopic identification of diseased tissues expressing CSAp. They are also useful for intravascular identification of diseased tissues expressing CSAp, for detecting lesions during an endoscopic, laparoscopic, intravascular catheter or surgical procedure, and for detecting and treating target calls, tissues or pathogens in a mammal. A method using the antibody is useful for diagnosing or detecting a malignancy in a subject, where the malignancy is carcinoma, gastrointestinal cancer, colorectal or pancreatic cancer or ovarian cancer, the subject is human or a domestic pet. This sequence represents the light chain complementarity determining region I (CDRI) from the antibodies of the invention.
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1 RSSQSIVHSNGNTYLQ 16 1 RSSQSIVHSNGNTYLE 16 Local Similarity 93.8 ses 15; Conservative Matches

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ADD94147 standard; peptide; 16 AA. ADD94147; RESULT 6
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Mouse HU177 light chain CDR1 partial amino acid sequence SeqID32 (first entry) 29-JAN-2004

grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agoniet; collagen antagoniet; cancer metastasis; anti-cryptic collagen; antibody; HUI77; variable region light chain; mouse;

Mus musculus.

WO2003046204-A2

26-NOV-2002; 2002WO-US038147. 05-JUN-2003.

26-NOV-2001; 2001US-00995529, 06-DEC-2001; 2001US-00011250.

(CELL-) CELL MATRIX INC

Brooks PC; Broek D, Watking JD, Huse WD, Tang Y, WPI; 2003-513649/48.

N-PSDB; ADD94146.

New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.

The invention relates to a novel anti-osteopontin antibody or antibody fragment which inhibits the binding of and integrin recognising the RGD sequence to osteopontin (OPN) or its fragment and inhibits the binding of an integrin recognising the SVVGLR sequence to osteopontin or its fragment. An antibody of the invention has immunosuppressive, antiarthritic, anti-rheumatic, and osteopathic activity. The antibodies are useful in diagnostics and developing drugs for autoimmune diseases, rheumatism, rheumatoid arthritis and archritis deformans. With these antibodies, it is possible to distinguish rheumatoid arthritis from arthritis deformans. The present sequence is used in the exemplification

of the invention

Sequence 16 AA;

Claim 25; SEQ ID NO 32; 232pp; English.

This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity

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for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of antagonist which a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the partial amino acid sequence of a mouse anti-orryptic collagen site antibody Hu177 variable region light chain CDR which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant anti-osteopontin antibodies with human-origin heavy and light chain constant regions, useful in diagnostics and developing drugs for autoimmune diseases, rheumatism and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteopontin; antibody; integrin; OPN; immunosuppressive; anti-arthritic; anti-rheumatic; osteopathic; autoimmune disease; rheumatism; rheumatoid arthritis; arthritis deformans; mouse; 2K1; CDR1.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto N, Higuchi H, Torikai M, Tokieda Y;
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0
                                                                                                                                                                            96.3%; Score 78; DB 7; Length 16; 93.8%; Pred. No. 1.6e-06; 1. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse antibody 2K1 VL region CDR1 SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 24; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CO LID
                                                                                                                                                                                                                                                                                                                                            ADH61992 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMU-) IMMUNO BIOLOGICAL LAB
(FUJI ) FUJISAWA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-2002; 2002WO-JP009868.
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                                                                                                                                                                                                                                                      RSSQSIVHSNGNTYLE 16
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                         1 RSSOSIVHSNGNTYLO
                                                                                                                                                                                            Local Similarity 93.8
ses 15; Conservative
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m Maeda H;
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                                                                                                                                                   Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                         ADH61992;
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Matches
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The invention relates to a novel monoclonal antibody specific to adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity determining regions (CDRs) of a sequence having 6-18 amino acids. The invention further relates to: a composition comprising the monoclonal antibody for detecting a heart disease marker AK3; a kit comprising the monoclonal antibody for the diagnosis of heart disease; and a method of detecting a heart disease marker AK3. The for preparing a composition for detecting a heart disease marker AK3. The monoclonal antibody medices false positive results of the conventional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New monoclonal antibody specific to human mitochondrial adenylate kinase isozyme 3, useful for preparing a composition for detecting a heart disease marker AK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biochemical markers. This sequence represents a human antibody variable light chain CDR peptide region of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody, adenylate kinase isozyme 3; complementarity determining region; CDR; heart disease; marker AK3; biochemical; human; variable; light chain.
                                                            monocional antibody; adenylate kinase isozyme 3;
complementarity determining region; CDR; heart disease; marker AK3;
biochemical; human; variable; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human SJB3-39 antibody variable light chain CDR1 peptide region.
                   Human SJB3-38 antibody variable light chain CDR1 peptide region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.3%; Score 78; DB 8; Length 16; 93.8%; Pred. No. 1.6e-06; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 86; 126pp; English.
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Best Local Similarity 93.05
Best Local Similarity
Local Similarity
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                                                                                                                                                                                                         WO2004029094-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                             (KIMH/) KIM H.
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein. The antibodies are ECP6D8-1-1, EGP1376-1-2, and EGP13C6-1-1. The monoclonal antibodies of the invention are useful for treating or ameliorating an Ebola virus infection. The antibodies were found to be effective when administered 2 days after challenge, after significant viral replication had occurred. ADL27487-ADL27489 represent complementarity determining regions (CDRs) from the light chain of a monoclonal antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated monoclonal antibody that binds Ebola virus GP, which monoclonal antibody comprises a heavy chain variable region, useful for treating or ameliorating Ebola virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes monoclonal antibodies that bind Ebola virus
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                     Length 16;
                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein; EGP6D8-1-1; EGP13F6-1-2; EGP13C6-1-1; Ebola virus infection; antibody; light chain; Complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSA ) US ARMY MEDICAL RES INST INFECTIOUS DISE.
                                                                                                                                                                                                                                                                                                                                                                                                                        CDR from the light chain of antibody EGP6D8-1-2.
                   Score 78; DB 7;
Pred. No. 1.6e-06;
1; Mismatches 0
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                                                                                                                                                                                                                                                                             ADL27487 standard; peptide; 16 AA.
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                        96.3%;
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                                                                                                                                          RSSQSIVHSNGNTYLE 16
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Query Match
Best Local Similarity 93.0.
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les 15; Conservative
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ILD ADL2

ADL27487

ILD ADL2

ADL27487

ADL27487

EDD COLUMN

EDD CO
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The invention relates to a novel monoclonal antibody specific to adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity determining regions (CDRs) of a sequence having 6-18 amino acids. The invention further relates to: a composition comprising the monoclonal antibody for the diagnosis of heart disease, and a method of detecting a heart disease marker AK3; a kit comprising the monoclonal antibody for the diagnosis of heart disease; and a method of detecting a heart disease marker AK3. The monoclonal antibody is useful for preparing a composition for detecting a heart disease marker AK3. The monoclonal antibody reduces false positive results of the conventional biochemical markers. This sequence represents a human antibody variable light chain CDR peptide region of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New monoclonal antibody specific to human mitochondrial adenylate kinase isozyme 3, useful for preparing a composition for detecting a heart disease marker AK3.
                                                                                                                            New monoclonal antibody specific to human mitochondrial adenylate kinase isozyme 3, useful for preparing a composition for detecting a heart disease marker AK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monoclonal antibody, adenylate kinase isozyme 3; complementarity determining region; CDR; heart disease; marker AK3; biochemical; human; variable; light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.3%; Score 78; DB 8; Length 16; 93.8%; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                            Claim 1; SEQ ID NO 92; 126pp; English
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28-SEP-2002; 2002KR-00059211
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                                                                                           WPI; 2004-316088/29
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16 AA;
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                              (KIMH/) KIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                Kim H;
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Claim 1; SEQ ID NO 44; 126pp; English.

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               adenylate kinase iscayme 3, comprising 4 or more of 6 complementarity determining regions (CDRs) of a sequence having 6-18 amino acids. The invertion further relates to: a composition comprising the monoclonal antibody for detecting a heart disease marker AR3; a kit comprising the monoclonal antibody for the diagnosis of heart disease; and a method of detecting a heart disease marker AR3. The monoclonal antibody is useful for preparing a composition for detecting a heart disease marker AR3. The monoclonal antibody reduces false positive results of the conventional biochemical markers. This sequence represents a human antibody variable light chain CDR peptide region of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions hat separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (1g) superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (WH) and the variable light chain (WL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens, useful for diagnosis, treatment and prevention of tumors and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; Core-1 antigen; framework region; immunoglobulin superfamily; procease inhibitor; lectin; helix-bundle protein; lipocalin; variable heavy chain; VI; variable light chain; VI; vaccine; diagnosis; alleviation; treatment; tumour; breast; colon; stomach; pancreas; large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
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invention relates to a novel monoclonal antibody specific to
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                                                                                                                                                                                                                                                                                        96.3%; Score 78; DB 8; Length 16; 93.8%; Pred. No. 1.6e-06; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region SEQ ID NO 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 7; 136pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP84865 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                                                     15; Conservative
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                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                   Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-2004
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                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP84865
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tise a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A. B or D and/or their subclasses. It may be human, human, and the constructs are Ig domain. The additional sequences/structures in the constructs are Ig domains of various specifies, interacting or stabilising domains, signal sequences, various specificities, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MRC molecules, antigens, chelators for radioactive labels, inposomes, transmembrane domains, viruses and/or cells, specifically macrophages. The antibodies, also constructs containing them, nucleic acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), prostate, kidney and/or liver) and/or metastases (particularly to liver), prostate, kidney and/or liver) and/or metastases (particularly to liver), the invention provide simple, raliable and efficient detection of the invention provide simple, raliable and efficient detection of the both where these are positive for the Cl antigen. The products of the contains They are specific for carcinoma and show almost no binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          healthy tissue.
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Sequence 16 AA;

ô Gaps ö 96.3%; Score 78; DB 8; Length 16; 93.8%; Pred. No. 1.6e-06; ive 1; Mismatches 0; Indels 15; Conservative Best Local Similarity Query Match Matches

1 RSSQSIVHSNGNTYLQ 16

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ADR19270 standard; peptide; 16 AA ADR19270; RESULT 13 ADR19270

(first entry) 21-OCT-2004

Glycosylated MUC1 tumour epitope recognition peptide, SEQ ID 7.

Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1; tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary; liver; kidney cell; intestinal; lung cancer; multiple myeloma.

Unidentified

WO2004065423-A2.

05-AUG-2004.

23-JAN-2004; 2004WO-DE000132.

23-JAN-2003; 2003DE-01003664.

(NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

Karsten U;

Stahn R,

Danielczyk A,

Goletz S,

WPI; 2004-593433/57.

recognition molecules that bind the glycosylated MUC1 tumor epitope, inl for prevention, diagnosis, treatment and monitoring of tumors. useful

Claim 4; SEQ ID NO 7; 158pp; German.

that bind specifically to a glycosylated MUC1 tumour epitope. The novel recognition molecules comprise: sequences ADR19264 or ADR19267; sequences ADR19266 or ADR19267 and sequences ADR19268 and ADR19269, and bind specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The invention further comprises: a construct comprising the recognition The invention relates to novel recognition molecules comprising sequences

molecule fused, chemically coupled or non-covalently associated with additional sequences and/or structures; an isolated nucleic acid that encodation molecule or construct; expression cassette or vector that contains the isolated nucleic acid, operatively linked to a promoter; virus or host cell comprising at least one cassette or vector of Anglaysés, an organism containing at least one host cell of Anglaysé; a containing the recognition molecule and construct; and a kit containing the recognition molecule and/or construct; and a kit containing them, the nucleic acid encoding them, and derived viruses, containing them, the nucleic acid encoding them, and derived viruses, containing them, the nucleic acid encoding them, and derived viruses, containing of tumours and/or metastases, specifically where MUCI positive, particularly carcinoma of breast, colon, stomach, pancreas, ovary, liver or kidney calls; (gastro)intestinal or lung cancers and multiple myeloma. The recognition molecules show little or no binding to the infinite myeloma of tumours, even at an early stage (carcinoma in efficient detection of tumours, even at an early stage carcinoma in situh, and can differentiate between tumours and benign diseases. This execution and efficient expressents one of the invention. recognition molecules of the invention 8888888888888888888888888888888888

Sequence 16 AA;

Gaps ö Length 16; 96.3%; Score 78; DB 8; Length 16; 93.8%; Pred. No. 1.6e-06; ive 1; Mismatches 0; Indel8 Local Similarity 93.8 nes 15; Conservative Query Match Matches

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1 RSSQSIVHSNGNTYLQ 16 RSSOSIVHSNGNTYLE 16

8 셤 RESULT 14 ADS87339

ADS87339 standard; peptide; 16 AA.

ADS87339;

(first entry) 18-NOV-2004 Humanised antibody MN3 light chain variable region CDR1.

cystic fibrosis, granulocyte related disorder, atherosclerosis, infarction, cancer; ischemic lesion, complementarity determining region. cytostatic; vasotropic; antimicrobial; antiinflammatory; antipyret: antitatherosclercitic; cardiant; monoclonal antibody; NCA90; NCA95; chimeric antibody; humanized antibody; inflammation; appendicitis; inflammatory bowel disease; pelvic inflammatory disease; fever;

Ното варіелв

gb Mus

Chimeric.

WO2004029093-A2.

08-APR-2004.

30-SEP-2003; 2003WO-GB004229.

30-SEP-2002; 2002US-0414341P.

(IMMU-) IMMUNOMEDICS INC. (MCCA/) MCCALL J D.

Leung S; Goldenberg DM, Hansen H,

WPI; 2004-329873/30.

Monoclonal anti-granulocyte antibody that binds NCA90 and NCA95 antigens, useful for treating malignancy, inflammation, atherosclerosis, infarction, or other granulocyte related disorders.

Claim 4; Page 105; 134pp; English

The invention relates to a monoclonal antibody (Mab) (I) or its fragment that binds NCA90 or NCA95, where when the Mab or its fragment binds NCA90 the Mab or its fragment is chimeric, partially humanized or fully humanized and where when the Mab or its fragment binds NCA95 the Mab or its fragment is either fully humanized or chimeric, partially humanized or fully humanized BW 250/183. (I) is useful for treating, detecting or imaging sizes, palvic inflammation resulting from appendicitis, inflammatory bowel disease, pelvic inflammatory disease, fever and cystic fibrosis and treating granulocyte related disorders, atherosclerosis and infarction. (I) is useful for detecting or treating cancer or ischemic lesion. This sequence corresponds to the complementarity determining region I (CDRI) of the light chain of the antibody of the invention.

Sequence 16 AA;

Score 78; DB 8; Length 16; Pred. No. 1.6e-06; 1; Mismatches 0; Indels 96.3%; Query Match
Best Local Similarity 93...
Best Local Similarity 15... 셤 8

Search completed: December 30, 2005, 14:19:57 Job time : 139.5 secs

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Gaps ö

RESULT 15

AAU70349 standard; peptide; 16 AA

AAU70349;

(first entry) 14-FEB-2002 Mouse Kappa II light chain CDR1.

Immunoglobulin; antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

Mus musculus.

WO200183806-A1

08-NOV-2001.

02-MAY-2001; 2001WO-US014349.

02-MAY-2000; 2000US-00563222.

(EPIC-) EPICYTE PHARM INC.

Hein MB; Hiatt AC, WPI; 2002-055482/07

Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynuclectides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array.

Disclosure, Page 14; 129pp; English.

The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polymuclectides encoding different immunoglobulin binding protein (19BP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an 19BP that binds to a ligand, and transformed plant cells are selected, and preparing an 19BP array in plant cells. At least one peptide sequence has at least 75\$ sequence identity to a framework region (FR) of a native 19M, 19G, 19A, 19D, 19E, 19Y, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably AAU70349

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AAU7

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                      eukaryotic
chain binding protein (CHBP) array in eukaryotic cells especially
                  plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryor cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening asseys of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                           93.8%; Score 76; DB 5; Length 16; 87.5%; Pred. No. 3.6e-06; ive 2; Mismatches 0; Indels
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                                                                                                                                                                           Query Match 93.8
Best Local Similarity 87.5
Matches 14, Conservative
                                                                                                                                            Sequence 16 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 30, 2005, 14:07:14; Search time 22.5 Seconds (without alignments) 68.421 Million cell updates/sec Run on:

US-10-735-916A-2 81 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 RSSQSIVHSNGNTYLQ 16 Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

250 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 16 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	site-specific meth	T-cell surface gly	alpha-conotoxin MI	ribosomal protein	candidapepsin (EC	T-cell receptor be	hypothetical prote	conserved hypothet	inulin fructotrans	a]	protein P8 - curle		orf 61.1 - phage T	redoxyendonuclease		photosystem I prot	leu operon leader	rRNA N-glycosidase	T cell receptor al	receptor		25K kidney and gal	Ā	casein kinase II (protein-tyrosine-p	chitinase (EC 3.2.		T-cell-receptor be	T-cell receptor be
ΙD	A36285	B45895	A59046	G24304	A44352	H49039	842237	D89854	PD0002	851610	E28027	C39509	G45681	S23184	A49226	809732	A36889	801669	PH1778	G49039	PH0777	E58501	MTDFBS	C45133	C45143	F44908	910	9	G53284
DB	2	~	~	7	~	~	7	N	~	~	N	~	~	~	7	7	7	~	~	~	N	~	н	7	~	~	~	~	N
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	34	25	2	2.	22	2	5	5	22	2	ĕ	ä	ä	ä	ä	ä	ä	ĩ	∺	<u></u>	7	ĩ	H	H	H	H	H	H	H
Score	28	21	18	18	18	18	18	18	18	17	16.5	16	16	16	16	16	16	15	15	15	15	15	14	14	14	14	14	14	14
Result No.	-	8	e	4	2	y	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig H chain V-D-J r beta-crystallin A4 carbamcyl-phosphat 7K protein - Bsche dihydrolipoamide S protein kinase C i T-cell receptor ga casein kinase II (proteoglycan assoc crystal protein, 7 T cell receptor al	r-cell receptor at T-cell receptor be T-cell receptor be T-cell receptor be Ig H chain V-D-J r
PH1622 833589 869361 84820 800123 810807 A36300 A45133 C58503 B24099	141299 PH0137 E49255 E53284 PH1588
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	100 100 100 100
177.33 177.33 177.33 176.00 176.00 176.00	16.0 16.0 16.0
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## ALIGNMENTS

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agment) War-1996	e binding	0; Gaps
(£r	nin nin	0,
RESULT 1 A36285 site-specific methyltransferase (BC 2.1.1) - Escherichia coli (fragment) C;Species: Escherichia coli C:Apecies: Bscherichia coli	C;Date: 18-Jenn-1991 #Bequence_revision is-con-1991 #text_ciansge_zi_nai_200 C;Accession: A36285 R;Reich, N.O.; Bverett, E.A. J. Biol. Chem. 265, 8929-8934, 1990 A;Title: Identification of peptides involved in S-adenosylmethionine binding in the A;Reterence number: A36285, MUID:90256827; PMID:2341412 A;Accession: A36285 A;Status: preliminary A;Molecule type: protein	A;Kestudes: 1-16 cKE1> A;Cross-references: UNIPARC:UPI000017AA66 C;Keywords: methyltransferase C;Keywords: methyltransferase Query Match Best Local Similarity 30.8%; Pred. No. 1.8e+02; Matches 4; Conservative 5; Mismatches 4; Indels 0
	14.	

Eco

3 SQSIVHSNGNTYL 15 2 TEAXIDSNGNXII 14 ઠ g

RESULT 2

T-cell surface glycoprotein CD28 short form - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Feb-1994
C;Accession: B45895
C;Accession: B45895
A;Title: The genomic organization of the CD28 gene. Implications for the regulation of A;Accession: B45895
A;Accession: B45895
A;Status: preliminary
A;Reterence number: A45895; MUID:90293482; PMID:2162892
A;Status: preliminary
A;Reterences: UNIPARC:UPI000017C3C5; GB:M37813
C;Keywords: glycoprotein

Gaps ö Query Match
25.9%; Score 21; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 2.7e+03;
Matches 3; Conservative 4; Mismatches 1; Indels

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|:|::|: 9 KSNGTIH 16 1 RSSQSIVH 8 ઠે g

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T-cell receptor beta chain V-D-J-C region (V beta 5, J beta 1.4) - human (fragment) C; Species: Homo sapiens (man) C; Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997 C; Accession: H49039 R; Rosenberg, W.M.; Moss, P.A.; Bell, J.I. Bur. J. Immunol. 22, 541-549, 1992 A; A; Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using A; Reference number: A49039; MUID:92164737; PMID:1311263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S42237
R;Noguchi, N.; Aoki, T.; Sasatsu, M.; Kono, M.; Shishido, K.; Ando, T.
R;Noguchi, N.; Aoki, T.; Sasatsu, M.; Kono, M.; Shishido, K.; Ando, T.
R;Noguchi, N.; Aoki, T.; Sasatsu, M.; Rono, M.; Shishido, K.; Ando, T.
R;Noguchi, N.; Aoki, T.; Sasatsu, M.; Sasatsu, M.; Sasatsu, Sasatsu
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C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Accession: D89854
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc R; Kuroda, M.; Ohta, T.; Robayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramstou, K.
Lancet 357, 1225-1240, 2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gross-references: UNIPARC:UPI000017C3B7
A;Note: sequence extracted from NCBI backbone (NCBIP:90720)
C;Keywords: T-cell receptor
Pred. No. 8.7e+03;
1; Mismatches 5;
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60.0%; Pred. No. 8.7e+03;
tive 1; Mismatches 1;
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25.0%;
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Best Local Similarity 60.0
Matches 3; Conservative
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5 TGSSVLLDSGTT 16
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Best Local Similarity
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                                                                                                                     8
                                                                  Alpha-conotoxin MII - cone shell (Conus magus)
C;Species: Conus magus (magus cone)
C;Species: Conus magus (magus cone)
C;Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: A59046
B;Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.
J. Biol. Chem. 271, 7322-7328, 1996
A;Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptor
A;Reference number: A59046; MUID:96205934; PMID:8631783
A;Accession: A59046
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <CAR>
A;Residues: UNIPROT:P56636; UNIPARC:UPI00001287CA
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot
F;1-16/Product: alpha-conotoxin MII #status experimental <AMT>
F;2-8,3-16/Disulfide bonds: #status experimental
F;16/Modified site: amidated carboxyl end (Cys) #status experimental
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ribosomal protein H [validated] - Haloarcula marismortui (fragment)
cibosomal protein H [validated] - Haloarcula marismortui
cibosomal protein H [validated] - Haloarcula marismortui
cibosomal protein G24304
g. May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
ciAccession: G24304
g. Rishoham, M.; Dilk, J.; Reinhardt, R.; Wittmann-Liebold, B.
FEBS Lett. 204, 323-330, 1986
A;Title: Purification and characterization of ribosomal proteins from the 30 S subunit of A;Accession: G24304
A;Accession: G24304
A;Molecule type: protein
A;Residues: 1-16 <SHO>
A;Cross-references: UNIPARC:UPI000017AEA2
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 8.7e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.2%; Score 18; DB 2; Length 16; 100.0%; Pred. No. 8.7e+03; tive 0; Mismatches 0; Indels
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Similarity 75.0%;
3; Conservative
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Best Local Similarity 100.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: E28027
R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Matl. Acad. Sci. US.A. 84, 4806-4810, 1987
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid A;Reference number: A94167
A;Accession: E28027
A;Accession: E28027
A;Abolecule type: protein
A;Residues: 1-16 <ABU>
A;Coss-references: UNIPROT:Q7MIV7; UNIPARC:UPI000017B09F
A;Coss-references: Uniparciond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C39509

mannose-specific lectin B-SJA-II chain b-1, bark - Japanese pagoda tree (fragment)

C;Species Sophora japonica (Japanese pagoda tree)

C;Species 30-Dec-1991 #Bequence_revision 30-Dec-1991 #text_change 31-Dec-2004

C;Date: 31-Dec-1991 #Bequence 1:; Seno, N.

J; Biol. Chem. 266, 3146-3153, 1991

A;Title: A novel mannose-specific and sugar specifically aggregatable lectin from the b

A;Title: A novel mannose-specific and sugar specifically aggregatable lectin from the b

A;Reference number: A39509; MUID:91131618; PMID:1993686

A;Status: preliminary
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G45681

Circles: phage T6 (fragment)

Circles: phage T6 (fragment)

Circles: phage T6

Cipate: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

Circles: phage T6

Cipate: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

Circles: phage T6

Circles:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-16 <UEN>
A;Cross-references: UNIPROT:P93537; UNIPARC:UPI000017B075
C;Superfamily: lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.5; DB 2;
Pred. No. 1.6e+04;
3; Mismatches 1;
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Pred. No. 1.9e+04;
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1; Conservative
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Best Local Similarity 50.0%;
Matches 5; Conservative
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nes 4; Conservative
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7 IVANDGSKTY 16
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Best Local Similarity
Matches 1; Conserv
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Best Local
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Cippedies: Lycopersion esculentum (tomato)
Cippedies: Lycopersion esculentum
Cippedies: Lycopersion esculentum
Cippedies: Lycopersion esculentum
Cippedies: Lycopersion: S51610
Rikrolkiewicz, S.; Saenger, H.L.; Niesbach-Kloesgen, U.
Rykrolkiewicz, S.; Saenger, H.L.; Niesbach-Kloesgen, U.
Rytitle: Structural and functional characterisation of the signal recognition particle-s
A;Reference number: S51597; MUID:95107255; PMID:7808407
B;Reterence number: S51610
A;Recession: S51610
A;Recession: S51610
A;Recession: S51610
A;Residues: 1-16 < KRO>
                                                         A; Accession: D89854
A; Status: preliminary
A; Molecule Cype: DNA
A; Residues: 1-16 < KUUR>
A; Cross-references: UNIPROT: Q99VH9; UNIPARC: UPI00000CA988; GB: BA000018; PID: g13700694;
A; Experimental source: strain N315
C; Genetics:
A; Gene: SAS021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bacillus sp.
C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Accession: Ploudous Pochem. 62, 628-631, 1998
A;Title: Purification and properties of inulin fructotransferase (DPA III-producing) fareference number: PD0002
A;Reference number: PD0002
A;Residues: 1-16 *CANA.
A;Residues: 1-16 *CANA.
A;Cross-references: UNIPROT:Q7M0Z5; UNIPARC:UP1000017CD57
C;Keywords: glycosyltransferase; hexosyltransferase
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                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 2; Length 10, Pred. No. 8.78+03;
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C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
                                      A; Reference number: A89758; MUID: 21311952; PMID: 11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI000017B08B; EMBL:Z34527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.2%;
Best Local Similarity 42.9%;
Matches 6; Conservative
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Best Local Similarity 100.0
Matches 3; Conservative
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Length 16;

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RESULT 15
A49226
major outer membrane protein - Haemophilus somnus (fragment)
C;Species: Haemophilus somnus
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49226
R;Tagawa, Y; Ishikawa, H.; Yuasa, N.
Infect. Immun. 61, 91-96, 1993
A;Title: Purification and partial characterization of the major outer membrane protein c
A;Reference number: A49226; MUID:93114910; PMID:8418069
A;Contents: 8042
A;Accession: A49226
A;Status: preliminary
A;Accession: A49226
A;Status: preliminary
A;Accession: C;Accession: A49226
A;Conserver expre: protein
A;Residues: 1-16 c;TAG>
A;Cross-references: UNIPROT:Q9R5E9; UNIPARC:UPI00000BE2A7
A;Note: sequence extracted from NCBI backbone (NCBIP:121595)
redoxyendonuclease (EC 4.2.99.-) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S23184
R;Huq, I.; Haukanes, B.I.; Helland, D.E.
Bur. J. Biochem. 206, 331-839, 1992
A;Title: Purification to homogeneity and characterization of a redoxyendonuclease from CA;Reference number: S23184; MUID:92299012; PMID:1376689
A;Accession: S23184
A;Accession: S23184
A;Accession: S23184
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A;Accession: S23184
A;Accession: Locken.
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19.8%; Score 16; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 2; Indels
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                                                                     December 30, 2005, 14:06:48; Search time 141.5 Seconds (without alignments) 79.777 Million cell updates/sec
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008mj12
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0049g00
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008m8b7
007m12s
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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07Y033 MAIZE
09MAT2 HORSE
09LAP2_ENTFC
089560 HHV8
04XP0 PLABE
08M8B6_PINTA
08M8B7 PINEL
09S8Y6_LUPAR
09S8Y6_LUPAR
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Q7M0Z5_BACSP
Q6GB29_STAAS
Q6GI19_STAAR
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vulpes vulp
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                                              Q6q142 |
Q7jfv3 |
Q9tr88 |
Q9tsk2
     Q7m1v7
                  P70034 EMENI
0750C4 NEUCR
086UF7 HUMAN
09UC75 HUMAN
05C009 SCHUA
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06Q142 BOVIN
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## ALIGNMENTS

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OBNO355 SPRIM PRELIMINARY; PRT; 16 AA.
OBNO355.
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytcohrome c oxidase polypeptide VIIa-heart (Fragment).
Nycticebus sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirhini; Loridae;
                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
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MUCLEOTIDE SEQUENCE.

MUCLEOTIDE SEQUENCE.

MEDILINE=99268136; PubMed=10335655;

Schmidt T.R., Goodman M., Grossman L.I.;

Molacular evolution of the COX7A gene family in primates.";

Mol. Biol. Evol. 16:619-656(1999).

EMBL; AF127786; AAF72744.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.6%; Score 24; DB 2; Length 16; 66.7%; Pred. No. 4.18+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88B1DFEA0AF61AE5 CRC64;
                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                          Created)
                                                           PRT;
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                                                                                                                01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, Elastase 2a (Fragment).
                                                     QBMUV9 SCHMA PRELIMINARY;
Q8MUV9;
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NCBI_TaxID=108082;
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NGRTFL 8
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01-03-098 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Minor capsid protein (Fragment)
Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus)
Viruses; dsDAM viruses, no RNA stage; Herpesviridae;
Gammaharpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Detection of human herpesvirus 8 DNA sequences in tissues and bodily fluids.";
                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecium (Streptococcus faecium).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1) TREATURE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MEDLINE=20307504; PubMed=10846225;
Dahl K.H., Lundblad E.W., Rokenes T.P., Olsvik O., Sundsfjord A.;
"Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin-
resistant enterococci and characterization of two novel insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]

NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

MEDLINE=99034644; PubMed=9815212; DOI=10.1086/314514;

Labuca J.R., Love J.L., Abbott L.Z., Dube S., Freidman-Kien A.E.,

Poiesz B.J.;
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Pred. No. 2.1e+04;
2; Mismatches 1; Indels
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44.4%; Pred. No. 2.1e+04;
tive 2; Mismatches 3; Indels
Indels
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                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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EMBL, AF042149; AAC25060.1; -; Genomic_DNA.
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3; Conservative
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PubMed=15377761; DOI=10.1105/tpc.104.025700;
Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Mammalia; Butheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
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Jubsection of maize kernel composition and starch production by candidate gene association.";
Plant Cell 16:2719-2733(2004).
EMBL; AY290277; AAP44840.1; -; Genomic_DNA.
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Pred. No. 2.1e+04;
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Pred. No. 1.4e+04;
2; Mismatches 1; Indels
                                                                        Score 22; DB 2; Length 16;
Pred. No. 9.3e+03;
3; Mismatches 2; Indels
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ARP292647; ARM544951; -; MENA.
InterPro; IRR000034; Laminin B.
ProDom; PD003031; Laminin B.
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                          E586241C602C15E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequen
01-OCT-2003 (TrEMBLrel. 25, Last annotain
starch branching enzyme IIb (Fragment).
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Equus caballus (Horse).
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  16
1822 MW;
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25.9%;
Best Local Similarity 50.0%;
Matches 3; Conservative
                                                                      h 27.2%;
Similarity 44.4%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBMJT2_HORSE PRELIMINARY;
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RVSQALIRS 13
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Best Local Similarity
16
16 AA;
                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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1 HASSNT 6
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QSS8Y6_LUPAR PRELIMINARY;
Q9S8Y6;
                                 01-OCT-2002 (TrEMBLrel. 22
01-OCT-2002 (TrEMBLrel. 22
01-JUN-2003 (TrEMBLrel. 24
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 5/...
Local 4; Conservative
          Q8M8B7_PINEL PRELIMINARY;
O8M8B7;
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Q8M8B7
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                                                                                                                                            NUCLEOTIDE SEQUENCE.
Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
Hall N., Karras M., Raine J.D., Carlton J.M., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Blidwell S.L., Rajandraem M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
"A comprehensive survey of the Plasmodium life cycle by genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Wararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus, Pinus.
NCBI_TaxID=3352;
                                                                                                                                                                                                                                                                       -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                        Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5821;
                                                                                                                                                                                                                                                                                                                                                                      h Similarity 33.3%; Score 19; DB 2; Length 16; Similarity 33.3%; Pred. No. 3.1e+04; 4; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 2; Length 16;
Pred. No. 3.1e+04;
0; Mismatches 3; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ATEA (ACT-2501) to The EMBL; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                 13-5EP-2005 (TYEMBLrel. 31, Created)
13-5EP-2005 (TYEMBLrel. 31, Last sequence update)
13-SEP-2005 (TYEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PB403344.00.0;
                                                                                                                                                                                                                                                                                                preliminary data.
; CAAI01005266; CAI02827.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 AA.
            16 AA
                                                                                                                                                                                                                                                transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH dehydrogenase subunit 3 (Fragment)
              PRT;
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Q8M8B6;
         Q4YGPO_PLABE PRELIMINARY;
Q4YGPO;
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
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Matches 4; Conserv
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Bukaryota, Viridiplantae, Strepophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabbles, Fabbaceae, Papilionoideae, Genisteae, Lupinus.
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MEDLINE=92344803; PubMed=1368361; DOI=10.1016/0031-9422(92)83098-J;
Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
Farnden K.J.;
                                                                                                                                            Pinus elliottii (Slash pine).
Mitochondrion.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
NCBI_TAXID=42064;
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Pred. No. 3.1e+04;
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Pred. No. 3.1e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
Chen J., Tauer C., Huang Y.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF426451, AAM21488.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytochemietry 31:1519-1527(1992).
GO; GO:0004067; F:asparaginase activity; IEA.
SEQUENCE 16 AA; 1499 MW; 90136390E527BF0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;
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QBMBBS;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last amortation update)
NADH dehydrogenase subunit 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
L-apparaginase isoform A (EC 3.5.1.1) (Fragment).
                                                                  Last sequence update)
Last annotation update)
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16 AA
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                                                                                                                   NADH dehydrogenase subunit 3 (Fragment).
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57.1%;
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Local Similarity 66.7%;
les 4; Conservative
                                              (TrEMBLrel. 22, (TrEMBLrel. 22,
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ID Q8I
AC Q8I
DT 01
DT 01
DE NA
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(Pyrophosphate phospho-hydrolase) (PPase) (Fragment)
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Immunodeficiency virus type 1, viral sample FLPBR4C (Florida patient B), partial env cds, V4 region. (Fragment)
Human immunodeficiency virus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
NCBI_TaxID=71631;
                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDIINE=92271245; PubMed=1589796;
OL C.-Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
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90-MAY-2000 (Rel. 39, Last sequence update)
01-FEB-2005 (Rel. 46, Last amocation update)
Manganese-dependent inorganic pyrophosphatase (BC 3.6.1.1)
                                                                                                                                                                  Score 19; DB 2; Length 16;
Pred. No. 3.1e+04;
0; Mismatches 3; Indels
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Pred. No. 3.1e+04;
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                                                                      NUCLEOTIDE SEQUENCE.
Chen J., Tauer C., Huang Y.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF426454; AAM21492.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.
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Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases
EMBL; M92120; AAA44490.1; -; Genomic_RNA.
                                                                                                                                     NON TER 1 1 SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AA; 1745 MW; 72260DC174FF6428 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
                                                                                                                                                                                                                                                                                        PRT;
            .nus echinata (Shortleaf pine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.5%;
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Q78377;
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Best Local Similarity 57.1.
4; Conservative
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                                                                                                                              tochondrion.
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SEQUENCE
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PPAC BACME
ID PPAC BACM
AC PS6948;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                           Young T.W., Kuhn N.J., Wadeson A., Ward S., Burges D., Cooke G.D.;
"Bacillus subtilis ORF yyb0 encodes a manganese-dependent inorganic pyrophosphatease with distinctive properties: the first of a new class of soluble pyrophosphatase?";
Microbiology 144:2563-2571(1998).
-!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
-!- COPACTOR: Binds 2 manganese ions per subunit (By similarity).
-!- SINCELLULAR LOCATION: Oytoplasmic (By similarity).
-!- SINLARITY: Belongs to the PPase class C family.
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Direct protein sequencing; Hydrolase; Manganese; Metal-binding
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Pred. No. 4.7e+04;
1; Mismatches 2; Indels
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3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manganese 1 (By similarity)
Manganese 1 (By similarity)
Manganese 2 (By similarity)
Name=ppaC;
Bactilus megaterium.
Bacteris, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                          PROTEIN SEQUENCE.
MEDLINE=98455825; PubMed=9782505;
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50.0%;
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30.8%;
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Best Local Similarity 30.8
Matches 4; Conservative
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DESTITE STREET, SERVICE PRESIDENTIARY; PRT; 16 AA.

CORAJSE PLAYO

DE OTRAZES PLAYO PRELIMINARY; PRT; 16 AA.

CORAJSE PLAYO (TERMELrel. 26, Created)

DT 01-WAR-2004 (TERMELrel. 26, Last sequence update)

DT 01-WAR-2004 (TERMELrel. 26, Last sequence update)

DT 01-WAR-2004 (TERMELrel. 26, Last sequence update)

DT 01-WAR-2004 (TERMELrel. 26, Last annotation update)

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Search completed: December 30, 2005, 14:24:46 Job time : 144.5 secs

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Best Local Similarity 100.
Matches 16; Conservative
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Sequence 32, Appl
Sequence 53, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 56, Appl
Sequence 119, App
Sequence 119, App
Sequence 118, App
Sequence 118, App
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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                                                                December 30, 2005, 14:25:05; Search time 110 Seconds (without alignments) 60.775 Million cell updates/sec
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Sequence 110,
Sequence 146,
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Sequence 32
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Sequence 6
Sequence 1
Sequence 1
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'cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-947-839-30
US-09-947-839-30
US-09-95-529-32
US-10-470-045-53
US-10-70-697-1
US-09-563-22-29
US-10-810-811A-56
US-09-955-529-119
US-09-955-529-119
US-09-955-529-118
US-09-955-529-118
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US-10-627-629-20
US-10-762-629-20
US-10-762-629-20
US-10-762-629-20
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                                                                                                                                                                                             1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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seq length: 16
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16, Appl
4, Appli
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US-10-946-910
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US-10-946-9113
US-10-948-105-8
US-10-909-313
US-10-909-313
US-10-909-5113
US-09-995-529-113
US-09-995-529-113
US-09-995-529-113
US-10-706-852-16
US-10-706-852-16
US-10-877-774-101
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APPLICANT: CORTSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HECK, Alain
APPLICANT: Length 16; 100.0%; Score 81; DB 5; I 100.0%; Pred. No. 9.1e-07; :ive 0; Mismatches 0; FILE REFERENCE: 101/73-183

FILE REFERENCE: 101/73-183

CURRENT FILING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: FR 03/08 538

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2002-01-18

SRICH FILING DATE: 2002-01-18

FRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

FRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

FRIOR FILING DATE: 2002-01-18 ORGANISM: Mus musculus US-10-735-916A-2

Indels Sequence 32, Application US/09995529; Publication No. US20030099655A1; GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying 1 RSSQSIVHSNGNTYLO 16 RSSQSIVHSNGNTYLQ 16 US-09-995-529-32

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Gaps

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MEDIUM TYER: Floppy disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839

FILING DATE: 6-Sep-2001

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/976,288

FILING DATE: CURROWN-

APPLICATION NUMBER: 07/977,696

FILING DATE: NO. US20030138428Alember 16, 1992

ATORNEY/AGENT INFORMATION:

NAME: Viviana Amzel Ph.D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: 30,930

TELEPHONE: (213) 6.022-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ceriani Dr., Roberto L.
Peterson Dr., Jerry A.
Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
Carcinoma Specificity, and Kit and
Diagnostic Vaccination and
Therapeutic Methods
                                                                                                                                                                                                                                                                                            96.3%; Score 78; DB 3; Length 16; 93.8%; Pred. No. 3e-06; tive 1; Mismatches 0; Indels
TITLE OF INVENTION: Humanized Collagen Antibodies and TITLE OF INVENTION: Related Methods FILE REFERENCE: P-IX 4976 CURRENT APPLICATION NUMBER: US/09/995,529 CURRENT FILING DATE: 2001-11-26 NUMBER OF SEQ ID NOS: 358 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSER: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: do Couto Dr., Fernando J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 16 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TYPE: Dinear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-839-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30, Application US/09947839 Publication No. US20030138428A1 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                             ; ORGANISM: Mus musculus US-09-995-529-32
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US-09-947-839-30
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Publication No. US20040053865A1

GENERAL INFORMATION:
APPLICANT: HARY, MAXY KATE
APPLICANT: WILSON, JULIE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
FILE REPERENCE: ARMY 166
CURRENT APPLICATION NUMBER: US/10/226, 795
CURRENT FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic light;
OTHER INFORMATION: chain of Mab EGF6D8-1-2 amino acid sequence
US-10-226-795-28
                                                                 Gaps
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APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
ITTLE OF INVENTION: Humanized Collagen Antibodies and
ITTLE OF INVENTION: Related Methods
ITTLE OF INVENTION: Related Methods
CURRENT APPLICATION WINGER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
                       ; DB 3;
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93.8%; Pred. No. 3e-06;
cive 1; Mismatches
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                                                               1; Mismatches
                       Score 78;
Pred. No.
                                                                                                                                                                                                                                          ; Sequence 32, Application US/09995529; Publication No. US20040091482A9; GENERAL INFORMATION:
                       96.3%;
93.8%;
                                                                                                                          1 RSSQSIVHSNGNTYLE 16
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Query Match
Best Local Similarity 93.00,
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Best Local Similarity 93.8
Matches 15; Conservative
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SEQ ID NO 28
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t TYPE: PRT
CRGANISM: Mus musculus
US-09-995-529-32
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US-10-226-795-28
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SEQ ID NO 29
LENGTH: 16
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JAPPLICANT: QU, ZERNCXING
JAPPLICANT: HANSEN, HANS
JAPPLICANT: HANSEN, HANS
JAPPLICANT: GOLDENBERG, DAVID M.
JAPPLICANT: GOLDENBERG, DAVID M.
JITLE OF INVENTION: CHIMERIC, HUMAN AND HUMANIZED ANTI-CSAP MONOCLONAL
JITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 018733/1064
CURRENT APPLICATION NUMBER: US/10/116,116
PRIOR APPLICATION NUMBER: US/10/116,116
PRIOR APPLICATION NUMBER: 09/823,746
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-10-14
PRIOR PILING DATE: 1999-10-14
PRIOR PILING DATE: 1999-10-14
PRIOR PILING DATE: 1999-10-14
PRIOR PILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.3%; Score 78; DB 4; Length 16; Best Local Similarity 93.8%; Pred. No. 3e-06; Matches 15; Conservative 1; Mismatches 0; Indels
         Sequence 53, Application US/10470045
Publication No. US20040146505A1
GENERAL INFORMATION:
APPLICANT: Scancell Limited
APPLICANT: Barsons, Tina
APPLICANT: Parsons, Tina
APPLICANT: Parsons, Tina
CURRENT APPLICATION: Substances
FILE REFERENCE: P32181WO/NJL
CURRENT APPLICATION NUMBER: US/10/470,045
CURRENT FILING DATE: 2003-07-24
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 53
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/11070697
Publication No. US20050169926A1
GENERAL INFORMATION:
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US-10-470-045-53
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Sequence 29, Application US/10783950

Sequence 29, Application US/10783950

Publication No. US20040199945A1

GENERAL INFORMATION:
APPLICANT: BPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
TITLE OF INVENTION: UMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
CURRENT APPLICATION NUMBER: US/10/783,950

CURRENT APPLICATION NUMBER: US/09/563,222
PRIOR PELING DATE: 2004-02-19
PRIOR FILING DATE: 2000-05-02
PRIOR PELING DATE: 2001-05-02
PRIOR PRILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 182

SOFTWARE PATEUTIN Ver. 2.1
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Sequence 56, Application US/10810881A

Sequence 56, Application US/10810881A

Publication No. US20050129695A1

GENERAL INFORMATION:

APPLICANT: Mercken, Marc; Benson, Jacqueline M.

TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES

TILE REPERENCE: CENSO21 NP

CURRENT APPLICATION NUMBER: US/10/810,881A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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AGE-09-563-222-29
; Sequence 29, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hister, Andrew
; APPLICANT: Hister, Andrew
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: BUKKRYOTIC CELLS
; TITLE OF INVENTION: BUKKRYOTIC CELLS
; TURENT APPLICATION UNBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FRASESQ for Windows Version 4.0
; SEQ ID NO 29
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87.5%; Pred. No. 6.5e-06;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 16;
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Pred. No. 6.5e-06;
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
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CORGANISM: Mus musculus
US-10-783-950-29
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; ORGANISM: Mus musculus
US-09-563-222-29
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Gaps
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Sequence 8, Application US/09518737

Publication No. US20030008321A1

GENERAL INFORMATION:

APPLICANT: FUKUI, YASUHISA

APPLICANT: SHIRAI, RYUICHI

APPLICANT: SHIRAI, RYUICHI

TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE

TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE

TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE

FILE REFERENCE: 1955/49618

CURRENT RPLICATION NUMBER: US/09/518,737

CURRENT FILING DATE: 2000-03-03

PRIOR APPLICATION NUMBER: JP 1999-250209

SPRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                   Length 16;
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Sequence 118, Application US/0995529

Publication No. US2003009655A1

GENERAL INFORMATION:

APPLICANT: Watkins, Jeffry D.

APPLICANT: Tang, Ying

TITLE OF INVENTION: Related Methods

TITLE OF INVENTION: Related Methods

FILE REPERBENCE: PLX 4976

CURRENT APPLICATION NUMBER: US/09/995,529

CURRENT FILING DATE: 201-11-26

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastERG for Windows Version 4.0

FINGENTIAL OF 118
                                                                                                                                                                                                                                                                                                 Query Match
92.6%; Score 75; DB 3; I
Best Local Similarity 87.5%; Pred. No. 9.5e-06;
Matches 14; Conservative 2; Mismatches 0;
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                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-119
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 119
LENGTH: 16
                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     1 RSSQSIVHSNGNTYLQ 16
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ORGANISM: Artificial Sequence
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Best Local Similarity 93.33
Matches 14; Conservative
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'Sequence 119, Application US/09995529
'Sequence 119, Application US/09995529
'Sequence 119, Application US/09995529
'Sequence 119, Application No. US20030099655A1
'GENERAL INFORMATION:
'APPLICANT: Watkins, Jeffry D.
'APPLICANT: Tang, Ying
'TITLE OF INVENTION: Humanized Collagen Antibodies and TITLE OF INVENTION: Humanized Collagen Antibodies and TITLE OF INVENTION: Related Methods
'FILE REFERENCE: PIX 4976
'CURRENT APPLICATION NUMBER: US/09/995,529
'CURRENT FILING DATE: 2001-11-26
'SOFTWARE: PASSEQ for Windows Version 4.0
'SEQ ID NOS :358
'LENGTH: 16
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Sequence 119, Application US/09995529

Publication No. US20040091482A9

GENERAL INFORMATION:

APPLICANT: Watkins, Ueffry D.

APPLICANT: Tang, Ying

TITLE OF INVENTION: Humanized Collagen Antibodies and

TITLE OF INVENTION: Related Methods

FILE REFERENCE: P-IX 4976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: synthetic antibody mutation US-09-995-529-119
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 60/458,474
PRIOR FILING DATE: 2003-28
PRIOR FILING DATE: 2003-08
PRIOR PILING DATE: 2003-03-28
PRIOR PILING DATE: 2003-03-28
PRIOR PILING DATE: 2003-03-28
PRIOR PILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin version 3.3
LENGTH: 16
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSSQSIVHSNGNTYLQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSSOSIVHSNGNTYLO 16
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Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION; (1). (16)
; OTHER INFORMATION: LC CDR1
US-10-810-881A-56
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                   Query Match
91.4%; Score 74; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 91.4%; Score 74; DB 3; Length 16; Best Local Similarity 87.5%; Pred. No. 1.4e-05; Matches 14; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-995-529-118
is Application US/09995529
sequence 118, Application US/09995529
sequence 118, Application US/09995529
sequence 118, Application No. US20040091482A9
sequence 118, Application No. US20040091482A9
sequence 118, Application No. US-09-095-529
sequence 11 TILE OF INVENTION: Humanized Collagen Antibodies and TILLE OF INVENTION WUMBER: US/09/995,529
cURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
software: FastSEQ for Windows Version 4.0
seq ID NO 118
LENGTH: 16
TYPE: PRT
sequence reaction Artificial Sequence reaction Artificial Sequence reaction US-09-995-529-118
// FEATURE:
// OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-118
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Job time : 111 secs
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Sequence 12, Appli Sequence 3, Appli Sequence 4, Appli Sequence 10, Appli Sequence 11, Appl Sequence 12, Appl Sequence 2728, Appl Sequence 2728, Appl Sequence 312, Appl Sequence 44, Appli Sequence 44, Appli Sequence 44, Appli

US-11-090-908-5
US-11-060-005-34
US-11-089-764-4
US-11-089-764-4
US-11-089-764-10
US-11-089-764-11
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US-11-089-764-12
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US-11-089-764-11
US-11-089-944
US-11-060-939-34
US-11-060-939-34
US-11-069-939-34

Sequence Sequence Sequence

8935, Ap

Sequence 8 Sequence 9 Sequence 1

Seguence 18, Appī Seguence 281, App

ALIGNMENTS

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Query Match
100.0%; Score 81; DB 7; I
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 16; Conservative 0; Mismatches 0;
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US-11-125-837-13
; Sequence 13, Application US/11125837
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Sequence 3, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 18, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 5, Appli
Sequence 50, Appli
Sequence 20, Appli
Sequence 10, Appli
Sequence 126, Appli
Sequence 126, Appli
Sequence 126, Appli
Sequence 126, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 6, Appli
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                                                                                December 30, 2005, 14:25:45; Search time 8 Seconds (without alignments)
14.978 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USOJ NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USOJ NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USOJ NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USOJ NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USOJ NEW PUB.pep:*
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-102-33-13
US-10-932-334-4
US-11-102-743-3
US-11-105-743-3
US-11-005-743-13
US-11-005-793-18
US-10-99-866-59
US-11-055-163-20
US-11-010-748A-77
US-11-010-748A-128
US-11-010-748A-138
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US-10-919-492-10
US-11-052-168A-32
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                              57103 seqs, 7488799 residues
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                        1 RSSQSIVHSNGNTYLQ 16
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Match Length
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Maximum DB seq length: 16
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                                                                                                                                                                                Scoring table:
                                                                                                                                              Perfect score:
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Gaps

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Length 16 0; Indels us-10-735-916a-2.sizlim.rapbn

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US-11-009-939-18
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Sequence 3, Application US/11102743

Publication No. US20050266002A1

GENERAL INFORMATION:

APPLICANT: Siegall, Clay

APPLICANT: Francisco, Joseph

APPLICANT: Francisco, Joseph

APPLICANT: Francisco, Joseph

TITLE OF INVENTIOR: Reall, H. Perry

TITLE OF INVENTIOR: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%; Score 70; DB 7; Length 16; 86.7%; Pred. No. 9.8e-07; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10932334

Publication No. US20050249728A1

GENERAL INFORMATION:

APPLICANT: ImmunoGen, Inc.

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

CURRENT APPLICATION NUMBER: US/10/932,334

CURRENT FILING DATE: 2004-09-02

PRIOR PIPLICATION NUMBER: US/10/729,441

PRIOR FILING DATE: 2003-12-08
             GENERAL INFORMATION:
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-Jiun
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 13062-011001
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR FILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PastSEQ for Windows Version 4.0
SSEQ ID NO 13
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/102,743
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: US/09/328,296
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHIN Ver: 2.0
SEQ ID NO 3
LENGTH: 16
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Publication No. US20050266003A1
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Best Local Similarity
Matches 13; Conserva
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US-10-932-334-4
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Sequence 18, Application US/11009939
Publication No. US20050265998A1
GENERAL INFORMATION:
APPLICANT: ElBon, Geng Christopher Andrew
FILE REFERENCE: 23135-402
CURRENT APPLICATION NUMBER: US/11/009,939
CURRENT PILING DATE: 2005-12-10
PRIOR APPLICATION NUMBER: 60/528,811
PRIOR APPLICATION NUMBER: 60/528,812
PRIOR APPLICATION NUMBER: 60/528,912
PRIOR FILING DATE: 2003-12-10
SEQ ID NOS: 44
SEQ ID NOS: 44
LENGTH: 16
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                                                                                                                                                                                                                                                                             Query Match 85.2%; Score 69; DB 6; I
Best Local Similarity 87.5%; Pred. No. 1.5e-06;
Matches 14; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.5%; Score 66; DB 7; 175.0%; Pred. No. 4.9e-06; tive 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-Jiun
APPLICANT: Huang, Chiu-Chen
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 1306.2-011001
CURRENT PEPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2005-05-10
PRIOR FILING DATE: 2005-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 16
TYBE: PRT
PRIOR APPLICATION NUMBER: 10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/11125837; Publication No. US20050266003A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           1 RSSOSIVHSNVNTYLE 16
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                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                              1 RSSQSIVHSNGNTYLQ 16
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Best Local Similarity 75.09
Matches 12, Conservative
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US-11-125-837-1
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; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-726-554-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 VHSNGNTY 14
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2 ISSGGSTY 9
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Sequence 17, Application US/11105708

Publication No. US20050281821A1

GENERAL INPORMATION:

APPLICANT: Pernaetti, Flavia

APPLICANT: Pernaetti, Flavia

APPLICANT: Pernaetti, Flavia

APPLICANT: Preimark, Bruce

APPLICANT: Preimark, Bruce

PAPLICANT: Procomark, Bruce

TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition

FILE REFERENCE: 30797-704.501

CURRENT FILING DATE: 2005-04-13

PRIOR APPLICATION NUMBER: 60/149, 977

PRIOR APPLICATION NUMBER: 60/149, 534

PRIOR PLING DATE: 1999-00-02

PRIOR PLING DATE: 1999-01-06

PRIOR PLING DATE: 1999-01-06

PRIOR FILING DATE: 1999-01-06

PRIOR FILING DATE: 1999-01-06

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 17

LENTH: 16
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TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST
TITLE OF INVENTION: THE HBV S-SURPACE
TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
FILE REFERENCE: 1599-0197P
CURRENT PELING DATE: 2003-12-04
PRIOR PILING DATE: 2003-12-04
PRIOR PLING DATE: 15/09/865,483
FRIOR PILING DATE: PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                     Query Match 75.3%; Score 61; DB 7; 1
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 12; Conservative 2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.8%; Score 59; DB 7;
81.2%; Pred. No. 8.2e-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic peptide US-11-105-708-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/10726554 Publication No. US20050249753A1 GENERAL INFORMATION:
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                                                                                                                                                                                               1 RSSQSIVHSNGNTYL 15
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Matches 13; Conservative
    ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial
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US-10-999-866-59

Sequence 59, Application US/1099866

Publication No. US2005026604A1

GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS A

TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS A

TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS A

TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS A

FILE REFERENCE: CENSO42NP

CURRENT PILING DATE: 2004-11-30

PRIOR FILING DATE: 2003-12-08

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PATENTING

SEQ ID NO 59

LENGTH: 16

TYPE: PRT

ORGANISM: HOMO sapiens
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; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BLOGEN, INC.
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TILLE REFERENCE: Al36PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PATCHIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.2%; Score 22; DB 6; Length 16; Best Local Similarity 37.5%; Pred. No. 2.4e+02; Matches 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.9%; Score 25; DB 6; Length 16; 50.0%; Pred. No. 72;
Score 25; DB 6; Length 16;
Pred. No. 72;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
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Best Local Similarity 50.00,
1008 4; Conservative
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LOCATION: (1)...(16)

OTHER INFORMATION: HC CDR 2

US-10-999-866-59
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Sequence 89, Application US/11010748A
; Sequence 89, Application No. US2005024421A1
; Sequence 89, Application No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STATTWATTER, Wolfgang
APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010, 748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-06-13
; PRIOR FILING DATE: 2003-06-13
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTRARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.9%; Score 21; DB 7; Length 16; 100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 16;
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Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0;
                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: CD15 peptide fragment US-11-010-748A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-126
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Query Match
Best Local Similarity 100.4
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SERIERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moll, Heidrun
APPLICANT: SCHARM, Burkhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MRR-136
CURRENT APPLICANTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MRR-136
CURRENT PELING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SEQ ID NO 77
LENGTH: 16
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                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-77
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ORGANISM: Artificial Sequence
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Best Local Similarity 33.3
Matches 3; Conservative
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Length 16;

DB 7;

25.9%; Score 21;

Query Match

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RESULT 15
US-11-010-748A-138
Sequence 138, Application US/11010748A
Sequence 138, Application US/11010748A
Publication No. US2005024421A1
GENERAL INFORMATION:
APPLICANT: BATER PARTER, Wolfgang
APPLICANT: STRITTWATTER, Wolfgang
APPLICANT: STRITTWATTER, Wolfgang
APPLICANT: MILL Heidrun
APPLICANT: MILL Heidrun
APPLICANT: MILL HEIDRERNCE: MER-136
FILE REPERBRÜCE: MER-136
CURRENT APPLICATION NUMBER: DS/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR PLIING DATE: 2002-06-13
PRIOR PLIING DATE: 2002-06-13
PRIOR PLIING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: Patentin version 3.1
SEQ ID NO 138
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Best Local Similarity 100.0%; Pred. No. 3.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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Job time : 9 secs
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ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-138
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RESULT 1 ADJ76838

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Description	<i><b>666666666666666666666666666666666666</b></i>	
SUMMARIES	ADJ76838 ADZ67008 ADZ67008 ADJ76899 ADJ76899 ADZ67058 ADZ67058 ADZ67053 ADJ76891 ADJ76901 ADJ76901 ADJ76901 ADZ67071 ADG69372 ADG69372 ADG69372 ADG69372 ADG69372 ADG69372 ADG69370 ADG	
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; or epidermal tumor; cancer; osteosarcoma; complementarity determining region; CDR. CDR sequence for anti-IGF-1R antibody. cytostatic; antipsoriatic; antibody; (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76838 standard; peptide; 7 AA. Leger 0; 18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-00000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. (first entry) Goetsch L, Corvaia N, WPI; 2003-569653/53. WO2003059951-A2. Mus musculus. 06-MAY-2004 24-JUL-2003 ADJ76838; 

N-PSDB; ADJ76837

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Claim 1; SEQ ID NO 4; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (1) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with

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hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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                                                                                                                                                                                    100.0%; Score 35; DB 7; Length 7; 100.0%; Pred. No. 2e+06; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                        ADZ67008 standard; peptide; 7 AA.
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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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Best Local Similarity
Matches 7; Conserv
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CORVAIA N.
LEGER O.
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specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined is amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGR-IR and/or EGRR, and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of the transduction pathway of the signal mediated by the interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral clean and/or EGP-dependent, especially IGP1 and/or IGP2.

Conaracter, preferably IGP-dependent, especially IGP1 and/or IGP2.

Consetul for preparation of twore cells, preferably IGP-dependent, and/or the proliferation of two medicament intended to inhibit the growth and/or EGP-dependent and/or EGP-dependen
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18-JAN-2002; 2002FR-0000054.
07-MAY-2002; 2002FR-00005753.
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Disclosure; SEQ ID NO 65; 164pp; French.
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18-JAN-2002; 2002FR-0000654.
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Matches 7; Conservative
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                                                                                                                       The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or procession and/or abnormal activity of IGF-1R and/or procession and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or
                                                                                                                                                                                                                                                     proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; antipsoriatic; antibody; IGF-IR; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGFR; signal transduction pathway; or epidermal growth factor receptor; RGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                            New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                     Gabs
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100.0%; Pred. No. 7.7;
tive 0; Mismatches 0; Indels
                                                                                                 Disclosure; SEQ ID NO 54; 164pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ76899 standard; protein; 112 AA.
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             Leger 0
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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Best Local Similarity 100.
Matches 7; Conservative
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             Corvaia N,
                                     WPI; 2003-569653/53.
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                                                                                                                                                                                                                                                                                                                                    Sequence 112 AA;
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             Goetsch L,
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with the presentivity of signal transduction pathways mediated by interaction of these receptors with thair ligands. Especially they inhibit trowth and/or transformation of numor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also seteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or proliferation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gymecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriaais; dermatological disease; immune disorder; immunoglobulin; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-and and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:54.
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                                                                                                                                                                                                                                           100.0%; Score 35; DB 7; Length 112; 100.0%; Pred. No. 7.7; ive 0; Mismatches 0; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ADZ67058 standard; protein; 112 AA.
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2002FR-00005753.
2003WO-FR000178.
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                                                                                                                                                                                                                                                           Local Similarity 100
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                              1 KVSNRLY 7
                                                                                                                                                                                                             Sequence 112 AA;
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07-MAY-2002;
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                                                                                                                                                                                                                                             Query Match
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(LEGE/)
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                                                                                                                                                                                                                                                                             Matches
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The inversion relates to a novel isolated anti-insulinity being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of capable of binding tyroaline kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the prevention of restment of an illness connected with an overexpression and/or an abnormal cof an illness connected with an overexpression and/or an abnormal cof an illness connected with an overexpression and/or or EGF. IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced a different connected with inhibition of the insulin creceptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral capendant and/or EGF-dependent and/or EGF and/
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relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
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Best Local Similarity luv...
7, Conservative
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The invertion relates to a novel isolated anti-insulin-inseq growth ractor capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ670014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal cof an illness connected with an overexpression and/or an abnormal cof interactivation of the Iransduction pathway of the signal mediated by the interaction of the Iransduction pathway of the signal mediated by the interaction of IGFI or IGF2-NK and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induced a medicament does not induce or only slightly creceptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral construction of tumor calls, preferably IGF-dependent, especially IGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, of the cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the special cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the special cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the special cancer or colon cancer. (I) is useful in the composite cancer, endometrial cancer or colon cancer. (I) is useful in vitro diagnosis of a biologically active compound to cancer is characterial to inversepressing the IGF-IR and/or EGF entore.
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                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                     Beck A;
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                                                                                                                                                                                                                                                                                                     Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 12; SEQ ID NO 65; 125pp; English.
                                                                                                                                                                                                                                                                                                     Leger O,
              18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-F0000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating cancer.
                                                                                                                                                                                                                                                                                                     Goetsch L, Corvaia N,
                                                                                                                                                                                                                                                                                                                                                WPI; 2005-321968/33
                                                                                                                                 GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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                                                                                                                                    GOET/)
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ö Gaps ö 100.0%; Score 35; DB 9; Length 112; llarity 100.0%; Pred. No. 7.7; Conservative 0; Mismatches 0; Indela Query Match Best Local Similarity Matches 7; Conserv

Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region. Human antibody 7C10 1 light chain variable region SEQ ID NO:61. Beck A; Haeuw J, Duflos A, Example 12; SEQ ID NO 61; 125pp; English. Location/Qualifiers ADZ67065 standard; protein; 112 AA. Leger O, /note-55. .61 2002FR-00000654. 2002FR-00005753. 2003WO-FR000178. "CDR1" 94. .102 /note= "CDR3" 16-DEC-2003; 2003US-00735916 2002FR-00000653 11-JUL-2003; 2003FR-00008538 useful for treating cancer. (first entry) ĕ, Goetsch L, Corvaia N, WPI; 2005-321968/33 CORVAIA N. LEGER O. DUFLOS A. HAEUW J. N-PSDB; ADZ67066. JS2005084906-A1. BECK A. Homo sapiens. 30-JUN-2005 18-JAN-2002; 07-MAY-2002; 20-JAN-2003; 21-APR-2005 ADZ67065; (GOET/) (CORV/) (DUFL/) (BECK/) (LEGE/) Region Region Region 

1 receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of apable of binding to human IGF-IR and, if necessary, capable of positional fragment, being capable of binding to human IGF-IR and, if necessary, capable of expecifically inhibiting tyroalme kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino caps (ADZ67006 and ADZ67014). An antibody of the invention 1s useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal of interaction of the IGF-IR and/or EGFR, and/or connected with a chiperaction of IGF1 or IGP2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only alightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral The invention relates to a novel isolated anti-insulin-like growth factor Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,

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character, preferably IGF-dependent, especially IGF1 and/or IGF2-
dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
useful for preparation of a medicament intended to inhibit the growth
and/or the proliferation of tumor cells, preferably IGF-dependent,
especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
HER2/neu-dependent cells. (I) is useful in the preparation of a
medicament intended for prevention or for the treatment of cancer, where
the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
breast cancer, endometrial cancer or colon cancer. (I) is useful in the
preparation of a medicament intended for the prevention or for the
treatment of psoriasis. (I) is useful in preparation of a medicament
intended for the specific targeting of a biologically active compound to
calls expressing or vowerexpressing the IGF-IR and/or EGFR receptor. (I)
is useful for in vitro diagnosis of illnesses induced by an
overexpression or an underexpression of the IGF-IR and/or EGFR receptor
ER and/or EGFR receptor is suspected, which involves contacting the
biological sample with (I), which is optionally labeled. The present
expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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Best Local Similarity 100.
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55 KVSNRLY 61
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factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of the second and activity of the second and activity of the second activity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipporiatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; light chain variable region.
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100.0%; Pred. No. 8.4;
ive 0; Mismatches
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'note= "leader peptide"
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                                                                                                                                                                                                                                                                                                                                                                              ADZ67053 standard; protein; 122 AA.
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"CDR2"
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; 2002FR-00005753.
; 2003WO-FR000178.
; 2003FR-00008538.
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/note= "CDR3"
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Best Local Similarity luv...
7; Conservative
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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07-MAY-2002;
20-JAN-2003;
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(LEGE/)
(DUFL/)
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New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                Goetsch L, Corvaia N,
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                                                                   WO2003059951-A2
                                  Homo sapiens.
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BXBXSXXXXXXXXXXXXXX
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                                                                                                                                                                                                   The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tynosine kinase activity of the receptor, operation of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tynosine kinase activity of the receptor, determining region (CDR) consisting of the or complementary determining region (CDR) consisting of the invention is useful in activation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or a banormal activation of the IGF-IR and/or EGFR, and/or connected with a abnormal activation of the IGF-IR and/or EGFR, and/or connected with a ctivation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where interaction of IGF or EGFR, and/or of EGF with EGFR, where connected with inhibition of the insulin trended to IGF-IR and/or EGF-IR and/or EGF-IR and/or EGF-IR and/or EGF-IR and/or EGF-dependent and/or EGFR receptor (I) is useful in the preparation of a medicament intended for prevention or for the treatment of postials (I) is useful in the preparation of a medicament intended for prevention or for the preparation of a medicament intended for the specific targeting of a biological part or an endeapendent and/or EGFR receptor
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                                                                                    Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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 Beck A;
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 Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J,
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Best Local Similarity 100.
Matches 7; Conservative
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KVSNRLY 71
                                      2005-321968/33.
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                                        WPI; 2005-321968,
N-PSDB; ADZ67052
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the
                                                                                                                                                                                                                                                                                                                                                                                                   prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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Best Local Similarity 100.
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/note= "CDR3"

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (Ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or for epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of typeractivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                                  Leger 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .80
.CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "CDR1"
               20-JAN-2003; 2003WO-FR000178.
                                                                 18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                 2002FR-00000653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43. .58
/note= "C
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les 7; Conservative
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/note=
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                                                                                                                                                  Goetsch L, Corvaia N,
                                                                                                                                                                                   WPI; 2003-569653/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 131 AA;
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                                                 18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADZ67071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, capable of specifically inhibiting tyrosine kinase activity of the receptor, determining a light or heavy chain having a least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67004 and ADZ67014). An antibody of the invention is useful in a lilness connected with an overexpression and/or an abnormal activation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal appreasation of the transduction pathway of the signal mediated by the interaction of IdF1 and/or EGFR, and/or CDFF with EGFR, where interaction of the remaductan pathway of the signal mediated by the interaction of IdF2 with IGF-IR and/or EGF with EGFR, where condary effects connected with inhibition of the insulint condances secondary effects connected with inhibition of the insulint condances secondary offects connected with inhibition of the insulint condances. The antibody is useful for preparation of a medicament and/or HER2/neu-dependent and/or EGF-dependent, especially IGF-dependent to for preparation of the medicament intended for prevention of tunder calls, into calls with the andorer, where the cancer is chosen from prostate cancer. Osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention of a medicament intended for the prevention or endometrial cancer or colon cancer. (I) is useful for in vitro diagnosis the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an endocament intended for the specific targeting to a biological sample in which the abnormal prevention. (I) is useful in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corvaia N, Leger O, Duflos A, Haeuw J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 9 Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 12; SEQ ID NO 67; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
100.0%;
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18-JAN-2002; 2002FR-00006554.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WD-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                  16-DEC-2003; 2003US-00735916
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N-PSDB; ADZ67070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DUFLOS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAEUW J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BECK A.
US2005084906-A1
                                                                           21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BECK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GOET/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LEGE/)
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ADQ08646;
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ö
                                                                                                                                                                                                                                                                                                   Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoms; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
Gaps
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                                                                                                                                                                                                                                                                     Human antibody 7C10 1 light chain variable region SEQ ID NO:63
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                           ADZ67067 standard; protein; 131 AA
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.e. "CDR1"
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74. .80
/note= "CDR2"
113. .121
/note= "CDR3"
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2002FR-00005753.
2003WO-FR000178.
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                                                                                                                                                                                                                                  (first entry)
   7; Conservative
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                                                                    74 KVSNRLY 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOETSCH L.
CORVAIA N.
LEGER O.
                                   7
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                                     1 KVSNRLY
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18-JAN-2002;
07-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JAN-2003;
                                                                                                                                                                                                                                  30-JUN-2005
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                                                                                                                                                                                                ADZ67067;
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(HAEU/)
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   Matches
                                                                                                                            RESULT 14
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determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with an illness connected with a coverexpression and/or an abnormal consistence in the IGF-IR and/or EGFR, and/or of EGF with EGFR, where interaction of IGF or IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin the receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, and/or HERZ/neu-dependent and/or EGF-dependent cells. (I) is useful in the preparation of a medicament intended for preparation of a medicament intended for the preparation of a medicament of proparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor (I) is useful in preparation of a medicament intended for the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the receptor is suspected, which involves contacting the receptor is suspected which involves contacting the present of sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel genes derived from Ciona intestinalis (sea squirt), expressed in nervous system in the tailbud embryo or larva, useful for studying the development of nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ08646 standard; protein; 841 AA.
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Matches 7; Conservative
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N-PSDB; ADQ08645.
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This invention relates to a novel gene cluster, where the encoded proteins are expressed in the nervous system of sea-squirt tailbud embryo or larva. The invention is useful for studying the development of the nervous system of the sea-squirt and for research purposes. The genes may be used for determining the disease-development mechanisms in the nervous system. In addition, novel gene clusters expressed in nervous system of sea-squirt tailbud embryo or larva allows development of diagnostics and therapeutics related to nervous system diseases. The present sequence is that of a protein encoded by a C intestinalis gene of the invention.
                         Claim 4; SEQ ID NO 48; 897pp; Japanese.
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Sequence 841 AA;

ö Gaps .; 0 Query Match 100.0%; Score 35; DB 8; Length 841; Best Local Similarity 100.0%; Pred. No. 74; Matches 7; Conservative 0; Mismatches 0; Indels

||||||| 801 KVSNRLY 807 1 KVSNRLY 7 ઠે 셤

Search completed: December 30, 2005, 13:23:57 Job time : 64.2097 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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sw model - protein search, using OM protein December 30, 2005, 13:11:41; Search time 9.93548 Seconds (without alignments) 67.789 Million cell updates/sec Run on:

US-10-735-916A-4 35 1 KVSNRLY 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		Ig kappa chain V r	histone acetyltran	cytotoxin homolog	hypothetical prote		conserved hypothet	heat shock protein	conserved hypothet	dipeptidyl-peptida	ATP-binding protei	synaptonemal compl	synaptonemal compl	microcystin synthe	hypothetical secre	lipoate-protein li	Δ	peroxidase (EC 1.1	leukocyte elastase	elastase inhibitor	germination respon	hypothetical prote	DNA primase - phag	penicillin-binding	penicillin-binding	Ä			hypothetical prote
OI	B32530	D28195	A57583	JS0299	PQ0299	AI2079	G89972	A41252	E69820	S66504	A12454	148176	S49461	AD2136	G97182	E90500	D90153	T04710	A42421	S27383	139859	AI2321	\$07508	B71802	E64715	833533	E71492	C71139	T21712
ength DB	108		374 2	64 2	216 2	305 2	375 2	405 1	435 2	463 2	600 2	845 2	993 2	1102 2	184 2	264 2	293 2	329 2	379 2	379 2	407 2	528 2	566 2	588 2	588 2	809 2	832 2	1003 2	2144 2
Query Match Length	88.6	88.6	98.6	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9
Score	31	31	31	30	30	30	30	30	30	30	30	30	30	30	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29
Result No.	н	7	e	4	ιΩ	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25		27	28	29

hypothetical prote Ig kappa chain V r	conserved hypothet hypothetical prote	hypothetical prote ORF MSV146 hypothe	repressor - Staphy	ribose-phosphare d ribose-phosphate d	phosphoribosylpyro ribose-phosphate d	phosphoribosylpyro	ribose-phosphate d	class I histocompa	membrane associate	hypothetical prote
F82884 S52449	T39328 S72336	T25745 T28307	T00165	KIECRY	E85700 AF0720	H90842	AG0245	839599	B97335	D83777
00	0 0	20	0		0 0	1 74	~	7	~	N
5005	160	232	256	315 315	315	315	315	328	367	391
82.9	80.0 80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
7 7 8 7 8	7 7 8 8 7 8 7 8	78 78 78	58	8 8 7 7	7 7 8 8 8 8	78	28	28	28	28
30 31		3.4	36	37 38	39	41	42	43	44	45

## ALIGNMENTS

Ig kappa chain V region (DB3) - mouse (fragment)

Ig kappa chain V region (DB3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004

C;Accession: E32530

R;Deverson, E.; Berek, C.; Taussig, M.; Feinstein, A.

Eur. J. Immunol. 17, 9-13, 1987

A;Title: Monoclonal BALB/c anti-progesterone antibodies use family IX variable region h
A;Reference number: A32530; MUID:87133855; PMID:3102254

A;Accession: E32530

A;Accession: E32530

A;Accession: E32530

A;Accession: E32530

A;Cross-references: UNIPROT:08VCI6; UNIPARC:UPI0000176B00; GB:M27587

A;Cross-references: UNIPARC:immunoglobulin homology

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Gaps ö 88.6%; Score 31; DB 2; Length 108; 85.7%; Pred. No. 7.4; 1.1ve 0; Mismatches 1; Indels 

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Ig kappa chain V region (anti-haloperidol antibody D) - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Ol-Dec-1989 #sequence_revision Ol-Dec-1989 #text_change 09-Jul-2004
C;Accession: D28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
C;Accession: D28195
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: D28195
A;Accession: D28195
A;Accession: D28195
A;Accession: D28195
A;Accession: J28195
A;Gross-references: UNIPROT:099M37; UNIPARC:UPI0000176B01; GB:M19769
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>

Gaps ö Length 112; 1; Indels Query Match 88.6%; Score 31; DB 2; Best Local Similarity 85.7%; Pred. No. 7.7; Matches 6; Conservative 0; Mismatches 1

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A;Cross_references: UNIPROT: P32815; UNIPARC: UPI000013B0F1; GB:M65289; NID:g142976; PIDN: A;Experimental source: strain var. non-diastaticus
P;20-94/Domain: ferredoxin 2[4Fe-48] homology <FER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Uul-2004
C;Accession: A12079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, £ A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q8YUZO; UNIPARC:UPI0000CE359; GB:BA000019; PIDN:BAB73890.1; A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004
C;Accession: 689972
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                             hypothetical protein 5 (gldA 3' region) - Bacillus stearothermophilus (fragment)
C;Species: Bacillus stearothermophilus
C;Species: 17-ul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Oct-2004
C;Accession: PQC929
R;Mallinder, P.R.; Pritchard, A.; Moir, A.
Gene 110, 9-16, 1992
A;Title: Cloning and characterization of a gene from Bacillus stearothermophilus var.
A;Reference number: JQ1474; MUID:92184120; PMID:1339360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein SA1673 [imported] - Staphylococcus aureus (strain N315)
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Pred. No. 26;
1; Mismatches
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Pred. No. 37;
1; Mismatches
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Similarity 71.4%; 1
5; Conservative 1:
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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                            KMSNRMY 30
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Best Local Similarity
Matches 5; Conserv
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A Molecule type: DNA
A Residues: 1-305 <KUR>
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Nathernate names: protein LPA16w; protein YP8132.12; protein YPL001w
Nathernate names: protein LPA16w; protein YP8132.12; protein YPL001w
Nathernate names: protein LPA16w; protein YP8132.12; protein YPL001w
C; Species: Saccharomyces cerevisia on September 18

C; Date: 08-Pab-1936 Heequence revision 08-Pab-1996 Htext_change 09-Jul-2004
C; Accession: A57583; 852530; 5596520.
C; Accession: A57583; MulD:9602752; PMID:7559580
A; Atternet number: A57583; MulD:96027552; PMID:7559580
A; Reference number: A57583
A; MulD:96027552; PMID:7559580
A; Reference number: A57583
A; Reference number: A57583
A; Reference number: A57583
A; Reference number: A77583
A; Reference number: A57583
A; Reference number: A57583
A; Residues: L194 KMLS
A; Residues: L195 KMPS:YPL001w
A; Residues: L194 KMLS
A; Residues: L195 KMPS:YPL001w
A; Residues: L194 KMLS
A; Residues: L195 KMLS
A; Residues: L195 KMLS
A; Residues: L195 KMLS
A; Residues: L195 KMLS
A; Residues: R05:R005922; MIPS:YPL001w
A; RDS
A; Residues: R05:R005922; MIPS:YPL001w
A; RMPS POSITION:R05 KMLS
A; Res
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Cytotoxin homolog S4C8 - shield snake
Cytotoxin homolog S4C8 - shield snake)
Cytotes: Aspidelaps scutatus (shield snake)
Cytotes: Or-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
Cytotesion: US0299
RyJoubert, F.J.
Int. J. Biochem. 20, 337-345, 1988
AyTitle: Snake venom toxins II. The primary structures of cytotoxin homologues S3C2 and AyReference number: US0299, MUID:88185648; PMID:3356299
AyAccession: US0299
AyAccession: US0299
AyAccession: UNIPROT:P19004; UNIPARC:UP100001287FC
AyCross-references: UNIPROT:P19004; UNIPARC:UP100001287FC
Cytotoxin
Cytotoxin
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chanderich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 249-256, 1990, 259-256, 1990, 259-256, 1990, 259-256, 1990, 259-256, 1990, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 259-256, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:P97030; UNIPARC:UPI0000060111; GB:Z99108; GB:AL009126; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1.463 < PAR>
A;Cross-references: UNIPROT:PS3634; UNIPARC:UPI0000127099; EMBL:X87212; NID:gl006656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-435 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dipeptidyl-peptidase I (EC 3.4.14.1) precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66504
R;Paris, A.; Strukelj, B.; Pungercar, J.; Renko, M.; Dolenc, I.; Turk, V. PEBS. Latt. 369, 226-330, 1995
A;Title: Molecular cloning and sequence analysis of human preprocathepsin C. A;Reference number: S66504; MUID:95377428; PMID:7649281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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F;258,405,427/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: yhbA
F;230-304/Domain: ferredoxin 2[4Fe-4S] homology <FER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB;
Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 53;
1; Mismatches
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Pred. No.
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Local Similarity 71.4%;
es 5; Conservative
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A,Map position: 8p22-8p22
C,Superfamily: papain
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Best Local Similarity 85.7
Matches 6; Conservative
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ATP-binding
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Biochem. Biophys. Res. Commun. 153, 428-434, 1988
A;Title: Characterization of a novel transformation-sensitive heat-shock protein (HSP47); A;Reference number: A27656; MUID:88240438; PMID:3377793
A;Reference protein
A;Residues: 16-51 <NAO>A;Residues: 16-51 <NAO>A;Cross-references: UNIPARC:UPI00001731FD
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c, Superfamily: serpin

C, Keywords: collagen binding; endoplasmic reticulum; glycoprotein; heat shock; molecular

F;1-15/Domain: signal sequence #status predicted <SIG>
F;4-40-Fyroduct: heat shock procein 4 # status predicted

F;402-405/Region: endoplasmic reticulum retention signal

F;107,112/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heat shock protein 47 precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: A41252; A27656; S16673
R;Hirayoshi, K.; Kudo, H.; Takechi, H.; Nakai, A.; Iwamatsu, A.; Yamada, K.M.; Nagata, K.Hirayoshi, K.; Kudo, Gasension: A3540464, 1991
A;Title: HSP47: a tissue-apecific, transformation-sensitive, collagen-binding heat shock
A;Reference number: A41252; MUID: 91304395; PMID: 2072906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Contents: annotation, review article
;Comment: This stress-induced glycoprotein of the ER lumen lacks protease inhibitor act
                                                              A;Molecule type: DNA
A;Residues: 1-375 <KUR>
A;Cross-references: UNIPROT:Q99T22; UNIPARC:UPI00000CACF6; GB:BA000018; PID:g13701649;
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1673
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
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                                                                                                                                                                                                                                                                                                          2; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Trele: Hsp47: a collagen-specific molecular chaperone.
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                                                                                                                                                                                                                                                                                                              Score 30; DB
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trends Biochem. Sci. 21, 23-26, 1996
                                                                                                                                                                                                                                                                                                              85.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      llarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 KIGNRLY 238
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les 5; Conserv
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A;Molecule type: mRNA
A;Residues: 1-405 <HIR>
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                                    A;Status: preliminary
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A;Molecule type: mRNA
A;Residues: 1-993 <SAG>
A;Cross-references: UNIPARC:UPI0000028B49; EMBL:Z38118; NID:g1360015; PIDN:CAA86262.1; P
                                                                                                                                                     Query Match 85.7%; Score 30; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0;
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Best Local Similarity 71.4
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 927 VSNRLY 932
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A; Residues: 1-184 < KUR>
                                                                                                                                                                                                                                                                                                                      2 VSNRLY 7
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A, Molecule type: DNA
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence.
C;Date: 20-Feb-1995 #sext_change 05 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #Cooler 1994
A;Reference number: 349461
A;Reference number: 349461
A;Residues: 1-99 *Jul-A;Residues: 1-99 *Jul-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pynationemal complex protein - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Uul-2004
C;Accession: 148176
R;Dobson, M.J.; Pearlman, R.E.; Karaiskakis, A.; Spyropoulos, B.; Moens, P.B.
A;Title: Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disjumiration: Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disjumiration: 148176
A;Accession: 148176
A;Accession: 148176
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-845 <RES>
A;Residues: 1-845 <RES>
C;Genetics:
A;Gene: synl
                            Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Triguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 205-213, 2001

A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUD:21592285; PMID:11759840

A; Reference number: AB1807; MUD:21592285; PMID:11759840

A; Residues: preliminary

A; Mesidues: 1-600 < KUR>
A; Residues: 1-600 < KUR>
A; Residues: 1-600 < KUR>
A; Residues: 1-600 < KUR>
A; Experimental source: strain PCC 7120
C; Genetics: al15193
C; Superfamily: Escherichia coli ABC transporter mdlA; ATP-binding cassette homology
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85.7%; Score 30; DB 2; Length 600;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 1; Indels
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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microcystin synthetase B [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2136
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
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C;Superfamily: peptide synthetase ppsB; acetate-CoA ligase homology; acyl carrier protei
C;Keywords: carrier protein
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A.Residues: 1-1102 <KUR>
A.Cross-references: UNIPROT:Q8YTSO; UNIPARC:UPI00000CE4E9; GB:BA000019; PIDN:BAB74342.1;
A.Experimental source: strain PCC 7120
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0;
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Pred. No. 37;
2; Mismatches
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Search completed: December 30, 2005, 13:34:53 Job time : 10.9355 secs

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QSher8 staphylococ QShn80 staphylococ QBCrrX staphylococ QS12r3 geobacillus G50me4 entemoeba h P1371 gallus gall P97030 bacillus gull P5265 magnaporthe P53634 h dipeptidy Q60hg6 m dipeptidy Q53993 homo sapien Q71e76 homo sapien Q5wy99 pomo sapien Q5xb02 pongo pygma

Perfect score:

Sequence:

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MUCLEOTIDE SEQUENCE.

MEDLINE=96226405; PubMed=8634155;

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Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxIb=7955;
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85.7%; Pred. No. 42;
ive 1; Mismatches 0; Indels
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                 OSHN80_STAEQ
QBCKX0_STAEP
OSL12R3_GEOKA
QS OME4_BWTHI
HSP47_GHICK
P9703_0 BACSU
OS 26J5_MAGGR
CATC_HUWAN
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Q71E76 HUMAN
Q8WY99 HUMAN
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 25HER8
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Q90420;
Q1-NOV-1996 (TrEMBLrel. 01, La
Q1-NOV-1996 (TrEMBLrel. 26, La
Q1-NOX-1996 (TrEMBLrel. 26, La
A7 kDa heat shock protein.
Name=hgp47; Synonyms=hsp7;
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115 KISNRLY 121
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Q5dw6 oncorhynchu
Q4372 helioobacte
Q6bsm3 debaryomyce
Q4pfh3 ustilago ma
Q12341 saccharomyc
Q12341 saccharomyc
Q12320 pisum sativ
P19004 aspidelaps
Q4093 theileria a
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Q57k6 brachydanio
Q567k6 brachydanio
Q4wh23 aspergillus
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Q9wy20 anabaena sp
Q9afk9 shigella fi
Q9afk9 shigella fi
Q9afk9 shigella fi
Q9m425 spinacia ol
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Q5076 entamoeba h
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Q6iqv2 brachydanio
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                                                                                                                                December 30, 2005, 13:11:26 ; Search time 63 Seconds (without alignments) 78.392 Million cell updates/sec
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                       5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                             2166443 seqs, 705528306 residues
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0567K6 BRARE
04WH23 ASPFU
04WH44 ASPFU
09AU08 SHIFL
09VSA9 SHIFL
09ARS9 SHIFL
09ARS2 SHIFL
09MAZ2 ANASP
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050Q58 ENTHI
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Q75NZO_PEA
CXH48_ASPSC
Q6F8GS_CANGA
Q747U3_GEOSL
Q4U9D3_THEAN
YGL5_BACST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q90420_BRARE
Q61QV2_BRARE
Q5DW60_ONCMY
G6PD1_ARATH
Q6KKD3_HBLPY
Q6BSM3_DBBHA
Q4PFH3_USTWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q4L7G0_STAHJ
Q6G877_STAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                       GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                protein search, using sw model
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                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                       US-10-735-916A-4
35
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                                                                                                                                                                                                                                                  1 KVSNRLY 7
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Match
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Gaps

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SEQUENCE
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g
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                                                                                                                                                                                             TISSUE-Embryo;

KE STATE-Embryo;

KETALOBOET R. L., Felngold E. A., Grouse L.H., Derge J.G.,

KETALOBOET R. L., Felngold E. A., Grouse L.H., Derge J.G.,

KALTALOBOET R. L., Felngold E. A., Grouse L.H., Derge J.G.,

KALTALOBOET R. L., Felngold E. A., Grouse L.H., Derge J.G.,

KALTALOBOET R. L., Colling F. S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E.,

Rapleton M., Wodin T.B., Toshiyuki S., Carninol P., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R. D., Mullahy S.J.,

Rachards S., Worley K. M., McKernan K.J., Malek J. A., Gunaratne P.H.,

R. A. Helton B., Ketteman M., Madan A., Gibbs R.A.,

Willialon D. K., Muzny D.M., Sacyren B.J., Lu X., Gibbs R.A.,

Wilting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

R. Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.
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                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinoptergali; Neopterygil; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (UND-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (UND-2004) to the serpin family.

EMBL; BC071301; AAH71301.1; -; mRNA.
ZFIN; ZDB-GENE-990415-33; hap47.

ZFIN; ZDB-GENE-990415-33; hap47.

InterPro; IPR000886; ER_target_S.
InterPro; IPR000215; Prot_inh_serpin.

Frank; PR00079; Serpin; 1.

SMART; SM00093; SERPIN; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Last annotation update)
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PROSITE; PS00284; SERPIN; 1.
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QSDW60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat shock protein 47.
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                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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STRAIN=cv. Columbia;
MEDLINE=97471969; PubMed=9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome S. I. Sequence
features of the 1.6 Mb regions covered by twenty physically assigned
NUCLECTIDE SEQUENCE.
PubMed=15721272; DOI=10.1016/j.bbrc.2005.01.097;
Ojima N., Yamashita M., Watabe S.;
"Quantitative mRNA expression profiling of heat-shock protein families
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305; Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F., Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G., Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J., Chan M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
                                                                                                                                                                                                           in rainbow trout cells ";
Biochem. Biophys. Res. Commun. 329:51-57(2005).
-1- SIMILARITY: Belongs to the serpin family.
BAB96463; BAB90029.1; -; mRNA.
GO; GO:0004867; P:protein folding; IEA.
GO; GO:0004867; P:protein folding; IEA.
InterPro; IPR000886; ER target_S.
InterPro; IPR000015; Prot_inh_Serpin.
Ffam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
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Q47127; O65577; O9FPM5;
15-DEC-1998 [Rel. 37, Created)
15-DEC-1998 [Rel. 37, Created)
13-SEP-2003 (Rel. 41, Last sequence update)
13-SEP-2003 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation)
13-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 AA; 45451 MW; 897A18B5B427877C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%; Score 34; DB 2;
85.7%; Pred. No. 42;
vative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00014; ER TARGET; UNKNOWN 1.
PROSITE; PS00284; SERPIN; 1.
Heat shock; Serpin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 KISNRLY 123
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Fink A., Greppin H., Tacchini P.,

"Nucleotide sequence of a cDNA encoding the glucose-6-phosphate
dehydrogenase from Arabidopsis thaliana.";

"Nucleotide sequence of a cDNA encoding the glucose-6-phosphate
dehydrogenase from Arabidopsis thaliana.";

"I (er) Plant Gene Register PGR95-021.

-!- FUNCTION: Catalyzes the rate-limiting step of the oxidative
pentose-phosphate pathway, which represents a route for the
dissimilation of taxbohydrates besides glycolysis. The main
function of this enzyme is to provide reducing power (NADPH) and
pentose phosphates for fatty acid and nucleic acid synthesis which
are involved in membrane synthesis and cell division.

-!- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-
1.5-lactone 6-phosphate + NADPH.

-!- CATALYTIC ACTIVITY: Regulated by metabolites. Posttranslationally
inactivated by cysteine-mediated redox modification via the
inactivated by cysteine-mediated redox modification via the
ferredoxin-thioredoxin system in the light and this avoids futile
cycles with photosynthetic CO2 fixation (By similarity).
-!- PATHWAY: Pentose phosphate pathway; first step.
-!- CBUSULDIAR LOCATION: Chloroplast.
-!- SUBURIANAL STAGE: Increase of activity in the apex linked to
prover the early stages of the transition from vegetative to reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMED outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THERITY ALTONOSTICAL ALTONOSTIC
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Iamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: There are 6 glucose-6-phosphate 1-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes in A.thaliana.
-!- SIMILARITY: Belongs to the glucose-6-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: Ref.5 sequence differs from that shown due to a frameshift in position 65.
                                                                                                                                                                                                                                                                                                                                         Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                                                                                                                                                                                                                                                                                                                                Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
Feldmann K.A.;
"Pull-length CDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ001359; CAA04696.1; -; mRNA.
EMBL; AB002236; BAB09918.1; -; Genomic_DNA.
EMBL; AY099561; AAM20413.1; -; mRNA.
EMBL; AY086213; AAM72144.1; -; mRNA.
EMBL; AY086213; AAM64291.1; -; mRNA.
EMBL; K84230; CAA59012.1; ALT_FRAME; mRNA.
INTERPRO; IPH001282; G6PD.
                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 17-576.
                                                                                                                                                                                                                                             Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia;
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Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WUCLECTIDE SEQUENCE.
MEDLINE=21972792; PubMed=11976306;
DOI=10.11284JB.4.10.2755-2766.2002;
Hofretter D., Hass R.,
"Characterization of two cryptic Helicobacter pylori plasmids: a putative source for horizontal gene transfer and gene shuffling."; J. Bacteriol. 184:2755-2766(2002).
BMBL; AF469113; AAM22664.1; -; Genomic_DNA.
BMBL; AF469113; Dotein; Plasmid.
SEQUENCE 355 AA; 41561 MW; C9090A779A04693F CRC64;
                                                                                     Redox modulation (By similarity).
A -> D (in Ref. 5).
IPPNITVUV -> STPKLIVDE (in Ref. 1).
Q -> B (in Ref. 5).
G -> A (in Ref. 5).
G -> A (in Ref. 1).
G -> A (in Ref. 1).
L -> R (in Ref. 1).
L -> R (in Ref. 1).
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similarity)
                                     (By
                                                             Substrate; phosphate group (By similarity).
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                                                                                                                                                                                                                                      Score 34; DB 1; Length 576; Pred. No. 61;
                                       Substrate; phosphate group similarity).
                                                                                                                                                                                                            65428 MW; 6559FFCCF76F44DF CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
26-OCT-2004 (TrEMBLrel. 28, Last annotation update)
26-OCT-2004 (TrEMBLrel. 28, Last annotation update)
26-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proton acceptor (By E
NADP (By similarity)
NADP (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                        355 AA.
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                                                                                                                                                                                                                                        97.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein orf5B.
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QEBSM3;
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Q8KKD3;
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Best Local Similarity 85.,
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1110
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                                                                                                                                                                                                              576 AA;
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131
264
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Prangeul L., Aigle M., Anthourad V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Royer J., Cattolico L., Confanioleri F., de Daruvar A.,
Hantraye F., Hemnequin C., Janniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.-M., Nikolski M., Oztas S., Oztaer P., Suleau A.,
Swennen D., Tekaia P., Wesolowski-Louvel M., Westhoff E., Wirth B.,
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Mincker P., Souciet J.-L.;
Genome evolution in yeasts.";
Nature 430:35-44(2004).
BMBL; CR882136; CAG86941.1; -; Genomic_DNA.
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Bukaryota; Kungi, Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=237631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMO0487; DEXDC: 1.
SMART; SMO0487; DEXDC: 1.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
ATP-binding; Complete proteome; Helicase; Hydrolase;
Nucleotide-binding; RNA-binding.
SROUENCE 614 AA; 70389 MW; 9ABSF7CC840C5DIB CRC64;
                                                                                                                                                                                                                                                                                                                    GO:0005524; F:ATP binding; IEA. — GO:0008026; F:ATP-dependent helicase activity; IEA. GO:00016787; F:hydrolase activity; IEA. GO:0003676; F:nucleic acid binding; IEA.
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
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Last annotation update)
                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=ATCC 36239 / CBS 767;
PubMed=15229592; DOI=10.1038/nature02579;
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                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR001410; DEAD.
Interpro; IPR011545; DEAD/DEAH_N.
Interpro; IPR001629; DEAD_box.
Interpro; IPR001650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 USTWA
Q4PFH3 USTWA PRELIMINARY;
Q4PFH3;
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71 KLSNRLY 77
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            NCBI_TaxID=4959;
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Matches
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David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorie P.,

Dorie K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,

Exickson J., Farina A., Faro S., Ferreira P., Fischer H.,

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Ghirke A., Goyette A., Gage D., Galagan J., Gearin G., Gnerre S.,

Androptan D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,

Andron T., Horn A., Houde N., Hughes L., Hulme W., Husby B., Iliev I.,

RA Honan T., Horn A., Kisner P., Kodira C., Kulbokas E., Labutti K.,

RA Lindblad-toh K., Liu X., Lokyttesng T., Manclen C., Major J.,

RA Lindblad-toh K., Marbitt R., Macdonald J., Maclean C., Major J.,

RA Maria D., Marabella R., Maru K., Matthews C., Mauceli E.,

Mccarthy M., Mcdonough S., Mcghee T., Meldrim J., Mencel E.,

RA Morathy M., Mcdonough S., Mcghee T., Mikelsen T., Menga V., Moru K.,

RA Morathy M., Milalev A., Mihova T., Mikelsen T., Menga V., Moru K.,

RA Moryen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,

RA Orbu N., O'donnell P., Okoawo O., O'leary S., Cmotosho B.,

Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,

Ra Sheridan J., Sherpa N., Shil J., Sairnov S., Sharpe T.,

Ra Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,

Ra Tenzing P., Tesfaye S., Theodore J., Thollutsang Y., Topham K.,

Ra Tenzing P., Tesfaye S., Theodore J., Wu Y., Wayman D., Yadav S.,

Ra Tenzing P., Tesfaye S., Theodore J., Wu Y., Wayman D., Yadav S.,

Ra Tenzing P., Tesfaye S., Theodore J., Wu Y., Wayman D., Yadav S.,

Ra Tenzing P., Lestine E., Yaller B., Wu Y., Wayman D., Yadav S.,

Ra Tenzing P., Lestine E., Young G., Zainoun J., Zohon R.,

Ra Mangdi T., Whitcher C., Wilkinson J., Wu Y., Ware C., Wang S.,

Ra Mang S., Yang X., Yesger E., Young G., Zainoun J., Zohon R.,

Ra Mang S., Yang X., Yesger E., Young G., Zainoun J., Zainoun J., Von M., Retter R.,

Ra Mang S., Yesser E., Yesser E., You
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Q12341; Q6Q515;
Q1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
13-SRP-2005 (Rel. 48, Last annotation update)
Histone acetyltransferase type B catalytic subunit (BC 2.3.1.48).
Name=HAT1; OrderedLocusNames=YPL001W; ORFNames=LPA16W, YP8132.12;
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Bukaryota, Pungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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85.7%; Pred. No. 3.8e+02;
tive 1; Mismatches 0; Indels
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SEQUENCE 1220 AA; 130516 MW; 588850F6ACA5C65C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence of Ustilago maydis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
PubMed=7559580; DOI=10.1074/jbc.270.42.24674;
Kleff S., Andrulis E.D., Anderson C.W., Sternglanz R.;
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EMBL; AACF01000040; EAK81699.1; -; Genomic_DNA.
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GO; GO:000537; C:cytoplasm; IDA.

GO; GO:0000123; C:histone acetyltransferase complex; IPI.

GO; GO:0005634; C:mcleus; IDA.

GO; GO:0004406; F:H3/H4 histone acetyltransferase activity; IMP.

GO; GO:000548; P:H3/H4 histone acetyltransferase activity; IMP.

GO; GO:000548; P:histone acetylarion; IDA.

3D-structure; Acyltransferase; Complete proteome;

Direct protein sequencing; Nuclear protein; Transferase.

COMPBIAS 314 317 Poly-Leu.

CONFLICT 87 10 L -> V (in Ref. 4).
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Best Local Similarity 85.7
Matches 6; Conservative
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139
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302
304
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374 AA;
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SEQUENCE
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                                                                                     NUCLECOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=S288c / AB972;

MEDINES-97313271; PubMed=9169875;

MEDINES-97313271; PubMed=9169875;

MEDINES-97313271; PubMed=9169875;

Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietrich E., Churcher C.M., Coster F., Davis R., Davis R.W., Dietrich E., Churcher C.M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Dietrich E., Hobling U., Heumann K., Hilbert H., Hillier L.W., Hall J., Hebling U., Heumann R.W., Johnston M., Kalman S., Kleine K., Amarathe R.W., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Amarathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Amarathe R., Nommann S., Rieger M., Schaefer P., Pearson D., Petel F.X., Pohl T.M., Purnelle B., Rajandream M.A., Rchmann S., Schroeder M., Schaefer 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S2886;
Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher B.,
Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-320.
MEDLINE=98394469; PubMed=9727486; DOI=10.1016/S0092-8674(00)81584-6;
Dutnall R.W., Tafrov S.T., Sternglanz R., Ramakrishnan V.;
"Structure of the histone acetyltransferase Hatl: a paradigm for the GCN5-related N-acetyltransferase superfamily.";
Cell 94:427-438(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- FUNCTION: Acetylates the lysine at residue 12 of free histone H4 but does not modify histone H4 when packaged in chromatin. HATI has intrinsic substrate specificity that modifies lysine in recognition sequence GXGXXG.
--- CATALYTIC ACTIVITY: Acetyl-CoA + histone = CoA + acetylhistone.
--- SUBUNIT: Oligomer (>200 kDa) of HATI and HAT2 subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Labaer J.;
"Creation of the YFLEX clone resource: cloning of Saccharomyces
cerevisiae ORFs in the Gateway recombinational cloning system.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P39994:HAT2; NbExp=1; IntAct=EBI-8176, EBI-8185; P53861:YNL230C; NbExp=1; IntAct=EBI-8176, EBI-29191; -1- SUBCELLULAR LOCATION: Cytoplasmic, also detected in nuclear
             "Identification of a gene encoding a yeast histone H4 acetyltransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GermOnline; 143983; -.
Ensembl; YPL001W; Saccharomyces cerevisiae.
SGD; S000005922; HAT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z48483; CAA88385.1; -; Genomic_DNA.
EMBL; Z7125; CAA85040.1; -; Genomic_DNA.
EMBL; U3335; AAB68104.1; -; Genomic_DNA.
EMBL; AY558042; AAS56368.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: To S.pombe SPAC139.06.
                                   acetyltransferase.";
J. Biol. Chem. 270:24674-24677(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A57583; A57583.
PDB; 1BOB; X-ray; @=1-320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  012341;
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Gaps

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24 KMSNRMY 30
Transit peptide.
TRANSIT
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                                   SEQUENCE
                                                              Query Match
                                                                                                                                                                                    CXH48_ASPSC
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Matches
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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"Cloning of pea sulfite reductase.";

"Embi, AB168112, BAD12837.1; -; mRNA.

"RSP; P17846; 1AOP.

"GO; OG:0066118; PEGICTON transport; IEA.

"InterPro; IPR006067; Nir_Si.

"InterPro; IPR006067; Nir_Si.

"InterPro; IPR00117; Nir_Si.

"Pfam; PF01077; NIR_SIR, 2.

"Pfam; PF0460; NIR_SIR, 2.

"Pfam; PF0460; NIR_SIR, ferr; 2.

"PRINTS; PR00397; SIROHĀEM.

"TIGRRAMS; TIGRO3042; SIROHĀEM.

"PROSITE; PS00365; NIR_SIR; 1.
                                                                                                                                  NUCLEOTIDE SEQUENCE.

Keaton M.A., Cannon G.C., Heinhorst S.;

"CDNA sequence for soybean ferredoxin:sulfite reductase.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AX017473, AAGS9996.1; -; mRNA.

HSSP; P17846; 4AOP.
                                                                                                                                                                                                                                                                                                                                                                                                          88.6%; Score 31; DB 2; Length 573; 85.7%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                           ferredoxin:sulfite reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                         56 >573 ferredoxin:sulfite reducts
573 573
573 AA, 63821 MW, FD02A907B746B2D9 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Ferredoxin:sulfite reductase precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  685 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                          GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR006066; Nir Si.
InterPro; IPR006067; Nir Sir 4Pe4S.
InterPro; IPR005117; NiR SiR beta_fer.
InterPro; IPR011787; Sir.
                                                                                                                                                                                                                                                                     Pfam; PF01177; NIR SIR; 1.
Pfam; PF03460; NIR SIR ferr; 2.
PRINTS; PF00397; SIROHAEM.
TIGREAMS; TIGRO2042; sir; 1.
PROSITE; PS00365; NIR SIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Sulfite reductase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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Q75NZO;
05-JUL-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                55
>573
573
                                                 Glycine max (Soybean)
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135 KVSNQLY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                 Glycine.
NCBI_TaxID=3847;
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                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
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SIGNAL
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nose snake) venom.";
Int. J. Biochem. 20:337-345(1988).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- TOXIC DOSE: LD(50) is 9.4 mg/kg by intravenous injection.
-!- TOXIC DOSE: LD(50) is 9.4 mg/kg by intravenous group XIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Joubert F.J.;
"Snake venom toxins -- II. The primary structures of cytotoxin
homologues S3C2 and S4C8 from Aspidelaps scutatus (shield or shield-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Venom;
MEDLINE=88185648; PubMed=3356299; DOI=10.1016/0020-711X(88)90361-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspidelaps scutatus (Ghield-nose snake).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Elepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophiinae; Aspidelaps.
                                                                                                                               ;
                                                                                   Length 685;
                                                                              Similarity 85.7%; Score 31; DB 2; Length 685 Similarity 85.7%; Pred. No. 3.6e+02; 6; Conservative 1; Mismatches 0; Indels
                585 sulfite reductase.
76839 MW; 170660B32E867D40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
110-MAY-2005 (Rel. 47, Last annotation update)
Cytotoxin homolog 84C8.
                                                                                                                                                                                                                                                                                                                                   64 AA
Potential.
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                                                                                                                                                                                                                                                                                                                                   STANDARD;
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133 KVSNQLY 139
                  52 6
685 AA;
                                                                                                                                                                        1 KVSNRLY 7
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                                                                                                   Local Similarity
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ORFNames=TA08960
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NCBI_TaxID=5874;
TIGR; GSU3172;
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Note of the Carray of the Carray Carr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
                                                                                                                                                                                                                                                                            OrderedLocusNames=CAGLOH00704g;
candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%; Score 30; DB 2; Length 130
71.4%; Pred. No. 1.1e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AA; 14887 MW; A222586437A66578 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=GSU3172;
                                                                                                                                                             Last sequence update)
Last annotation update)
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PubMed=14671304; DOI=10.1126/science.1088727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AA.
                                             130 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE017180; AAR36563.1; -; Genomic_DNA
                                                                                                                       Created)
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                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q747U3 GEOSL PRELIMINARY;
Q747U3;
                                 QEFSGS CANGA PRELIMINARY;
QEFSGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 430:35-44(2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5478;
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Q747U3 GROSL
Q747U3 GROSL
D7 Q5-JUL-20
D7 O5-JUL-20
D8 Hypotheti
G8 Geobacter
C9 Geob
            Q6FSG5
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
Hall N., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                   Gaps
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MEDLINE=92184120; PubMed=1339360; DOI=10.1016/0378-1119(92)90438-U;
Mallinder P.R., Pittchard A., Moir A.;
"Cloning and characterization of a gene from Bacillus
stearothermophilus var. non-diastaticus encoding a glycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Alveolata; Apicomplexa; Piroplasmida; Theilerlidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Hypotherical protein in gldA 3'region (ORF5) (Fragment).
Bacillus stearchermophilus.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Geobacillus.
NGI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The chromosome 3 genome sequence of Theileria annulata.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CR940353; CAI76570.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dehydrogenase.";
Gene 110:9-16(1992).
-!- SIMILARITY: Contains 2 4Fe-4S type ferredoxin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%; Score 30; DB 2; Length 189; 71.4%; Pred. No. 1.6e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                 Length 161;
                                                                                                                                                                                                Indels
InterPro; IRR008312; UCP028301.
Pfam; PF05591; DUF770; 1.
PIRSF; PIRSF028301; UCP03301; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 161 AA; 18185 MW; 29EB10B908B5BFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 189 AA; 21158 MW; 41DA80AA475E3237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                    85.7%; Score 30; DB 2; Li
100.0%; Pred. No. 1.4e+02;
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                                                                                                                                                                   100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q4U9D3_THEAN PRELIMINARY;
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Best Local Similarity 71.4.
                                                                                                                                                                                                     6, Conservative
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                                                                                                                                                      Query Match
Best Local Similarity
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77 VSNRLY 82
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Tue Jan
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the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                              Gaps
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                                                                                                                                              Query Match
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                   24210 MW; 0A95D704B2CA0695 CRC64;
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71 KIGNRLY 77
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SEQUENCE
            removed.
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Search completed: December 30, 2005, 13:33:23 Job time : 66 secs

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TYPE: PRT
ORGANISM: Glycine max
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Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 4604, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 4, Appli
Sequence 5170, Ap
Sequence 25, Appl
Sequence 2, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 73, Appl
Sequence 154, Appl
Sequence 6134, Appl
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Sequence 27, Appl
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                                                                                                        December 30, 2005, 13:14:26; Search time 15.6935 Seconds (without alignments) 36.877 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-726-44-4

US-10-726-114-4

US-09-218-328-325-170

US-09-134-001C-3820

US-08-134-001C-3820

US-08-134-001C-3820

US-08-134-001C-3820

US-08-134-03-154

US-09-99-016-6132

US-09-999-016-7306

5223423-3

US-09-999-016-7306

5223423-3

US-09-299-016-7306

S223423-3

US-08-27-112-8

US-08-171-108A-8

US-08-477-112-8

US-08-477-112-8

US-08-477-112-8

US-08-477-112-9

US-08-477-112-4

US-08-477-112-4
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                                                                                                                                                                                                                                                                                                             572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        sw model
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Gapop 10.0 , Gapext 0.5
                                                                        - protein search, using
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Maximum DB seq length: 200000000
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35
1 KVSNRLY 7
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Match
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                                                                          OM protein
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No.
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10330, A
21, Appl
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Sequence 3
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  Sequence
US-09-513-999C-6825
US-09-840-495-26
US-09-499-039A-10330
US-09-489-039A-10330
US-10-303-162-21
US-10-303-118-21
US-10-303-118-21
US-10-303-118-21
US-10-303-118-21
US-10-303-118-21
US-09-282-92A-30497
US-09-282-92A-19547
US-09-248-796A-18957
US-09-382-077-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-916-576B-6
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## ALIGNMENTS

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Sequence 20. Application US/09232290A
; Sequence 20. Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: NIEBA, LARS
; TITLE OF INVENTION: IMMUNOGLOBULIN SUBER FAMILY DOWAINS AND FRAGMENTS WITH
; TITLE OF INVENTION: INFREASED SOLUBILITY
; FILE REFERENCE: MORPHO/7
; CURRENT FILING DATE: 1999-01-15
; CURRENT FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-720-524-4
; Sequence 4, Application US/09720524
; Sequence 4, Application US/09720524
; Sequence 4, Application US/09720524
; Benent No. 6720172
; GENERAL INFORMATION:
    APPLICANT: B. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
; FILE REPRENCE: BB-1167-D
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/092,833
; RIOR PILING DATE: 1998-07-14
; NUMBER: OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 687
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Best Local Similarity 85.7
Matches 6; Conservative
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55 KVSNRFY
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CRGANISM: Murine
US-09-232-290-20
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 3820
LENGTH: 388
            APPLICANT: SANTAWARIA, Ignio
APPLICANT: VELASCO, Gloria
APPLICANT: CAZORLA, Maite
APPLICANT: CAZORLA, Maite
APPLICANT: CAMPO, Elias
APPLICANT: CAMPO, Elias
APPLICANT: LOPEZ-CTIN, Carlos
APPLICANT: LOPEZ-CTIN, Carlos
APPLICANT: WATA, Kazush
APPLICANT: WATA, Kazush
TITLE OF INVENTION: NOVEL HUMAN CATHERSIN L2 PROTEIN, GENE ENCODING SAID
TITLE OF INVENTION: NOVEL HUMAN CATHERSOP
FILE REPERENCE: 99-410A/WMC/0132
CURRENT FILIAG DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US/09/290,586A
CURRENT FILIAG DATE: 1999-06-05
NUMBER: OF SECIENT PLICATION NUMBER: JP 10-172147
NUMBER: OF SECIENT PLICATION NUMBER: JP 10-172147
NUMBER: OF SECIENT PLICATION NUMBER: JP 10-172147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 365;
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85;
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Sequence 2, Application US/08426428

Patent No. 5637462

GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: NEW CATHEPSIN C HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB;
Pred. No. 85;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-134-001C-3820
; Sequence 3820, Application US/09134001C
; Patent No. 6380370
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Sequence 5170, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENTE: 6799-0378
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5170
LENGTH: 323
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GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-D
CURRENT APPLICATION NUMBER: US/10/757,114
CURRENT FILING DATE: 2004-01-14
FRIOR APPLICATION NUMBER: 05/09/720,524
FRIOR PILING DATE: 2001-05-10
FRIOR APPLICATION NUMBER: 60/092,833
FRIOR PILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 687
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                                      Score 31; DB 2; Length 687;
Pred. No. 97;
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85.7%; Pred. No. 97;
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Pred. No. 75;
2; Mismatches 0; Indels
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8.09-290-586A-25
; Sequence 25, Application US/09290586A
; Patent No. 6800473
                                                                                                                                                                                                                                                                     Sequence 4, Application US/10757114
Patent No. 6939710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Acinetobacter baumannii
                                         88.6%;
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Similarity 71.4%;
5; Conservative
                 Query Match
Best Local Similarity 85.,
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Matches 6; Conservative
                                                                                                                                                  135 KVSNQLY 141
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135 KVSNQLY 141
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241 KMSNRIY 247
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Best Local Similarity
Matches 5; Conserv
                                                                                                                      1 KVSNRLY 7
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US-09-328-352-5170
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US-10-757-114-4
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US-09-720-524-4
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Werner, Sabine

APPLICANT: Halle, Jorn-Peter

APPLICANT: Halle, Jorn-Peter

APPLICANT: Regenbogen, Johannes

APPLICANT: Regenbogen, Johannes

APPLICANT: Regenbogen, Johannes

TITLE OF INVENTION: Use of Follypeptides or Nucleic Acids for

TITLE OF INVENTION: Healing and for the Identification of Pharmacologically

TITLE OF INVENTION: Active Substances

TITLE OF INVENTION: Active Substances

TITLE OF INVENTION: Active Substances

TITLE OF INVENTION NUMBER: US/09/886,319A

CURRENT APPLICATION NUMBER: US 60/222,081

PRIOR APPLICATION NUMBER: DE 10030149.5

PRIOR FILING DATE: 2000-06-10

PRIOR FILING DATE: 2000-06-20

WUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 73
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Batent NO. 6727066

GRNERAL INFORMATION:
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT FAPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 2; Length 463;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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         REFERENCE/DOCKET NUMBER: PF-0032 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 73, Application US/09886319A Patent No. 6586185
                                    TELECOMMUNICATION INFORMATION:
TELEPRONS: 415-85-055
TELEPRAX: 415-85-0195
TELEPRAX: 415-85-0195
SEQUENCE CHARACTERISTICS:
ENGTH: 463 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Amino acid
TYPE: Amino acid
SCOULLOCY: linear
MOLECULE TYPE: protein
US-08-871-314-2
                                                                                                                                                                                                                                                                                                                                                                                       85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3330 Hillview Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,428
FILING DATE:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/871,314
FILING DATE: 6/9/1997
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i Sequence 2, Application US/08871314

i Patent No. 6066488

i GENERAL INFORMATION:

APPLICANT: Coleman: Roger

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: NEW CATHEPSIN C HOWOLOG

NUMBER OF ENGURNES: 2

CORRESPONDENCE ADDRESS:

ADDRESSES: Incyte Pharmaceuticals, Inc.

STREE: 3330 Hillytew Avenue

CITY: Palo Alto
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ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: 9F-0032 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR EGG ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
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APPLICATION NUMBER: 08/426,428
FILING DATE: 04/19/1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Luther, Barbara J. REGISTRATION NUMBER: 33954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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ZIP: 9430
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5223423-3
; Patent No. 5223423
; Patent No. 5223423
; Patent No. 5223423
; GALLO, ROBERT
; TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
; HUMAN IMMUNOBERICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION DATA:
; APPLICATION DATE: 03-31-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08667809B
; Sequence 2, Application US/08667809B
; Patent No. 5986174
; GENERAL INFORMATION:
APPLICANT: Bazczynski, Chris
APPLICANT: Rosichan, Jeffrey L.
APPLICANT: Rosichan, Jeffrey L.
APPLICANT: Hoscowitz, Jeanine
TITLE OF INVENTION: MAIZE PROMOTER SEQUENCE FOR LEAF- AND TITLE OF INVENTION: STALK-PREFERRED GENE EXPRESSION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3025;
                                                                                          Length 474;
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CITRET: Box 1000
STREET: IOWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,809B
FILING DATE: 21-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: SWeeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.7%; Score 30; DB 6; Le
100.0%; Pred. No. 7.4e+02;
tive 0; Mismatches 0;
                                                                                       85.7%; Score 30; DB 2; 1
ilarity 85.7%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 1.
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TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                   173 KYSNRLY 179
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                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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; LENGTH: 3025
TYPE: PRT
ORGANISM: Human
                                               US-09-949-016-7306
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PELLING DATE: 2000-04-14
PRIOR FILING DATE: 2000-00-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-09
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFFWARE: FREISEQ FOR WINDOWS Version 4.0
SEQ ID NO 7306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 08/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,468
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRESEQ for Windows Version 4.0
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                 ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 014284CD1
US-09-919-039-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6132, Application US/09949016
Patent No. 6812339
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; Sequence 7306, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                         85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-6132
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                          LENGTH: 463
    SEQ ID NO 154
                                                                                                 FEATURE
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Qy 1 KVSNRLY 7
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Db 229 RVNNRLY 235
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Search completed: December 30, 2005, 13:37:17 Job time: 16.6935 secs

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Sequence 54, Application US/10735916A Publication No. US20050084906A1 GRNERAL INFORMATION: APPLICANT: CORTSCH, Liliane APPLICANT: CORVAIA, Nathalie APPLICANT: LEGER, Olivier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-10-735-916A-54
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Sequence 54, Appl
Sequence 61, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 64, Appl
Sequence 24199,
Sequence 281410,
Sequence 283410,
Sequence 283410,
Sequence 225929,
Sequence 225929,
Sequence 13411,
Sequence 134241,
Sequence 16, Appli
Sequence 23, Appli
Sequence 66, Appli
Sequence 23, Appli
Sequence 66, Appli
Sequence 66, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 23, Appli
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                                                                                                                                    December 30, 2005, 13:33:42; Search time 52.0484 Seconds (without alignments) 56.194 Million cell updates/sec
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Sequence
Sequence
Sequence
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(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-735-916A-54
US-10-735-916A-61
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US-10-725-115-303579
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US-10-424-599-283410
US-10-757-114-4
US-10-757-114-4
US-10-757-114-4
US-10-757-114-4
US-10-757-114-4
US-10-757-114-4
US-10-757-114-4
US-10-757-115-33315
US-10-297-509-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Gapop 10.0 , Gapext 0.5
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35
1 KVSNRLY 7
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Perfect
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No.
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Sequence 734, App
Sequence 19065, A
Sequence 23102, A
Sequence 249121,
Sequence 228278,
Sequence 250209,
Sequence 256646,
Sequence 248390,
Sequence 615, App
Sequence 615, App
Sequence 615, App
Sequence 617, App
Sequence 24730, A
Sequence 24730, A
Sequence 68597, A
Sequence 28, Applised
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yeduence 4, Application US/10735916A

yeblication No. US20050084906A1

general information No. US20050084906A1

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  US-10-631-467-734
US-10-369-493-19065
US-10-732-923-23102
US-10-425-115-249121
US-10-437-963-194958
US-10-425-115-256209
US-10-425-115-256209
US-10-425-115-25646
US-10-425-115-264709
US-10-389-566-615
US-10-389-566-615
US-10-282-122A-68597
US-10-282-122A-68597
US-10-034-644-9
US-10-033-644-9
US-10-023-644-9
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; ORGANISM: Mus musculus
US-10-735-916A-4
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Matches 7; Conserv
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Best Local Similarity 100..
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CORGANISM: Homo sapiens
US-10-735-916A-65
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APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: W 03/08 538
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/05 54
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PATENTIN Ver. 2.1
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Sequence oi, Application No. US20050084906A1

SEDERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: CORVALA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE REFERENCE: 017753-183
TITLE REFERENCE: 017753-183
TITLE REFERENCE: 017753-183
FILE REFERENCE: 0107753-183
FRIOR APPLICATION NUMBER: PR 04/00 653
FRIOR PILING DATE: 2003-07-11
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR PILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FIL
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US-10-735-916A-61
; Sequence 61, Application US/10735916A
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Best Local Similarity 100.
Matches 7; Conservative
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US-10-735-916A-54
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                                                                                                                                                                                 Sequence 67, Application US/10735916A
; Sequence 67, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: GORTSCH, Nathalie
APPLICANT: BECER, Alain
APPLICANT: BECK, Alain
APPLICANT: HARUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735, 916A
CURRENT FILING DATE: 2003-12-16
; PRIOR PILING DATE: 2003-07-11
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                                                      100.0%; Score 35; DB 5; Length 122; 100.0%; Pred. No. 13;
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Best Local Similarity 100.
Matches 7; Conservative
                                                      Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
           ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-49
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74 KVSNRLY 80
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65 KVSNRLY 71
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LENGTH: 122
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Squence 303579, Application US/10425115
Squence 303579, Application US/10425115
Squence 303579, Application No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-2163229
FILE REFERENCE: 38-2163229
FILE REFERENCE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 303579
LENGTH: 214
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; Publication No. US20040214272A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
; APPLICANT: Encour, Yihua
APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
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US-10-425-115-303579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.4%; Score 32; DB 4;
85.7%; Pred. No. 1e+02;
tive 1; Mismatches
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FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
PRIOR APPLICATION NUMBER: PCT/FK UJ/UV IN-
PRIOR FILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-80
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 67
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Best Local Similarity 85.7.
E. Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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116 KVTNRLY 122
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ORGANISM: Zea mays
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Gaps

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APPLICANT: La Kovalic David K
APPLICANT: La Kovalic David K
APPLICANT: Abou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwi I
ATTLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                   US-10-757-114-4

Sequence 4, Application US/10757114

Sequence 4, Application WS/10757114

Publication No. US20040137496A1

GENERAL INFORMATION:

APPLICANT: E. I. du Font de Nemours and Company

TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins

FILE REPERENCE: BB-1167-D

CURRENT APPLICATION NUMBER: US/04/757,114

CURRENT PILING DATE: 2004-01-14

PRIOR PILING DATE: 2001-05-10

PRIOR PILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 8

SOFTWARR: MICROSOFT OFFICE 97

SEROTH: 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 687;
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Pred. No. 5.5e+02;
1; Mismatches 0; Indels
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                                                                                                                                         Query Match 88.6%; Score 31; DB 4; Length 687 Best Local Similarity 85.7%; Pred. No. 5.5e+02; Matches 6; Conservative 1; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Glycine max
; PEATURE:
; PEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97942C.1.pep
US-10-424-599-283410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_46044C.1.pep
US-10-424-599-225929
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Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 225929, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Glycine max US-10-757-114-4
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                               135 KVSNOLY 141
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REPERRENCE: 38-21 (5323.)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 283409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 283410, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REPRENCE: 38-21(5223.3) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 283410
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                                                                                                                                                                                                                                                          88.6%; Score 31; DB 4; Length 92; 71.4%; Pred. No. 68; 0; Indels ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_97941C.1.pep
US-10-424-599-283409
                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_17309C.1.pep
US-10-425-115-264792
                        TYPE: PRT
ORGANISM: Zea mays
PEATURE:
NAME/KSY: ungure
LOCATION: (1)..(92)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: ungure
LOCATION: (1)..(223)
OTHER INFORMATION: ungure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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85 KISNKLY 91
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US-10-424-599-283410
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US-10-424-599-283409
    LENGIH: 92
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Gaps

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Gaps

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RESULT 14
US-10-739-930-6956
is Sequence 6556, Application US/10739930
is Publication No. US20040216190A1
is GENERAL INFORMATION:
is APPLICANT: KOVALIC, David K.
is TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
is TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
is TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
is TITLE OF INVENTION: UNUMBER: US/10/739,930
is CURRENT PILING DATE: 2003-12-18
is NUMBER OF SEQ ID NOS: 11088
is SEQ ID NO 6956
it ERNOTH: 176
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Sequence 336315, Application US/10425115

Publication No. US20040214272A1

Sequence 336315, Application US/10425115

Publication No. US20040214272A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE REFERENCE: 38-21 (53222)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEG ID NO 336315

LENGTH: 223
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85.7%; Score 30; DB 5; Length 176;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
COGANISM: Brassica napus
PEATURE:
COTHER INFORMATION: Clone ID: BRANA-23APR03-C27607_1.p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_69828C.1.pep
US-10-425-115-336315
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47 KIKNRLY 53
|:||| |
32 KISNRFY 38
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ORGANISM: Zea mays
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Search completed: December 30, 2005, 14:14:51 Job time : 53.0484 secs

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December 30, 2005, 13:35:07; Search time 2.59677 Seconds (without alignments) 20.187 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06 NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07 NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 57103 seqs, 7488799 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                 protein search, using
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Maximum DB seq length: 200000000
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35
                                                                                                                                                                                                                                                                                                     1 KVSNRLY 7
                                                                                                                                                                                                                                                                               score:
                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                          Sequence:
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Perfect
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 4, Appli Sequence 54, Appl Sequence 61, Appl Sequence 63, Appl Sequence 63, Appl Sequence 67, Appl Sequence 61, Appl Sequence 1000, Ap Sequence 11, Appli Sequence 1, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Description US-11-012-353-4
US-11-012-353-61
US-11-012-353-65
US-11-012-353-65
US-11-012-353-63
US-11-012-353-67
US-10-012-353-67
US-10-012-353-67
US-10-1012-353-67
US-10-1012-353-67
US-11-108-17-5A-11
US-11-113-775A-1
US-11-113-775A-1
US-11-113-775A-1
US-11-113-775A-1
US-11-113-7799-1
US-11-113-7799-1
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US-11-113-7799-3
US-11-113-779-3
US-11-113-779-3
US-11-113-779-3
US-11-082-389-80
US-11-082-389-80
US-10-818-628-1030
US-10-818-628-1030
US-10-818-628-1030
US-11-082-389-78 Query Match Length DB Score Result No. 

US-11-012-353-4
; Sequence 4, Application US/11012353
; Fublication No. US20050249730A1
; GENERAL INFORMATION: US200550249730A1
; GENERAL INFORMATION: LILIANE
; APPLICANT: CORVER, LILIANE
; APPLICANT: CORVER, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: DUFLOS, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 01753-198
; CURRENT FILING DATE: 2004-12-16
; PRIOR PILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: FR 020553
; PRIOR PILING DATE: 2003-07-20
; PRIOR PILING DATE: 2002-01-18
; PRIOR PILING DATE: 2002-01-18 242, App 2142, Ap 1248, Ap 12, Appli 2, Appli 14, Appl 18, Appl 67, Appl 75, Appl Sequence 2 Sequence 2 Sequence 1 Sequence 2 Sequence 2 Sequence 6 Sequence 6 Sequence 6 Sequence 5 Sequence 1 Sequence 2 Sequence 3 Sequence 5 Sequence 5 Sequence 1 Sequence 1 Sequence 1 ALIGNMENTS 43 TYPE: PRT
ORGANISM: Mus musculus
US-11-012-353-4 SEQ ID NO 4 

Gaps ö Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Batches 7; Conservative 0; Mismatches 0; Indels

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KVSNRLY 7 1 KVSNRLY

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US-11-012-353-54 ; Sequence 54, Application US/11012353

RESULT 2

Sequence 188, Sequence 1030, Sequence 112,

Sequence

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RESULT 5
US-11-012-353-49
    LENGTH: 112
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Sequence 61, Application NS/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIAME
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: LEGRE, OLIVIER
APPLICANT: LEGRE, OLIVIER
APPLICANT: LEGRE, OLIVIER
APPLICANT: LEGRE, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYRRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01753-196
FILE REPERENCE: 01753-196
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-07-11
PRIOR FILING DATE: 2002-07-11
PRIOR FILING DATE: 2002-01-18
PRIOR PRIOR DATE: 2002-01-18
PRIOR PRIOR DATE: 2002-01-18
PRIOR PRIOR DATE: 2002-01-18
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                   GENERAL INFORMATION:

APPLICANT: GORISCH, LILIANE
APPLICANT: CORVALA, NATHALIE
APPLICANT: CORVALA, NATHALIE
APPLICANT: CORVALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
ITILE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
ITILE OF INVENTION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR PLING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2003-01-18
PRIOR FILING DATE: 2003-01-18
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PRIOR FILING DATE: 2003-01-18
PRIOR F
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Publication No. US20050249730A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 KVSNRLY 61
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Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAGUW, JEAN-FRANCOIS
APPLICANT: HEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
ITLE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-01-18
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Publication No. US20050249730A1

Publication No. US20050249730A1

Publication No. US20050249730A1

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: HAEUW, JEAN-PRANCOIS

APPLICANT: HEGER, OLIVIER

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

FILE REFERENCE: 017753-198
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                                                                                              Query Match 100.0%; Score 35; DB 7; Length 112; Best Local Similarity 100.0%; Pred. No. 0.21; Matches 7; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 65
LENGTH: 112
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-11-012-353-65
TYPE: PRT
CORGANISM: Homo sapiens
US-11-012-353-61
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55 KVSNRLY 61
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US-10-821-234-1000

US-10-821-234-1000

Sequence 1000, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Adarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REPRENCE: 82.1A

CURRENT FILING DATE: 2004-04-07

PRIOR PRILNG DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SEQ ID NO 1000

LENGTH: 488

LENGTH: 488
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: GORISCH, LILIANE
APPLICANT: CORVALA, NATHALIE
APPLICANT: CORVALA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, DEAN-FRANCOIS
APPLICANT: HAEUW, DAIN
TITLE OF INVENTION: RECEPTORS ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTI-IOE-IR AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR PLILING DATE: 2003-01-12-16
PRIOR PELLING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 020553
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLILING DATE: 2002-01-18
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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                RESULT 7
US-11-012-353-67
US-11-012-353-67
Sequence 67, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-821-234-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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        74 KVSNRLY 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KVSNRLY 7
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GROENGAL INCUMATION:
APPLICANT: GOCFGCH, LILIANE
APPLICANT: COCVAIA, NATHALIE
APPLICANT: COCVAIA, NATHALIE
APPLICANT: COCVAIA, ALAIN
TAPLICANT: BUEKA, ALAIN
TILLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TILLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: US/35,916
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 020553
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLILING DATE: 2002-01-20
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLILING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
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CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR PLICATION NUMBER: FR 0308538
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2002-01-20
PRIOR PLING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 020653
PRIOR APPLICATION NUMBER: FR 020653
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQ 1D NO 49
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-49
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US-11-012-353-63
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Score 30; DB 6; Length 488; Pred. No. 13; 85.7%; Query Match Best Local Similarity

1 KVSNRLY 7

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Query Match 77.1
Best Local Similarity 57.1
Matches 4; Conservative
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US-11-108-172-631
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172 KLNNRIY 178
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US-11-113-775A-2
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US-11-113-775A-1
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                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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  Gaps
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APPLICANT: King Gordon E.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Reager, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Ordick Thomas S.
APPLICANT: Ordick Thomas S.
TITLE OF INVENTION: COMPOUND FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OP COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C15
CURRENT FILING DATE: 2005-04-15
CURRENT FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 09/833,263
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 09/649,811
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                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: PONTANA MATIA Rita
APPLICANT: PONTANA MATIA Rita
APPLICANT: PIZZA MATIAGRAZIA
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR PULING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 6; Length 232;
Pred. No. 16;
1; Mismatches 1; Indels
  Indels
  1;
Mismatches
                                                                                                                                                                       Sequence 4338, Application US/10467657
Publication No. US20050260581A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 631, Application US/11108172; Publication No. US20050260177A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           raype: PRT (CRGANISM: Neisseria gonorrhoeae US-10-467-657-4338)
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 9218
SOFTWARES SEGWHI99, Version 1.04
SEQ ID NO 4338
LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Smith, Carole L.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| ||||
211 RVENRLY 217
                                                                      187 KYSNRLY 193
                                    1 KVSNRLY 7
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Matches
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PRIOR PILLION APPLICATION WARRENERS US 09/515,251
PRIOR PILLION DATE: 2000-06-20
PRIOR PILLION DATE: 2000-06-21
PRIOR APPLICATION NAMER: US 09/40-231
PRIOR APPLICATION NAMER: US 09/40-231
PRIOR PILLION DATE: 1000-02-130
PRIOR PILLION DATE: 2000-04-13
PRIOR PILLION PARTICATION WARREN DE 12000-04-13
PRIOR PILLION PARTICATION WARREN DE 12000-04-13
PRIOR PILLION PARTICATION PA
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US-10-630-203-12
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| Sequence 2, Application US/11113799 |
| Sequence 2, Application US/11113799 |
| Sequence 2, Application W. US20050261156A1 |
| GENERAL INFORMATION: |
| APPLICANT: Kottwitz, Beatrix |
| APPLICANT: Pegelow, UIxid: |
| TITLE OF INVENTION: DETERGENT WITH SULFO-POLYMER RINSE AID AND A SPECIAL |
| TITLE OF INVENTION: ALPHA-AMYLASE |
| FILE REFRERENCE HERK-0123 / H 06113 |
| CURRENT APPLICATION NUMBER: US/11/113,799 |
| CURRENT PILING DATE: 2005-04-25 |
| PRIOR APPLICATION NUMBER: DE 102004020431.4 |
| PRIOR FILING DATE: 2004-04-27 |
| PRIOR FILING DATE: 2004-04-27 |
| PRIOR FILING DATE: 2004-04-10-04 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/11113799;
Sequence 1, Application US/11113799;
Publication No. US20050261156A1
GENERAL INFORMATION:
APPLICANT: Kottwitz, Beatrix
APPLICANT: Fegelow, Ulrich
TITLE OF INVENTION: DETERGENT WITH SULFO-POLYMER RINSE AID AND A SPECIAL
TITLE OF INVENTION: DALPHA-AMYLASE
FILE REFERENCE: HENK-0123, 74 06113
CURRENT FILING DATE: 2005-04-25
CURRENT FILING DATE: 2004-04-27
PRIOR FILING DATE: 2004-04-27
PRIOR FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 3
SOFFWARE: PATENTIN VETSION 3.3
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                                                                                                                                                                                                                                                                                                    Query Match
77.1%; Score 27; DB 7; Length 483;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 3; Mismatches 0; Indels
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; CURRENT FILING DATE: 2005-04-25
; PRICR APPLICATION NUMBER: DE 102004020430.6
; PRICR FILING DATE: 2004-04-27
; PRICR APPLICATION NUMBER: DE 10200408591.7
; PRICR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Variant of Seq. ID No. 3 US-11-113-799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    |::||:|
172 KLNNRIY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |::||:|
172 KLNNRIY 178
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Bacillus sp
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                                                                                                                                                                                                                                                                                                                                                                                                      1 KVSNRLY 7
                                                                                                                                                                                                                                                             US-11-113-775A-2
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LENGTH: 483
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US-11-113-799-1
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US-10-630-203-12
is Sequence 12, Application US/10630203
j Publication No. US20050250663A1
j GENERAL INFORMATION:
j APPLICANT: Wovozymes A/S
j APPLICANT: Thisted, Thomas
j APPLICANT: Fyuglasmy, Claus Crome
j APPLICANT: Fyuglasmy, Claus Crome
j APPLICANT: Andersen, Carsten
j APPLICANT: Andersen, Carsten
j APPLICANT: Aughasmy, Claus Crome
j TITLE OF INVENTION: Alpha-amylase mutants with altered properties
j TILE REFERENCE: 10062.200-US
j CURRENT APPLICATION NUMBER: US/10/630,203
j CURRENT PILING DATE: 2001-07-31
j NUMBER OF SEQ ID NOS: 30
j SOFTWARE: Patentin version 3.1
j SEQ ID NO 12.
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                                                                                                                                                                                                    Score 27; DB 7; Length 483; Pred. No. 59; 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                         ; OTHER INFORMATION: Variant of Seq. ID No. 3 US-11-113-799-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: December 30, 2005, 14:15:20 Job time : 2.59677 secs
NUMBER OF SEQ ID NOS: 3
SOFWARE: Patentin version 3.3
SEQ ID NO 2
LENGTH: 483
                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bacillus sp.
                                                                                                                                                                                                                                                                                                                                  172 KLNNRIY 178
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172 KLANARIY 178
                                                                                    TYPE: PRT ORGANISM: Artificial
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December 30, 2005, 14:26:51; Search time 183 Seconds (without alignments) 16.807 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                 - protein search, using
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35
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                                                                      OM protein
                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                        Perfect
                                                                                                    Run on:
                                                                                                                                                                        Title:
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geneseqp20018:* geneseqp20028:* geneseqp2003a8:* geneseqp2003bs:* geneseqp20048:* geneseqp1990s:* geneseqp1980s:* geneseqp2000s:* Geneseq 21:* Database

Listing first 45 summaries

100%

Match

Maximum

Post-processing: Minimum Match 0%

Minimum DB seq length: 7 Maximum DB seq length: 7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20058:*

#### CDR2 of t CDR2 of t Anti-huma Humanised Anti-huma Mouse ant Human lig Complemen Murine an Murine mo Murine pe Mouse HUI Mouse ant Mouse ant CDRL2 reg CDR seque Murine in Murine an Mouse Kap Mouse lec Murine 26 Mouse FGF Mouse HUI Human Adzeroos Nadgeroos Nadgero Aab97135 | Aab97199 | Abb62375 | Aau70350 | Abp58277 Abr40266 SUMMARIES ADR68225 AAR75492 AAW31748 AAW70921 AAW71895 AAY80282 AAB12906 ADZ67008 ADD94240 ABP72121 AAB97199 ADD28189 ADD94239 ADE36487 ADL35323 AAB21365 ABP62375 ADJ76838 AAW70927 DB Length Query 100.00 1774-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744-13 1744 Score Result No.

ABR40266

Abr39455 Anti-Abet	_	Abr39783 Anti-Abet	Aag79999 Humanised	Adc03152 Colon spe	_		Ade94056 Anti-Abet	Adh61993 Mouse ant	Adh17765 Murine an	Ad193522 Human CD4	Adn61704 Humanised	Adm78082 Human SJB	Adm78106 Human SJB	Adm78124 Human SJB	Adm78130 Human SJB	Adp84868 Complemen	Adr19272 Glycosyla	Ads87340 Humanised	Adr68224 Murine 26	Adr68226 Murine 26
7 6 ABR39455	7 6 ABU08302	7 6 ABR39783	7 6 AAG79999	7 7 ADC03152	7 7 ADE27681	7 7 ADD94149	7 7 ADE94056	7 7 ADH61993	7 8 ADH17765	7 8 ADL93522	7 8 ADN61704	7 8 ADM78082	7 8 ADM78106	7 8 ADM78124	7 8 ADM78130	7 8 ADP84868	7 8 ADR19272	7 8 ADS87340	7 8 ADR68224	7 8 ADR68226
24 68.6	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6		24 68.6	24	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6	24 68.6
25	56	27	28	52	30	31	32	33	34	35	36	37	38	68	40	41	42	43	44	45

# ALIGNMENTS

cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. CDR sequence for anti-IGF-1R antibody. ADJ76838 standard; peptide; 7 AA 06-MAY-2004 (first entry) WO2003059951-A2. Mus musculus. ADJ76838; ADJ76838 

24-JUL-2003

20-JAN-2003; 2003WO-FR000178

18-JAN-2002; 2002FR-0000053. 18-JAN-2002; 2002FR-0000054. 07-MAY-2002; 2002FR-00005753.

(FABR ) FABRE MEDICAMENT SA PIERRE

Leger 0;

Goetsch L, Corvaia N,

WPI; 2003-569653/53 N-PSDB; ADJ76837.

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Claim 1; SEQ ID NO 4; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (1) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with

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hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF1R and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetitics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 7; Length 7; 100.0%; Pred. No. 2e+06; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADZ67008 standard; peptide; 7 AA.
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR00178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002FR-00000653.
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                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100
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KVSNRLY 7
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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                                                                                                                                                                                                                                                                                   Sequence 7 AA;
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(BECK/)
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(DUFL/)
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Matches
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ID ADZ67008

XX ADZ67008

XX ADZ6

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XX INBU

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XX Endo

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comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS7006 and ADS7014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cartivation of the IGF-IR and/or EGFR, and/or of EGFR with EGFR, where the administration of the ranaducion pathway of the signal mediated by the intended secondary effects connected with inhibition of the Insulln contraction of IGF-IR and/or EGFR, and/or of EGFR with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the Insulln creceptor. The antibody is useful for preparation of a medicament intended to inhibit the grant connected with inhibition of the Insulln creceptor. The antibody is useful for HERZ/neu-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF-dependent calls (I) is useful in the preparation of a medicament intended to inhibit the granter, creceptally IGF-dependent and/or IGF-dependent calls (I) is useful in the preparation of a medicament intended for prevention or for the treatment of psoriasis (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to treatment of psoriasis (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to seatment of psoriasis (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to seatment of psoriasis (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to reatting from a biological sample in which involves contacting the presence is sequence is used in the exemp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
specifically inhibiting tyrosine kinase activity of the receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse HUI77 mutant light chain CDR amino acid sequence SeqID125.
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06-DEC-2001; 2001US-00011250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2002; 2002WO-US038147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100..
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVSNRLY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KVSNRLY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003046204-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD94240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
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cancer,

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Gaps

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Indels

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The invention relates to novel humanised antibodies and antibody fragments which react with fibroblast growth factor 8 (FGF8) and inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised antibodies and antibody fragments reacting with fibroblast growth factor 8 useful for the treatment and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                 Mouse FGF-8 related protein CDR2 SEQ ID 9.
                                                                                Claim 24; SEQ ID NO 125; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirota M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 69; 86pp; Japanese.
                                                                                                                                                                                                                                                                                                                                ABP72121 standard; peptide; 7 AA.
              Tang Y,
                                                                                                                                                                                                                                    77.18;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUN-2002; 2002WO-JP006591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-2001; 2001JP-00196176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                 03-JUN-2003 (first entry)
                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura K,
              Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-239169/23.
                              WPI; 2003-513649/48.
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                     1 KVSNRLY 7
                                                                                                                                                                                                                                                                                 KVSNRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003002608-A1
                                                                                                                                                                                                                   Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JAN-2003
              Watking JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shitara K,
                                                                                                                                                                                                                                                                                                                                                ABP72121;
                                                                                                                                                                                                                                                                                                               RESULT 4
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its biological functions. The polypeptides of the invention have cytostatic activity. The antibody is useful for the treatment of cancerincluding prostate, breast, ovarian and testicular cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drugs containing antibody compositions produced by cells tolerant t
lectin recognizing specific sugar-chain structure, appropriate for
patients suffering from PcgammaRIIIa polymorphism e.g. in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse; antibody; lectin; sugar; N-acetylglucosamine; For gamma receptor; IIIa; cytostatic; antiallergic; immunomodulator; For gamma receptor; IIIa; cytostatic; antibracy; inflammation; autoimeume disease; circulatory system; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okazaki A;
                                                                                                                                        Score 26; DB 6; Length 7; Pred. No. 2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse lectin tolerance related peptide SEQ ID NO:22.
                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Niwa R,
                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 22; 214pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura K, Shitara K, Hatanaka S,
                                                                                                                                                                                                                                                                                                                                                                  ADD28189 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-2002; 2002JP-00106951.
                                                                                                                                          74.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2003; 2003WO-JP004505
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-812677/76.
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  |||||:
KVSNRI 6
                                                                                                                                                                                                                           1 KVSNRL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003084570-A1.
                                                                                                     Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                           ADD28189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumors
                                                                                                                                                                                    Matcheв
                                                                                                                                                                                                                                                                                                                           RESULT 5
ADD28189
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                                                                                                                                                                                                                                                                 fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach the inner growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anti-cryptic collagen site antibody HUI77 variable region light chain CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; humanised; antibody; fibroblast growth factor 8; FGF8; cytostatic; cancer; prostate; breast; ovarian; testicular; CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cryptic collagen site antibody HUI77 variable region light chain CDR which may be used during the creation of an antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                            New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
                                                                                                                                                                                                                                                  This invention relates to a novel grafted antibody or its functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 7; Length 7; Pred. No. 2e+06; 1; Indels
                                                 Brooks PC;
                                                   Broek D,
            (CELL-) CELL MATRIX INC
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The invention relates to a novel drug containing as the active ingredient an antibody composition produced by cells tolerant to a lectin recognising a sugar-chain structure in which an alpha-bond is formed between the 6-position of N-acetylglucosamine at the reducing end of an N-glycoside bond-type complex sugar chain and the 1-position of fucose, which has affinity to human PC gamma receptor IIIa. A drug of the invention has cytostatic, antiallersic, immunomodulator, cardiant, virucide, and antibacterial activity. The drugs are useful in screening and treating patients not suitable for drugs not derived from these cells, particularly as diagnostics, preventives or remedies for diseases accompanying tumour, allergy or inflammation, autoimmune diseases, diseases of the circulatory system, and viral or bacterial infections. The present sequence is used in the exemplification of the invention. Sequence 7 AA;

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Shimada

Length 7;

Score 26; DB 7; Pred. No. 2e+06;

74.3%; 83.3%;

Similarity

Query Match Best Local

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Treatment and prevention of arthritis comprising the use of anti-FGF-8 (sic fibroblast growth factor) antibody.
                                                                                                                                                                                          arthritis, anti-FGF-8; sic fibroblast growth factor;
cartilage protection agent; joint destruction inhibitor;
synoviral proliferation inhibitor; mouse; murine.
                                                                                                                                                          Mouse anti-FGF-8 antibody-related peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 11; 193pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suda T, Miki I,
                                       ADE36487 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2001; 2001JP-00400677.
                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2002; 2002WO-JP013650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uchii M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-587078/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KVSNRL
                                                                                                                                                                                                                                                                                                                    WO2003057251-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7 AA;
                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                   29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                         17-JJL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL35323;
                                                                            ADE36487;
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RESULT 7
                    ADE36487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anticryptic collagen site antibody HUI77 variable region light chain CDR which may be used during the creation of an antibody of the invention.
                                                                                                                                                                                                                                                                                                                                    grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth, angiogenesis; tumour growth; cytostatic; collagen agonist; collagen anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
                                                                                                                                                                                                                                                                                                 Mouse HUI77 mutant light chain CDR amino acid sequence SeqID124.
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  Indels
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Broek D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 24; SEQ ID NO 124; 232pp; English
                                                                                                                                                                                ADD94239 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang Y,
    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2002; 2002WO-US038147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-00995529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-2001; 2001US-00011250.
                                                                                                                                                                                                                                                          (first entry)
  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CELL-) CELL MATRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-513649/48.
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Best Local Similarity
Matches 5; Conserv
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1 KVSNRFW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KVSNRLY 7
                                         KVSNRL 6
                                                                     KVSNRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003046204-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watking JD,
                                                                                                                                                                                                                                                          29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                       ADD94239;
                                           -
    Matches
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Tanaka A;

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The invention comprises a method for treating and preventing arthritis, the method involves the use of anti-FGF-8 (sic fibroblast growth factor) antibody. The antibody and method of the invention is useful for: the detection, treatment and prevention of arthritis; as a cartilage protection agent; as a joint destruction inhibitor; and as a synoviral proliferation inhibitor. The present amino acid sequence represents a mouse peptide that was used in an example of the invention.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine anti-Fcgamma receptor IIIa antibody-related peptide - SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody binding; Fcgamma receptor IIIa; Fc region sugar chain; cytostatic; antiallergic; antinflammatory; immunosuppressive; vasotropic; virucide; cancer; allergy; inflammatory; autoimmune; circulatory; viral infection; murine; mouse.
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                Length 7;
                                                                                                                                                                                                              Score 26; DB 7;
Pred. No. 2e+06;
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL35323 standard; peptide; 7 AA.
                                                                                                                                                                                                                  74.3%;
83.3%;
                                                                                                                                                                                          Query Match
Best Local Similarity 83.33,
Best Local Similarity 63.33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-2004 (first entry)
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The invention relates to a novel method for enhancing the binding activity of an antibody to the Fcgamma receptor IIIa by increasing the proportion of N-glycoside bond type complex sugar chains attached to the Fc region of the antibody which do not have the 1-position of fucose bound to the 6-position of N-acetylglucosamine at the reducing end of the sugar chain. The method of the invention has cytostatic, antiallargic, antiallammatory, immunosuppressive, vasotropic and virucide applications and may be useful for generating antibodies to be used in the treatment, prevention and diagnosis of diseases including cancer, allorgies, inflammatory disorders, autoimmune diseases, circulatory disorders and viral infections. The current sequence is that of an anti-Fcgamma receptor IIIa antibody-related peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                       Method of enhancing the binding activity of antibody to Fc-gamma receptor IIIa for production of antibodies with high cytotoxicity as cancer, allergic, viral and other disease therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; neuroprotective; nootropic; antibody therapy; antigen-binding; light chain; heavy chain; human; amyloid-beta peptide; complementarity determining region; Alzheimer's disease; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.3%; Score 26; DB 7; Length 7; 83.3%; Pred. No. 2e+06; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine 266 antibody light chain CDR2 variant #2.
                                                                                                                                                                                                                                                             Example 14; SEQ ID NO 80; 296pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR68225 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davies J, Tang Y, Watkins JD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-2004; 2004WO-US002004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2003; 2003US-0446380P
                                                           09-APR-2002; 2002JP-00106950
                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                              09-APR-2003; 2003WO-JP004504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                            Shitara K;
                                                                                                                                                           WPI; 2003-812729/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-625759/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  humanised antibody
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KVSNRI 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KVSNRL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004
                                                                                                                            Nakamura K,
16-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR68225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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The invention relates to an antibody, or its antigen-binding portion, comprising a light chain and a heavy chain that specifically binds human amyloid-beta (Abeta) peptide. The new antibody or its antigen-binding portion that specifically binds human Abeta comprises a light chain and a comprises a light chain and a comprise a light chain and a comparises a light chain and a determining region I (CDRI) comprising amino acid sequences ADR68228.

CC ADR68223; CDRZ comprising amino acid sequences ADR68228 and CDR3 comprising amino acid sequences ADR68229. The heavy chain comprising amino acid sequences ADR68239. The heavy chain comprising amino acid sequences ADR68239, and comprising amino acid sequences ADR68239. The heavy chain comprising amino acid sequences ADR68239, and comprising amino acid sequences ADR68239, and comprising amino acid sequence ADR68239, and comprising the sequence ADR68239; and comprising the sequence ADR68239; and comprising the sequence ADR68239; a heavy CDR2 comprising the sequence ADR68239; a heavy CDR3 comprising the sequence ADR68240; or a comprising the sequence ADR68249; a light chain CDR3 comprising ADR24; a light chain antibody is useful in the manufacture of a medicament for treating Alzheimer's disease. This comprises antibody light chain used to generate the humanised antibody of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer; amplification; PCR; mouse; kappa chain; heavy chain; Pab; antibody; immunotolerance; animal; variegated display library; CDR; variable region; antigen; immunorecessive; cell surface marker; foetal; cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma; familial hypercholesterolaemia; binding affinity; complementarity determining region.
New humanized antibody or its antigen-binding portion that specifically binds human amyloid-beta peptide, useful in the manufacture of a medicament for treating Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating new antibodies specific for immunorecessive epitopes - by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 8; Length 7;
Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse antibody variable region CDR2 peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                   Claim 1; SEQ ID NO 24; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR75492 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.3%;
71.4%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9515982-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75492;
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us-10-735-916a-4.sizlim.rag

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CDRs are derived from the heavy and light chain variable regions of the antibodies FB3-2 (AAQ92502-3) and H3-3 (AAQ92504-5).

The peptides AAR75488-92 represent CDR2 from the variable regions of the antibodies AAR75488-92 represent CDR2 from the variable regions of the above antibodies, used to generate a single variable regions of the sequences were isolated from a variegated display library (VDL) of variable regions derived from a variegated display library (VDL) of variable regions from the antibody coding sequences using the primers AAQ74155-74. The constructed antibody coding sequences using the primers AAQ74155-74. The constructed antibody coding sequences using the primers AAQ74155-74. The antigen e.g. a cell surface marker on a foetal, cancer or immunorecessive antigen e.g. a cell surface marker on a foetal, cancer of the antigen. The antibodies generated can be used in the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of production of the antibody allows rapid and sensitive isolation of antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than those produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                   Peptides AAR75462-92 are examples of complementarity determining regions
selection from variegated V gene library cloned from immuno:tolerance derived antibody repertoire, useful in diagnosis, purifcn. and therapy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-Fas recombinant antibodies - useful for treating auto-immune diseases, especially rheumatoid arthritis.
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100.0%; Pred. No. 2e+06;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementarity determining region.
                                                                          Claim 75; Page 96; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW31748 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    combinatorial/hybridoma methods
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Best Local Similarity
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                                      e.g. of cancer.
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              protein of the invention is a recombinant protein (A), that comprises at least one region corresponding to an immunoglobulin (Ig) variable region which enables the protein to recognise and specifically bind to an antigen, preferably human Fas, and has substantially no more useful for treating autoimmune diseases, especially rheumatism (rheumatoid arthritis). (A) is based on a murine monoclonal antibody. As the protein lacks the constant region, it has substantially no more immunogenicity in the human patient than a human antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - useful
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                                                                                                                                                                                                                                                                                                  Gaps
sequence represents a fragment of the protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody; respiratory syncytial virus; RSV; VP6 protein; rota virus; RV; viral infection; inhibit; fusion; protection; transcription; antiviral agent; prophylaxis; diagnosis; infection; contamination.
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                                                                                                                                                                                                                                                       68.6%; Score 24; DB 2; Length 7; 100.0%; Pred. No. 2e+06; 1ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW70921 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                    Conservative
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Best Local S
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Sequence 7 AA

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Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis; autoimmune disease; rheumatoid arthritis; therapy; human; mouse; antibody engineering; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                            Production of anti-Fas protein humanised antibodies - for use in apoptosis on Fas expressing cells in the treatment of auto:immune diseases, especially rheumatoid arthritis.
                                                                      Anti-human Fas monoclonal antibody CH11 light chain CDR2.
AAW71895 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                       (SANY ) SANKYO CO LID.
                                                                                                                                                                                                                                                                                                                                         WPI; 1998-482965/42.
                                                                                                                                                       Mus musculus.
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                                                  18-JAN-1999
                                                                                                                                                                                                         23-SEP-1998.
                                                                                                                                                                                 EP866131-A2.
                         AAW71895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody type reactions, at least 1 epitope of a pathogenic virus having tropism for the mucosa. AAM70905-16 and AAM70929-46 are analogous to CDR regions for monoclonal antibodies specific for respiratory syncytial virus (RSV). AAM70917-28 are analogous to CDR regions of monoclonal antibodies specific for respiratory syncytial virus specific for site III or IV of the VP6 protein of rota virus (RV). The peptides can neutralise viral infections and may also inhibit fusion between infected and uninfected cells or cells and viruses. They provide so are useful as antiviral agents or for prophylaxis, in human of veterinary medicine. The peptides can be labelled and used to diagnose infection or contamination by the virus. The peptides are particularly directed against RSV or RS but may also be used against papilloma, adeno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - useful
                                          Gaps
                                                                                                                                                                                                                                                              Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody; respiratory syncytial virus; RSV; VPG protein; rota virus; RV; viral infection; inhibit; fusion; protection; transcription; viral agent; prophylaxis; diagnosis; infection; contamination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide(s) recognising viral epitope with tropism to mucosa for, e.g. diagnosing, preventing and treating viral infection(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.6%; Score 24; DB 2; Length 7; llarity 100.0%; Pred. No. 2e+06; Conservative 0; Mismatches 0; Indels
             68.6%; Score 24; DB 2; Length 7;
100.0%; Pred. No. 2e+06;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       CDR2 of the light chain of monoclonal antibody RV-133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entero, polio, influenza or immune deficiency viruses
                                                                                                                                                           AAW70927 standard; peptide; 7 AA.
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    Query Match
Best Local Similarity 100.
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Best Local Similarity
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                                                                                           1 KVSNR 5
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for use in inducing

Yonehara

Takahashi T, Nakahara K,

98EP-00302113. 97JP-00067938

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This peptide comprises complementarity determining region 2 (CDR2) of the light chain variable region (see AAW71889) of the mouse anti-human Fas monoclonal antibody CH11. CDR1 (see AAW71894) and CDR3 (see AAW71896) have also been identified. The invention relates to novel humanised antibodies comprising humanised light and heavy chains (see AAW71876-81) of CH11. These humanised anti-human Fas antibodies are capable of inducing apoptosis in cells expressing Fas (e.g. synoviocytes) and are useful in the treatment of autoimmune disease and chronic rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised anti-Fas antibody light chain CDR2 peptide SEQ ID NO:6.
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                                                                                                                                                                                                                                                                                                                                                                             68.6%; Score 24; DB 2; Length 7;
100.0%; Pred. No. 2e+06;
tive 0; Mismatches 0; Indels
Example 4; Page 53; 187pp; English.
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                                                                                                                                                                                                                                                                                                                                                          immunosuppressive.
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JP2000014383-A.

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AAW71895

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The present invention describes a recombinant antibody (A) which binds to fas antigen, and controls and induces apoptosis in cells which expressed fas antigen. The complementarity determining regions (CDR) of (A) contain amino acid sequences obtained from a mammal other than human, other regions contain amino acid sequences from human and they partly contain modified amino acids. (A) has immunosuppressive activity. (A) is used for treating and/or diagnosing autoimmune diseases. The present sequence represents a specifically claimed light chain CDR2 of (A)
                                                                                                                                                                                                                       Novel recombinant antibody used for treating and diagnosing autoimmune diseases - is humanized anti-Fas antibody which controls and induces apoptosis in cells expressing fas antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.6%; Score 24; DB 3; Length 7; Best Local Similarity 100.0%; Pred. No. 2e+06; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                          (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                        Claim 5; Page 12; 25pp; Japanese.
                                                           98JP-00204318.
                                                                                                  98JP-00204318.
                                                                                                                                                                                   WPI; 2000-199626/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
                                                             03-JUL-1998;
                                                                                                  03-JUL-1998;
                     18-JAN-2000.
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Gaps ö

Search completed: December 30, 2005, 14:47:21 Job time : 186 secs

1 KVSNR 5 |||||| 1 KVSNR 5

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 30, 2005, 14:40:17 ; Search time 36 Seconds (without alignments) 18.709 Million cell updates/sec Run on:

US-10-735-916A-4 35 Title: Perfect score:

1 KVSNRLY 7 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

141 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 7 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	•~	aggrecan - bovine	aspartate transami	glucose isomerase	hypothalamic hepta	ribosomal protein	membrane protein -	phosphonoacetaldeh	omega-gliadine 1'	ribosomal protein	ă	myomodulin - Calif	catch-relaxing pep	fatty-acid synthas	phosphotransferase	hypothetical prote	T-cell receptor be	T-cell receptor be	- 1	dermorphin - Rohde	glutathione transf	glutathione transf	Met-enkephalin-Arg		dermorphin (Trp-4,	•	Ig mu chain D regi	T-cell receptor be	T-cell receptor be
ΩI	A38081	S42620	A11483	S17976	NYPG7	S19630	PQ0663	A28709	PN0150	S78024	PH0932	A28340	ECMUCR	A60139	B39127	140504	PT0520	PT0521	845311	A61324	S71870	S71867	A60224	S36662	821230	PH1602	E33932	PT0663	PT0567
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Query Match Length	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
uery atch	1.7	4.	4.	9.6		5.7	7.		7	5.7	5.7	5.7	5.7	22.9	22.9	22.9	22.9	22.9	22.9	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	0.0
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T-cell receptor be carnocin U149 - Ca probable H+-transp PMRFamide-related hypothetical L2 pr galactose oxidase peptidyl-dipeptida Ig heavy chain V ropacity protein P. opacity protein P. mabinlin II chain wicilin 72K chain 180K exoantigen - acetylcholinestera gene c-rel protein platelet glycoprot
PT0671 A58718 PC2370 PC2370 I56695 XEYDGD M10889 PH10889 S16365 S16365 S38516 A34818 A34026 I50210 C56793
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# ALIGNMENTS

RESULT 1	
A38081	
amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (Pichia angusta) (fragment)	<u> </u>
C;Species: Pichia angusta	
C;Date: 31-Dec-1993 #sequence revision 03-Feb-1994 #text_change 20-Apr-2000	
C;Accession: A38081	
R;M1, D.; Janes, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klinman, J.P.	
J. Biol. Chem. 267, 7979-7982, 1992	,
A;Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine	amine
A; Reference number: A38081; MUID: 92235001; PMID: 1569055	
A;Accession: A38081	
A; Molecule type: protein	
A;Residues: 1-7 <mua></mua>	
A;Cross-references: UNIPARC:UP1000017CA48	
C; Keywords: copper; oxidoreductase; quinoprotein; topaquinone	
F;4/Modified site: topaquinone (Tyr) #status experimental	
Query Match 37.1%; Score 13; DB 2; Length 7;	
Best Local Similarity 50.0%; Pred. No. 2.8e+05; Watches 3. Conservative 1: Mismatches 2: Indels 0: Gaps 0;	

2 |:| | 1 VANYEY 2 VSNRLY Š 셤

aggrecan - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus
C;Species: Bos primigenius taurus
C;Accession: S42620
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A;Title: Aggrecan in bovine tendon.
A;Title: Aggrecan in Bovitan
A;Molecule type: protein
A;Molecule type: Drotein
A;Molecule type: UNIPARC:UPI000017C497
A;Cross-references: UNIPARC:UPI000017C497
C;Keywords: cartilage RESULT 2

Query Match
31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 2 VSNR 5 ò

4 VSPR 7

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Gaps ;

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Int. J. Syst. Bacteriol. 42, 144-150, 1992
A;Title: Blectrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete ge
A;Reference number: S19630; MUID:92144363; PMID:1736962
A;Accession: S19630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment) C; Species: porcine epidemic diarrhea virus C; Species: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999 C; Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999 C; Accession: PQ0663 R; Bridgen, A; Duarre, M; Tobler, K; Laude, H; Ackermann, M. J. Gen. Virol. 74, 1795-1804, 1993 A; Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
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A;Residues: 1-7 <BRL>
A;Cross-references: UNIPARC:UPI0000170FAC; GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID.
C;Comment: This virus is coronavirus related to human coronavirus 229E.
C;Keywords: membrane protein
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C;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C;Accession: A28709
R;Olsen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D. Biochemistry 27, 2229-2234, 1988
A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase.
                                                                                                                                                                                                                                                                                                                                                                  ribosomal protein L30 - Streptomyces griseus (fragment)
C;Species: Streptomyces griseus
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Oct-2004
C;Accession: S1930
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A;Reference number: JQ2191; MUID:93389433; PMID:8397280
50.0%; Pred. No. 2.8e+05; ive 1; Mismatches 0;
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. 2.8e+05;
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A;Experimental source: etrain IFO 13189
C;Superfamally: Ribosomal protein L30p
C;Reywords: protein blosynthesis; ribosome
                                         Conservative
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                                                                Applicate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
NyAlternate names: aspartate aminotransferase, mitochondrial
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: Al1483
R;Campos-Cavieres, M.; Milatein, C.P.
Biochem. J. 147, 275-281, 1975
Biochem. J. 147, 275-281, 1975
A;Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitoch A;Reference number: Al1483; MUID:76039441; PMID:1180894
A;Reference number: Al1483
A;Molecule type: protein
A;Residues: 1-7 cCAM>
A;Residues: 1-7 cCAM>
A;Residues: 1-7 cCAM>
A;Experimental source: liver
C;Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
F;2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucose isomerase - Thermoanaerobacterium saccharolyticum (fragment)
C;Species: Thermoanaerobacterium saccharolyticum
C;Species: Thermoanaerobacterium saccharolyticum
C;Species: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 09-Jul-2004
C;Accession: 817976
R;Lee, C.; Zeikus, J.G.
B;Lee, C.; Zeikus, J.G.
B;Le
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R; Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, Horm. Metab. Res. 13, 228-232, 1981

A; Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasi A; Reference number: A01417; MUD:81213980; PMID:6263778

A; Accession: A01417

A; Molecule type: protein

A; Residues: 1-7 < CHA>

C; Superfamily: hypothalamic heptapeptide

C; Keywords: hypothalamus
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Sep_1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
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Evidence

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Length 7;

DB 2; Le... fn, 2.86+05; 0;

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R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergra, A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0932
A;Molecule type: MRNA
A;Residues: 1-7 <GOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Aplysia californica (California sea hare)
C;Accession: A28340
C;Accession: A28340
R;Cropper, B.C.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 5483-5486, 1987
A;Title: Wyomodulin: A bioactive neuropeptide present in an identified cholinergic bucc A;Reference number: A28340; MUID:87261010; PMID:3474664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catch-relaxing peptide - blue mussel
NyAlternate names: CARP
Cispecies: Mytilus edulis (blue mussel)
Cispecies: Mytilus equince_revision 20-Jun-2000 #text_change 16-Aug-2004
Cibacession: A29342
RiHirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shimamoto, N.; Muneoka, Y.
Brain Res. 422, 374-376, 1987
A; Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.
A; Reference number: A29342; MUID:88052022; PMID:3676797
                                                                                                                                                                                                            A;Cross-references: UNIPARC:UP1000017C9E4
A;Experimental source: complete Freund's adjuvant-immunized lymph node C;Keywords: T-cell receptor
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A;Cross-references: UNIPROT:P10420; UNIPARC:UDI0000126FB4
C;Comment: This peptide exhibits both potentiating (contraction) and C;Keywords: amidated carboxyl end; hormone; retractor muscle P;7/Modified site: amidated carboxyl end (Leu) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.7%; Score 9; DB 2; Length 7; 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Reaidues: 1-7 <CRO>
A;Cross-references: UNIPROT:P15513; UNIPARC:UPI000017BD99
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.8
Matches 2; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PRO150
R;Odintsova, T.I.; Egorov, T.A.
Bickhimia 55; 509-516, 1990
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of A;Reference number: PN0146; MUID:90283493; PMID:2354218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Saccharomyces cerevisiae
C;Species: Os-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C;Date: Os-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C;Accession: S78024
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma Bur, J. Biochem. 245, 449-456, 1997
A;Title: Identification and characterization of the genes for mitochondrial ribosomal pr A;Reference number: S78018; MUD:97296414; PMID:9151978
A;Accession: S78024
A;Accession: S78024
A;Residues: 1-7 <KIT>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0932
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C, Genetics:
A, Genome: nuclear
C, Keywords: mitochondrion; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             omega-gliadine 1' - Aegilops longissima (fragment)
                     A,Accession: A28709
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-7 <0LS>
A,Residues: 1-7 <0LS>
A,Cross-references: UNIPARC:UP1000017AC8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: PN0150
A;Molecule type: protein
A;Residues: 1-7 <0DI>A;Cross-references: UNIPARC:UPI00001780D2
A;Experimental source: strain K-907
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1 SRQL 4
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
C;Date: D. C; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
Biochim. Biophys. Acta 828, 380-382, 1985
A;Title: Amino acid sequence around the reactive serine residue of the thioesterase doma A;Fitle: Amino acid sequence around the reactive serine residue of the thioesterase doma A;Fitle: Diotein A;Fitle: Diotein A;Fitle: Diotein A;Fitle: Diotein A;Fitle: Diotein A;Fitle: Diotein B;Fitle: Diotein B;Fit
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 27.Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C;Accession: B39127
R;Hardesty, C.; Ferran, C.; DiRienzo, J.M.
J; Bacceriol: 173, 449-456, 1991
A;Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of so
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A;Accession: B39127
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-7 <HAR>
A;Cross-references: UNIPARC:UPI0000170D6E; GB:M38416; NID:g155142; PIDN:AAA98418.1; PID:C;Keywords: phosphotransferase
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fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
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P92442_TABCCM 047029_ENTCL 068GL04_BORBU 08GL12_BORBU P70804_AZOVI 1PYR_CANAL UFO4_MOUSE 015953_HUMAN 047505_ECOLI 055184_RAT 063480_RAT ALLL2_CĀRMA ALLL2_CĀRMA

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Kraig E.; "cis Elements and trans factors are both important in strain-specific regulation of the leukotoxin gene in Actinobacillus
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MEDLINE-96355846; PubMed-8751884;
Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
                                                                                                                                                                                                                                                                                                                            actinomycetemcomitans).
Bacteria, Proteobacteria, Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.9%; Score 15; DB 2; Length 7; ilarity 100.0%; Pred. No. 2.2e+06; Conservative 0; Mismatches 0; Indels
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065578 9ALPH

065578 9ALPH PRELIMINARY; PRT; 7 AA.

015578; 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein (Fragment).

Bypothetical protein (Fragment).

Showine herpesvirina 1.

Viruses; danny viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Varicellovirus.
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MEDLINE=95313343; PubMed=7793062;
Vlcek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA; 832 MW; 6DCB42D767340420 CRC64;
                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 17, Last annotation update
GlyA (Treagment).
Name-GlyA;
Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actinomycetemcomitans.";
Infect. Immun. 64:3451-3460(1996).
EMBL; U51862; AAB88721.1; -; Genomic_DNA.
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                                                                            December 30, 2005, 14:27:11; Search time 227 Seconds (without alignments) 21.756 Million cell updates/sec
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P92387_9POAL
P92393_HETPI
P92433_LOPEL
P92421_PSAFR
P92425_PSEPI
P92425_PSEPI
P92435_PPOAL
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UNO6_PIMPS
09YIG9_ADB04
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09YIR0_ADB07
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Astacoidea, Cambaridae, Procambarus.
                      NCBI_TaxID=6728;
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                "Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus 1 genome which exhibits a colinear gene arrangement with the UI21 to UL4 genes of herpes simplex virus."; virology 210:110-118(1995).

EMBL; Z48053; CAA88130.1; -; Genomic_DNA.
                                                                                                                                                                                                                                         Gaps
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MEDLINE-9804539; PubMed=9392829; DOI=10.1016/S0196-9781(97)00188-5;
MEDLINE-9804539; PubMed=9392829; DOI=10.1016/S0196-9781(97)00188-5;
Davey M., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Davey M., Bast P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
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Bukaryota, Wetazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
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01_OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cardioexcitatory FWRFamide homolog NF1.
Procambarus clarkii (Red swamp crayfish).
Bukaryota; Metacos, Arthropoda; Crustacea; Malacostraca; Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Astacidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h similarity 33.3%; Pred. No. 2.2e+06; 1; Conservative 2; Mismatches 0; Indels
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Pred. No. 2.2e+06;
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Last annotation update)
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Letchworth G.J., Schwyzer M.;
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30-MAY-2000 (Rel. 39,
10-MAY-2005 (Rel. 47,
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED untertation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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DOI=10.1002/(SICI)1522-2683(19990101)20:4/5<1098::AID-ELPS1098>3.3.CO;2-Q;
COSTA P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                         MEDLINE=93248032; PubMed=6387183; DOI=10.1016/0196-9781(93)90021-8;
Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
"Isolation of two FMRFamide-related peptides from crayfish pericardial
                                                                                                                                                           Gaps
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-!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 6.6, ifs MM is: 25 kDa.
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Spermatophyta, Coniferopaida, Coniferales, Pinaceae, Pinus, Pinus.
NCBI_TaxID=71647;
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15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of needles (N141) (Fragment).
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                              TISSUE-Pericardial organs;
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Last sequence update) Last annotation update)

Created)

7 A.

Length 7;

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NUCLECTIDE SEQUENCE.
MEDIJNE=88078100; PubMed=2825819; DOI=10.1016/0300-9084(87)90178-7; Rassedhaert D., Gelfid J., Laude H.; "Enteric coronavirus TGEV: partial sequence of the genomic RNA, its organization and expression."; Biochimie 69:591-600(1987).
                                                                                                                                                                                                                                                                                                                                                                                                  Human adenovirus 7 (HAdV-7).
Viruses, dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10519;
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Eleouet J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.;
"Complete sequence (20 kilobases) of the polyprotein-encoding gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus; Group 1 species.
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MEDLINE-99175282; PubMed=10074533;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
"Strain variation in adenovirus serotypes 4 and 7a causing acute
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Crawford-Miksza L.K.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP065065; AAD03662.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical fusion protein.
Transmissible gastroenteritis virus.
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7 AA; 980 MW; 7B5EA414140322A0 CRC64;
                                  Match
Jocal Similarity 66.7%; Pred. No. 2.2e+06;
les 2; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory disease.";
J. Clin. Microbiol. 37:1107-1112(1999)
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Q9YQ10;
01-MAY-1999 (TrEMBLrel. 10;
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Q9YVE3;
01-MAY-1999 (TrEMBLrel. 10,
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Best Local Similarity 66.7°,
2; Conservative
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBL_TaxID=28280;
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NCBL_TaxID=85755;
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MEDLINE=99175282; PubMed=10074533;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
"Strain variation in adenovirus serotypes 4 and 7a causing acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Z-G T95-873;
MEDLINE=99175282; PubMed=10074533;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
"Strain variation in adenovirus serotypes 4 and 7a causing acute
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Crawford Miksza L.K.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065068; AAD03668.1; -; Genomic_DNA.
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Crawford-Miksza L.K.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP065064; AAD03659.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
PVI core protein (Fragment)
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                                                                                                                                                                                                            PRT;
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    Best Local Similarity 100.0%; Matches 2; Conservative 0
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Q9YIQ9;
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Q9YIRO;
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1: Indels

7 AA.

Created) PRT;

Length 7;

Score 11; DB 2; 1 Pred. No. 2.2e+06; 0; Mismatches 1;

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01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last seq 05-JUL-2004 (Rel. 44, Last ann catch-relaxing peptide (CARP).
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Q95945;
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  NCBI_TaxID=29856;
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CARP MYTED
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                                                MEDLINE=99099045; PubMed=9882359;
Izeta A., Smerdou C., Alongo S., Penzeg Z., Mendez A., Plana-Duran J.,
Enjuanes L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUCLEOTIDE SEQUENCE.
MEDLINE=20072928; PubMed=10603257; DOI=10.1006/mpev.1999.0656;
Murphy W.J., Thomerson J.E., Collier G.E.;
"Phylogeny of the Neotropical killifish family Rivulidae
(Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopteryii, Percomorpha, Atherinomorpha,
Cyprinodontiformes, Aplocheilidae, Rivulinae, Gnatholebias.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
Blonectria ochroleuca (Gliocladium roseum).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
                                                                                         "Replication and packaging of transmissible gastroenteritis coronavirus-derived synthetic minigenomes.";
J. Virol. 73:1535-1545(1999).

EMBL; AJOI1482; CAA09625.1; -; Genomic_RNA.

Hypochetical protein.

SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.4%; Score 11; DB 2; Length 7; 100.0%; Pred. No. 2.2e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                      31.4%; Score 11; DB 2; Length 7; 100.0%; Pred. No. 2.2e+06; ative 0; Mismatches 0; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome oxidase I (Fragment).
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NON TER 1 1 1
SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;
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EMBL; AF002591; AAD01074.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.
f transmissible gastroenteritis virus.";
irology 206:817-822(1995).
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P83492 BIOOC
1D P83492;
AC P83492;
DT 01-JUN-2003 (TERMBLrel. 24,
DT 01-JUN-2003 (TERMBLrel. 24,
DT 01-MAR-2004 (TERMBLrel. 26,
DE Alkaline protease Gr3 (EC 3.
S Bionectria ochroleuca (Glioc
C Eukaryota; Fungi; Ascomycote;
C Hypocreomycetidae; Hypocreal
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099182 9SMEG PRELIMINARY;
099182;
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Best Local Similarity 100.
Matches 2; Conservative
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                                          NUCLEOTIDE SEQUENCE
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Best Local Similarity
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Saccharomycetales, Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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STRAIN=D273-10B;
MEDLINE=81069885; PubMed=6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino Hansembly of the mitochondrial membrane system. Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytochrome oxidase.";
                                              A Zhao M., Zhang K.;
Submitted (DEC-2002) to Swiss-Prot.
-!- FUNCTION: Acts as a serine protease.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
GO; GO:0004252; F: extracellular region; NAS.
GO; GO:004252; F: serine-type endopeptidase activity; NAS.
Interpro; IPR000209; Pept_S8_S53.
RPGOSITE; PS00137; SUBTILASE_ASP; PARTIAL.
RPGOSITE; PS00137; SUBTILASE_HIS; PARTIAL.
RPGOSITE; PS00139; SUBTILASE_SER; PARTIAL.
RPGOSITE; PS00139; SUBTILASE_SER; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7;
PROTEIN SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-TUN-2003 (TrEMBLrel. 24, Last annotation update)
Inside intron 5 (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
7 AA; 859 MW; 75B7232362CDC460 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              7 AA; 688 MW; 776DD455A6C1ADB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10; DB 2; L. Pred. No. 2.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 2;
Pred. No. 2.2e+06;
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Last annotation update)
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100.0%; Pred. No. ...
0; Mismatches
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EMBL; V00694; CAA24066.1; -; Genomic DNA.
GO; GO:0005739; C:mitochondrion; IEA.
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NCBI_TaxID=9823;
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21-JUL-1986
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                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                        "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
Brain Res. 422:374-376(1987)
-!- FUNCTION: This peptide exhibits both potentiating (contraction)
and inhibitory (relaxation) effects on the anterior byssus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Boptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIGOIA ILMELIA (DESEL LIES LIGA).
Bukaryota, Hetazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Mytilus edulis (Blue mussel).
Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilinae; Mytilus.
MCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amidation; Amphibian defense peptide; Direct protein sequencing.
7 7 Alanine amide.
SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                  MEDLINE-88052022; Pubmed=3676797;
Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
Muneoka Y.;
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                                                                                                                                                                                                                                                                                                                                                           Length 7;
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin glands.
                                                                                                                                                                                                                                                                                         PIR; A29342; ECMUCR.

Midation; Direct protein sequencing; Hormone.

MOD RE.

SEQÜENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                          25.7%; Score 9; DB 1; Le: 100.0%; Pred. No. 2.2e+06; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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                                                                                                                                                                                 retractor muscle.
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Best Local Similarity
..... 2; Conserve
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Matches 1; Conserv
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SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                            MEDILINE B1213980; PubMed=6263778; Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H., Chang R.C.C., Huang W.-Y., Arimura A., Rodn D.V., Schally A.V.; "Isolation, structure and synthesis of a heptapeptide with in vitro Horm. Metab. Res. 13:228-232(1981).
                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.7%; Score 9; DB 1; Lularity 50.0%; Pred. No. 2.2e+06; Conservative 1; Mismatches 0.
                                                                              Last sequence update)
Last annotation update)
7 AA.
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PRT;
                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE, AND SYNTHESIS
                                                       Created)
                                                                                                                                        Hypothalamic heptapeptide
STANDARD;
                                                    (Rel. 01, (Rel. 01, )
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nes 1; Conserv
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December 30, 2005, 14:44:07 ; Search time 45 Seconds (without alignments) 12.861 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                           572060 segs, 82675679 residues
                                                                           sw model
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Gapop 10.0 , Gapext 0.5
                                                                             - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
                                                                                                                                                                                           US-10-735-916A-4
35
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/laa/5_COMB.pep:*
/cgn2_6/ptodata/1/laa/6_COMB.pep:*
/cgn2_6/ptodata/1/laa/H_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/RE_COMB.pep:*
/cgn2_6/ptodata/1/laa/RE_COMB.pep:*

Listing first 45 summaries

Maximum Match 100%

Issued_Patents_AA:*

Database :

### Appl Appl Appli Appli Appli Appli Appli Appli Appli Sequence 3267, 3267, Sequence 28, 1 Sequence 30, 1 Sequence 30, 1 Sequence 30, Sequence 22, Sequence 9, Sequence 6, Sequence 8, Description Sequence Sequence Sequence Sequence (Sequence ( Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-00-560-558B-30 US-09-217-268B-30 US-09-914-695-22 US-09-914-695-22 US-09-518-737-9 US-09-518-737-9 US-09-254-180C-5 US-09-187-47 US-09-187-47 US-09-187-47 US-09-187-459-2693 US-09-187-859-2663 US-09-187-859-2663 US-09-187-859-2663 US-09-187-859-3267 US-09-187-859-3267 SUMMARIES Query Match Length DB Score Result No.

Sequence 521, App Sequence 611, App Sequence 23, Appl	Sequence 129, App Sequence 2663, Ap Sequence 2693, Ap	3267	Sequence 11, Appl Sequence 7, Appli	Sequence 45, Appl	Sequence 11, Appl Sequence 8, Appli Sequence 321, App	Sequence 21, Appl Sequence 11, Appl Sequence 321, Appl
7 2 US-09-535-852-521 7 2 US-09-535-852-611 7 2 US-09-206-786A-23	7 2 US-09-936-588-129 7 2 US-10-006-869-2663 7 2 US-10-006-869-2693		7 1 US-08-153-799-11 7 1 US-08-793-490-7	7 2 US-09-128-572-45 7 2 US-09-326-718-5	7 2 US-09-336-093-11 7 2 US-08-952-445-8 7 2 US-08-461-226-321	7 2 US-09-135-319A-21 7 2 US-08-135-319A-21 7 2 US-09-557-465D-11 7 2 US-10-012-542-321
28 17 48.6 29 17 48.6 30 17 48.6	31 17 48.6 32 17 48.6 33 17 48.6	34 17 48.6 35 17 48.6	36 16 45.7 37 16 45.7	38 16 45.7 39 16 45.7	40 16 45.7	43 16 45.7 44 16 45.7 45 16 45.7

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US-08-053-171-28

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                                                                                                                                                                                                                                                                                                                     COUNTAL: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFTCATION: 424
ATTONERY/AGENT INFORMATION:
NAME: SMITH, Willaim M
REGISTRATION NUMBER: 11823-54-1
TELECOMMUNICATION INFORMATION:
TELEPRAK: (415) 326-2400
Sequence 28, Application US/08053171
| Patent No. 5562903
| GENERAL INFORMATION:
| APPLICANT: Co. Loibner | TITLE OF INVENTION: Antibody Derivatives | NUMBER OF SEQUENCES: 32 | CORRESPONDENCE ADDRESS: ADDRESSER: Townsend and Townsend Khourie and Crew | STREET: 379 Lytton Avenue
                                                                                                                                                                               INKERT: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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| FALCHIC NO. 0099002U
| GENERAL INFORMATION:
| APPLICANT: BEICYTE PHARMACEUTICALS, INC.
| APPLICANT: HIATT, ANDREW C.
| APPLICANT: HIATT, ANDREW C.
| TITLE OF INVENTION: IMMUNGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
| FILE REFERENCE: 068904-0501
| CURRENT APPLICATION NUMBER: US/09/563,222C
| CURRENT PILING DATE: 2000-05-02
| PRIOR APPLICATION NUMBER: 09/563,222
| SOFTWARE: PARCHIN VOE: 2.1
| SOFTWARE: PARCHIN VOE: 2.1
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Patent No. 6706487

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Adel-Meguid, Sherin
APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Stephen D.
TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
FILE REPRENCE: 2001-08-31
FILE REPRENCE: POOG-03-17

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 60/125,299

PRIOR PILING DATE: 1999-03-19

PRIOR PILING DATE: 1999-03-19

PRIOR FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                         Length 7;
                                                                                                                                                                      Query Match 68.6%; Score 24; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0;
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; TYPE: PRT; ORGANISM: Murine; FEATURE; NAME/KEY: MISC_FEATURE; OTHER INFORMATION: CDR Of murine R3 antibody US-09-217-268B-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred.
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Matches 5; Conservative
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US-09-914-695-22
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Patent No. 6506883
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriquez, Rolando P
APPLICANT: Frias, Ernesto M
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
TITLE OP INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
FILE REPERENCE: 2720.1US
CURRENT APPLICATION NUMBER: US/09/217,268B
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ 1D NOS: 36
SOFTWARE PATENT OF SEQ 10 NOS: 36
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Humanized and chimeric monoclonal
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
TITLE OF INVENTION: EGF-R); diagnostic and therapeutic use.
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
STREET: P.O. Box 2250
CITY: Salt Lake City
STATE: Utah
COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS95
SOFTWARE: WordPerfect 5.1/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E
FILING DATE: No. 5891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: TUTNEY, Allen C:
REGISTRATION NUMBER: 33,041
REFERENCE/POCKET WUMBER: 2720US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                         Sequence 30, Application US/08560558E
Patent No. 5891996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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Matches 5; Conserv
                                                                                                                                                                                                                         GENERAL INFORMATION:
                                KVSNR 5
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     KVSNR 5
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US-08-560-558E-30
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US-09-217-268B-30
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LENGIH: 7
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TYPE: amino acid
TOPOLOGY: linear
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; Sequence 6, Application US/08244626
; Sequence 6, Application US/08244626
; Patent No. 5502167
; Patent INFORMATION:
APPLICANT: Waldmann, Herman
APPLICANT: Crowe, James Scott
APPLICANT: Lewis, Alan Peter
; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
                                                                                                                                                                                                                                                                                           GENERAL INCORMATION:
APPLICANT: PUKUI, YASUHISA
APPLICANT: FUKUI, YASUHISA
APPLICANT: SHIRAI, SATOSHI
APPLICANT: SHIRAI, RYUICHI
APPLICANT: SATO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: MONOCLONAL ANTIBODY PROPRATE
FILE REPERBENCE: 1955/49618
CURRENT PILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: UP 1999-250209
PRIOR PILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 10
SOCTHARR: PATCHIN Ver. 2.1
SEROI ID NO 9
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.6%; Score 24; DB 2; Length 7; 100.0%; Pred. No. 4.6e+05; Live 0; Mismatches 0; Indels
                               Query Match 68.6%; Score 24; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 5; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentII Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,626
FILING DATE: July 15, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c. STREET: 555 Thirteenth Street, N. W. CIIY: Washington
                                                                                                                                                                                                                       RESULT 6
18-09-518-737-9
'Sequence 9, Application US/09518737
'Patent No. 6709833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Mus musculus US-09-518-737-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KVSNR 5
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US-09-914-695-22
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US-10-226-795-29

US-10-226-795-29

Sequence 29, Application US/10226795

Sequence 29, Application US/10226795

Setent No. 6875433

GENERAL INFORMATION:

APPLICANT: HART: MARY KATE

APPLICANT: WILSON, JULIE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING

TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN

FILE REFERENCE: ARMY 166

CURRENT APPLICATION NUMBER: US/10/226,795

CURRENT FILING DATE: 2002-11-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 29

LENGTH: 7

LENGTH: 7
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Patent No. 6696620
GENERAL INPORMATION:
APPLICANT: BIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
CURRENT FILLS OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILLS REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/09/563,222C
CURRENT APPLICATION NUMBER: PCT/US01/14349
PRIOR PILLING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ') OTHER INFORMATION: Description of Artificial Sequence: Synthetic light; OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence US-10-226-795-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.0%; Score 21; DB 1; I
80.0%; Pred. No. 4.6e+05;
iive 1; Mismatches 0;
FILING DATE: December 4, 1992
CLASSIFICATION: 424
ATTONNEY, AGENT INFORMATION:
NAME: ETHST, BALDARA G.
REGISTRATION NUMBER: 30,377
REFERENCE/POCKET NUMBER: 1808-153A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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APPLICANT: Conjuchem, Inc.

APPLICANT: Bridon, Dominique

APPLICANT: Bridon, Dominique

APPLICANT: Bridon, Alan

APPLICANT: Hilber, Peter

APPLICANT: Hilber, Peter

APPLICANT: Hibaudeau, Karen

TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PREPTIDES FROM

TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PREPTIDES FROM

TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PREPTIDES FROM

TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THENOUGH CONJUGATION TO BLOOD

TITLE OF INVENTION: COMPONENTS

TITLE OF INVENTION: COMPONENTS

TITLE OF INVENTION TO BATE: 2000-09-05

CURRENT APPLICATION NUMBER: 60/134,406

PRIOR APPLICATION NUMBER: 60/153,406

PRIOR FILING DATE: 1999-05-10

PRIOR PILING DATE: 1999-10-10

PRIOR FILING DATE: 1999-10-18
                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09724530

Sequence 4, Application US/09724530

Patent No. 6843989

GRERAL INFORMATION:
APPLICANT: Wahl, Alan
APPLICANT: Wahl, Alan
APPLICANT: Fell, H. Perry
ITILE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REFERENCE: 9632-005
CURRENT FILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: US/09/724,530
CURRENT FILING DATE: CURRENT APPLICATION NUMBER: US/09/328,296
FRIOR APPLICATION NUMBER: TILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                         0; Indels
                                                                                                                                                   Length 7;
                                                                                                                                                 54.3%; Score 19; DB 2; Le
100.0%; Pred. No. 4.6e+05;
ative 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                 Query Match
Best Local Similarity 100.4
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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CORGANISM: Mus musculus
US-09-724-530-4
                                                                        TYPE: PRT
CRGANISM: Mus musculus
US-09-724-409-4
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US-09-623-548A-654
                                                           LENGTH:
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Sequence 4, Application US/09724409
Patent No. 683821
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Francisco, Joseph
APPLICANT: Francisco, Joseph
APPLICANT: Fell, H. Perry
TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REFERENCE: 9632-005
CURRENT APPLICATION NUMBER: US/09/724,409
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: US/09/328,296
PRIOR FILING DATE: 1999-06-08
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                                                                                                                                                                                       54.3%; Score 19; DB 2; Length 7; 100.0%; Pred. No. 4.6e+05; ive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 7
                                                                                                                                                                                         Query Match 54.3
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                              TYPE: PRT; ORGANISM: Homo sapiens
US-09-563-222C-9
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2 VSNR 5
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; ORGANISM: Mouse
US-09-254-180C-5
                                                                                                                                                                                                                                                                                                                                                                                    US-09-254-180C-5
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US-09-724-409-4
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JAPPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION: 1999-00-10
PRIOR PILING DATE: 1999-00-10
PRIOR PILING DATE: 1999-00-10
PRIOR PELING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
SOFTWARE: PATCHIN VAMBER: 60/153,406
PRIOR FILING DATE: 1999-10-18
SOFTWARE: PATCHIN VAMBER: 60/153,703
PRIOR FILING DATE: 1999-10-18
SOFTWARE: PATCHIN VET: 2.1
SEQ ID NO 654
LENGTH: T
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Patent No. 6946129
GRNERAL INFORMATION:
APPLICANT: Siegall, Clay
APPLICANT: Wahl, Alan
APPLICANT: Francisco, Joseph
APPLICANT: Fall, H. Perry
TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REPERENCE: 9632-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide US-09-657-276-654
                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-623-548A-654
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                                                                                                                                                                                                                                              Score 19; DB 2; Length 7; Pred. No. 4.6e+05; 1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 654, Application US/09657276
Patent No. 6887470
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 654
LENGTH: 7
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US-09-328-296-4
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; CURRENT APPLICATION NUMBER: US/09/328,296
; CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; TENETH: 7
; TENETH: 7
; ORGANISM: Mus musculus
US-09-328-296-4
Guery Match
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
OY 2 VSNR 5
Db 2 VSNR 5
Search completed: December 30, 2005, 14:52:47
Job time: 46 secs
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Sequence 125, Application US/09995529
Publication No. US20030099655A1
GENERAL INFORMATION:
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Sequence 124, App
Sequence 124, App
Sequence 11, Appl
Sequence 9, Appl
Sequence 22, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 30, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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                                                                                                     December 30, 2005, 14:51:25; Search time 159 Seconds (without alignments) 18.395 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

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(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *

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(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: *

(cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-995-529-125
US-09-995-529-125
US-09-995-529-124
US-10-495-629-124
US-10-492-618-0
US-10-409-611-80
US-10-409-611-80
US-10-409-611-80
US-09-217-268B-30
US-10-231-452-6
US-10-231-452-6
US-10-487-322-2
US-10-487-326-2
US-10-488-998-2
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US-10-488-998-2
US-10-488-998-2
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US-10-488-998-2
US-10-488-998-2
US-10-488-998-2
US-10-687-035-7
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                                                                                                                                                                                                                                                                                                           1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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Match Length DB
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| Sequence 4, Application US/10735916A
| Publication No. US20550084906A1
| GENERAL INFORMATION:
| APPLICANT: GORYSCH, Liliane
| APPLICANT: CORVAIA, Nathalie
| APPLICANT: DUFLOS, Alain
| APPLICANT: BECK, Alain
| APPLICANT: BECK, Alain
| APPLICANT: BECK, Alain
| APPLICANT: HACHW, Jean-Francois
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
| TILE REFERENCE: 017753-183
| TURBENT FILING DATE: 2003-01-16
| PRIOR APPLICATION NUMBER: PR 03/08 538
| PRIOR FILING DATE: 2003-01-18
| PRIOR PILING DATE: 2003-01-18
| PRIOR PILING DATE: 2002-01-18
| PRIOR FILING DATE: 2002-01-18
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                US-10-512-527-2
US-10-810-813-57-2
US-10-810-813-57
US-11-009-443-17
US-11-009-443-17
US-11-009-443-17
US-11-009-443-17
US-11-009-72-56-16
US-10-877-773-116
US-10-877-774-116
US-09-995-529-121
US-09-995-529-121
US-00-022-066-44
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US-10-022-066-443
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                                                                           Query Match
Best Local Similarity 100.
Matches 7; Conservative
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US-10-735-916A-4
TYPE: PRT ORGANISM:
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GENERAL INVENDENCIALINI

APPLICANT: Nobuo HANNI

APPLICANT: MCtoo YAMASAKI

APPLICANT: AKINC PURUTA

APPLICANT: AKINC PURUTA

APPLICANT: AKINC PURUTA

APPLICANT: Kenya SHITARA

APPLICANT: Kenya SHITARA

APPLICANT: Nacki SHIMADA

TITLE OF INVENTION: Anti-fiblroblast growth factor-8 monoclonal antibod

FILE REFERENCE: 249-310

CURRENT PFLICATION NUMBER: US/10/434,469

CURRENT PILING DATE: 1996-06-03

PRIOR PLICATION NUMBER: US 08/832,236

PRIOR APPLICATION NUMBER: US 08/832,236

PRIOR APPLICATION NUMBER: US 09/876,040

PRIOR PLILNG DATE: 1999-06-07

PRIOR PLILNG DATE: 1999-06-07

PRIOR PLILNG DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PALENTIN VEY: 2.1
                                                                                                                                                   Query Match 74.3%; Score 26; DB 3; Length 7; Best Local Similarity 71.4%; Pred. No. 1.7e+06; Matches 5; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                         US-09-995-529-124

US-09-995-529-124

Sequence 124, Application US/09995529

Publication No. US20040091482A9

GENERAL INFORMATION:

APPLICANT: Watkins, Jeffry D.

APPLICANT: Tang, Wing

TITLE OF INVENTION: Related Methods

TITLE OF INVENTION: Related Methods

FILE REFERENCE: PIX 4976

CURRENT APPLICATION NUMBER: US/09/995,529

CURRENT PILING DATE: 2001-11-26

NUMBER: PRILING DATE: 2001-11-26

SOFTWARE: FREEEC for Windows Version 4.0

SEQ ID NO: 124

TENGON 124
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; OTHER INFORMATION: synthetic antibody mutation US-09-995-529-124
               ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: synthetic antibody mutation
US-09-995-529-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11, Application US/10434469
; Publication No. US20040091480A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4
Matches 5; Conservative
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Publication No. US20030099655A1;
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.;
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976;
CURRENT FILION DAMER: US/09/995,529;
CURRENT FILION DAMER: 2001-11-26;
NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FaetSEQ for Windows Version 4.0
; SEQ ID NO 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 125, Application US/09995529
Publication No. US20040091482A9
GENERAL INFORMATION:
APPLICANT: Waskins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Reference: P. X 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 4.0
TITLE OF INVENTION: Humanized Collagen Antibodies and TITLE OF INVENTION: Related Methods FILE REPERENCE: P.IX 4976 CURRENT APPLICATION NUMBER: US/09/995,529 CURRENT FILING DATE: 2001-11-26 NUMBER OF SEQ ID NOS: 358 SOFTWARE: FRASEEQ for Windows Version 4.0 SEQ ID NO 125
                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: synthetic antibody mutation US-09-995-529-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: synthetic antibody mutation US-09-995-529-125
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4*
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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US-09-995-529-124
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RESULT 11

US-09-217-268B-30

Sequence 30, Application US/09217268B

Patent No. US20202065398A1

GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Mateo de Acosta del Rio, Chimeric Monoclonal Antibodies That Recognize Epid
TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epid
TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
FILE REFERENCE: 2720.1US
CURRENT APPLICATION NUMBER: US/09/217,268B

CURRENT PILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn version 3.1
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                            Sequence 22, Application US/10409608A

Publication No. US2005031613A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

THE REFERENCE:

TOTAL OF SO TO NUMBER:

TOTAL OF SEQ ID NOS:

TOTAL OF SE
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pred. No. 1.7e+06;
1; Mismatches 0; Indels
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Mus musculus
US-10-409-608A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mus musculus
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Best Local Similarity
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1 KVSNRI 6
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US-10-500-207A-11
                       US-10-409-608A-22
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Sequence 80, Application US/10409611

Sequence 80, Application US/10409611

Sequence 80, Application US/10409611

GENERAL INFORMATION:

APPLICANT: KYOWA HAKKO KOGYO CO., LTD.

TITLE OF INVENTION: Method of enhancing of binding activity of antibody composition of the Reperence 249-303

CURRENT PILIOR DATE: 2003-04-09

FILE REPERENCE: 249-303

CURRENT PILIOR DATE: 2002-106950

FRIOR PILIOR DATE: 2002-04-09

NUMBER OF SEQ ID NOS: 100

SEQ ID NOS: 100

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                          US-10-462-105-9

Sequence 9, Application US/10482105

Sequence 9, Application US/10482105

GENERAL INFORMATION:

APPLICANT: KYOMA HAKKO KOGYO CO., LTD

TITLE OF INVENTION: Humanized anti-FGF-8 antibody and the antibody fragment thereof

TITLE OF INVENTION: HUMBER: US/10/482,105

TITLE OF TAPPLICATION NUMBER: US/10/482,105

CURRENT PILING DATE: 2003-12-24

PRIOR FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9

LENGTH: 7
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ilarity 83.3%;
Conservative
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74.3%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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LENGTH: 7
TYPE: PRT
ORGANISM: Mus musculus
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US-10-409-611-80
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Matches 5; Conserv
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US-10-434-469-11
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US-09-563-222-30
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APPLICANT: SHOUT, EMI
APPLICANT: SAKURADA, MIKKIKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: NAMASHKI, MOTOO
TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-170
CURRENT APPLICATION NUMBER: US/09/796,744
CURRENT PILING DATE: 2000-03-03
FRIOR FILING DATE: 2000-03-03
FRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 9
LENGTH: 7
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                                                                                                                                                                             68.6%; Score 24; DB 3; Length 7; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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Publication No. US20030008321A1
GENERAL INFORMATION:
APPLICANT: FUKUI, YASUHISA
APPLICANT: SHIRAI, SATOSHI
APPLICANT: SHIRAI, RYUICHI
APPLICANT: SAITO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
FILE REFERENCE: 1965/49618
                                                                             FEATURE:
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-30
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CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: JP 1999-250209
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                             US-09-796-744-9; Sequence 9, Application US/09796744; Patent No. US20020098527A1
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Mus musculus
US-09-796-744-9
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ORGANISM: Murine
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APPLICANT: Hiatt, Mich B.
TITLE OF INVENTION: IMMUNOCLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: EUKARYOTIC CELLS
FILE REFERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 7
LENGTH: 
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Sequence 34, Application US/09995529

Publication No. US2003009655A1

GENERAL INFORMATION:

APPLICANT: Wackins, Jeffry D.

APPLICANT: Wackins, Jeffry D.

APPLICANT: Huse, William D.

APPLICANT: Tang, Ying

TITLE OF INVENTION: Humanized Collagen Antibodies and

TITLE OF INVENTION: Related Methods

FILE REFERENCE: PIX 4976

CURRENT APPLICATION NUMBER: US/09/995,529

CURRENT APPLICATION NUMBER: 201-11-26

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FREEKE FREEKE PREECE OF WINDOWS VERSION 4.0
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                                                     Patentin Ver. 2.1
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Best Local Similarity 100.
Matches 5; Conservative
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.;
SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-9
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1 KVSNR 5

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December 30, 2005, 14:52:09; Search time 12 Seconds (without alignments)
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1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10 NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US10 NEW_PUB.pep:*

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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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1 KVSNRLY 7
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Sequence 4, Appli Sequence 5, Appli Sequence 14, Appl Sequence 19, Appl Sequence 19, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 56, Appl Sequence 62, Appl 200, App 27, Appl 9189, Ap 29, Appl 76, Appl Sequence 202, App Sequence 204, App Sequence 13, Appl Sequence 191 Sequence 194 Sequence 200 Sequence 27, Description Sequence Sequence Sequence Sequence Sequence US-11-125-837-2 US-11-125-837-14 US-11-105-937-14 US-11-105-937-19 US-11-009-939-19 US-11-096-706-18 US-11-096-706-56 US-11-096-706-168 US-11-096-706-194 US-11-096-706-194 US-11-096-706-194 US-11-096-706-194 US-11-096-706-194 US-11-096-706-194 US-11-096-706-194 US-11-096-706-198 US-11-096-706-193 US-11-096-706-193 US-11-096-706-103 US-11-096-706-103 US-11-096-706-104 US-11-096-706-104 US-11-096-706-104 US-11-096-706-104 US-11-096-706-104 US-11-096-706-104 US-11-096-706-104 US-11-096-706-105 SUMMARIES Query Match Length DB Score . Ю Result

Sequence 34, Appli Sequence 284, Appli Sequence 284, Appli Sequence 46, Appl Sequence 150, Appl Sequence 150, Appl Sequence 56, Appl Sequence 27, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 274, Appl Sequence 274, Appl Sequence 274, Appl Sequence 274, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 175, Appl Sequence 11, Appl	
6 US-10-997-066-34 6 US-110-842-877A-4 7 US-11-096-708-40 7 US-11-096-706-46 7 US-11-096-706-46 7 US-11-096-706-150 7 US-11-099-814-12 6 US-10-999-866-56 6 US-10-999-866-56 6 US-10-842-877A-13 6 US-10-842-877A-13 6 US-10-842-877A-14 6 US-10-842-877A-17 6 US-10-842-877A-17 6 US-10-842-877A-17 6 US-10-948-778-164 6 US-11-096-706-175 7 US-11-096-706-175 6 US-10-917-759-117	
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## ALIGNMENTS

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US-11-012-353-4

Sequence 4, Application US/11012353

Publication No. USZ0050249730A1

GENERAL INFORMATION:
APPLICANT: GORYCH, LILIANE
APPLICANT: CORVAIA, NATRALIE
APPLICANT: BUFLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANTON NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: FR 0308538
PRIOR PILING DATE: 2003-01-20
PRIOR PLLING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 0200553
PRIOR APPLICATION NUMBER: FR 0200553
PRIOR APPLICATION NUMBER: FR 0200554
PRIOR PLLING DATE: 2002-01-18
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KVSNRLY 7
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RESULT 1
US-11-012-353-4
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US-10-932-334-5 ; Sequence 5, Application US/10932334 RESULT 2

Sequence

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Gaps

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APPLICANT: Permaekti, Flavia
APPLICANT: Permaekti, Flavia
APPLICANT: Permaekti, Bruce
APPLICANT: Premaekti, Bruce
APPLICANT: Van Epps, Dennis
APPLICANT: Van Epps, Dennis
APPLICANT: Van Epps, Dennis
APPLICANT: Van Epps, Dennis
TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
FILE REPERENCE: 30797-704.501
CURRENT FILING DATE: 2006-04-13
PRIOR APPLICATION NUMBER: 09/478,977
PRIOR APPLICATION NUMBER: 60/152,496
PRIOR APPLICATION NUMBER: 60/143,534
PRIOR APPLICATION NUMBER: 60/143,534
PRIOR APPLICATION NUMBER: 60/14,878
PRIOR PLILNG DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
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Publication No. US20050265998A1
GENERAL INFORMATION:
APPLICANT: Blson, Greg Christopher Andrew
ITILE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
FILE REPERBURE: 23135-402
CURRENT APPLICATION UNDERS: US/11/009,939
CURRENT FILING DATE: 2005-12-10
                                                                                                                                                                                                                                                                             ; DB 7; her.,
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100.0%; Pred. No. 4.3e+04;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                  68.6%; Scc. 100.0%; Pred. No. ... 0; Mismatches
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR PILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic peptide US-11-105-708-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 18, Application US/11105708; Publication No. US20050281821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
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US-11-125-837-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial
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Best Local Similarity
Matches 5; Conserv
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; OTHER INFORMATION: antibody light chain complementarity determining region
US-10-932-334-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.6%; Score 24; DB 6; Length 7; Best Local Similarity 100.0%; Pred. No. 4.3e+04; Matches 5; Conservative 0; Mismatches 0; Indels
                                                    TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR PLING DATE: 2003-12-08
PRIOR PLING DATE: 2003-12-08
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENTIN VETSION 3.2
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-Jiun
APPLICANT: Chen, Pei-Jiun
APPLICANT: Chen, Pei-Jiun
APPLICANT: Huang, Chiu-Chen
TITLE OF INVENTION: ANTIBODIES
FILE REFRENCE : 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT APPLICATION NUMBER: US 60/569,892
PRIOR PILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 7
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Publication No. US20050266003A1
GENERAL INFORMATION:
APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-Jiun
APPLICANT: Huang, Chiu-Chen
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 13062-011001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/11125837; Publication No. US20050266003A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
            Publication No. US20050249728A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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CORGANISM: Mus musculus
US-11-125-837-2
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Best Local Similarity
Matches 5; Conserv
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US-11-125-837-14
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Gaps

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; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition ; OTHER INFORMATION: region)
US-11-096-706-34
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yequence 56, Application US/11096706

publication No. US2005024547641

GENERAL INFORMATION:

APPLICANT: Collingwood, Trevor

TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins

FILE REFERENCE: 013496-00822005

FILE REFERENCE: 01065-04-01

FILE REFERENCE: 02/05-04-01

FILE REFERENCE: 02/05-04-01

PRIOR FILING DATE: 2004-06-02

PRIOR FILING DATE: 2004-06-02

PRIOR FILING DATE: 2004-06-02

NUMBER OF SEQ ID NOS: 227
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                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                      Length 7;
                                                                                                                                                                                    48.6%; Score 17; DB 6; I
60.0%; Pred. No. 4.3e+04;
tive 2; Mismatches 0;
PRIOR APPLICATION NUMBER: WO PCT/USO2/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: Patentin version 3.1
SEQ ID NO 334
LENGTH: 7
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Best Local Similarity 60.v.
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-334
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2 SHQLY 6
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US-11-096-706-34
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; Sequence 4, Application US/11102743
; Publication No. US20050266002A1
; GENERAL INFORMATION:
; APPLICANT: Siegal1, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TILLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REPERENCE: 9622-005
; CURRENT APPLICATION NUMBER: US/11/102,743
; CURRENT APPLICATION NUMBER: US/9/328,296
; PRIOR APPLICATION NUMBER: US/9/328,296
; RADOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 4
; LENGTH: 7
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Publication No. US20050282743A1

GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Carrick, Deanna Marie
APPLICANT: Schweizer, Johannes
APPLICANT: Carrick, Deanna Marie
APPLICANT: Carrick, Deanna Marie
APPLICANT: Corporation
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REPERENCE: 20054-00332008
CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2002-02-25
                                                                                                                                                                                                                                                                Score 21; DB 7; Le:
Pred. No. 4.3e+04;
1; Mismatches 0;
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100.0%; Pred. No. 4.3e+04;
Live 0; Mismatches 0;
       PRIOR APPLICATION NUMBER: 60/528,811
PRIOR FILING DATE: 2003-12-10
PRIOR PILING DATE: 2003-12-10
PRIOR FILING DATE: 2003-12-10
PRIOR PILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 60/528,962
PRIOR PILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PARCHILIN VET. 2.1
SEQ ID NO 19
                                                                                                                                                                                                                                                                    60.0%;
80.0%;
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Best Local Similarity 100.
Matches 4: Conservative
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus US-11-102-743-4
                                                                                                                                                                                                               ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                            1 KVSNR 5
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US-10-485-788A-334
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; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding ; OTHER INFORMATION: domain) US-11-096-706-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding OTHER INFORMATION: domain)
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US-11-096-706-194
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Collingwood, Trevor
TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
FILE REFERENCE: 019456-00822003
CURRENT APPLICATION NUMBER: US/11/096,706
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 60/560,535
PRIOR APPLICATION NUMBER: US 60/576,757
PRIOR APPLICATION NUMBER: US 60/576,757
PRIOR PILING DATE: 2004-06-02
NUMBER OF SEC ID NOS: 227
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                              Length 7;
                                                                                                   Db 4.3e+04;
                                                                                              48.6%; Score 17; DB 7;
llarity 75.0%; Pred. No. 4.3e+04
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                Sequence 101, Application US/11096706; Publication No. US20050245476A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 194, Application US/11096706
Publication No. US20050245476A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial
                                                                                          Query Match
Best Local Similarity
Matches 3, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                        3 SNRL 6
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US-11-096-706-194
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; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-62
                                                                         Chemically synthesized peptide (zinc finger protein recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ## Sequence 168, Application US/11096706
## Sequence 168, Application US/11096706
## Publication No. US20050245476A1
## GENERAL INFORMATION:
## APPLICANT: Collingwood, Trevor
## TITLE OF INVENTION Treatment of Neuropathic Pain with Zinc Finger Proteins
## TITLE OF INVENTION Treatment of Neuropathic Pain with Zinc Finger Proteins
## TITLE OF INVENTION Treatment of Neuropathic Pain with Zinc Finger Proteins
## FILE REFERENCE: 019496-008220US
## CURRENT PELING DATE: 2006-04-01
## PRIOR PILING DATE: 2004-04-08
## PRIOR PILING DATE: 2004-04-08
## PRIOR PILING DATE: 2004-06-02
## NUMBER OF SEQ ID NOS: 227
## SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 62, Application US/11096706

Publication No. US20050245476A1

GENERAL INFORMATION:
APPLICANT: Collingwood, Trevor
TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
FILE REPERENCE: 019496-00820US
CURRENT FILING DATE: 2004-04-01

PRIOR APPLICATION NUMBER: US/11/096,706
CURRENT FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: US 60/560,535
PRIOR APPLICATION NUMBER: US 60/576,757

PRIOR APPLICATION NUMBER: US 60/576,757

SOFTWARE: PAING DATE: 2004-06-02

NUMBER OF SEQ ID NOS: 227

SOFTWARE: PAICHING VERSION 3.3

SOFTWARE: PAICHING VERSION 3.3
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                                                                                                                                                                 Score 17; DB 7; Length 7; Pred. No. 4.3e+04; 1; Mismatches 0; Indels
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                                                                                                                                                                   48.6%;
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                              Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                 FEATURE:
OTHER INFORMATION: Chemical
COTHER INFORMATION: region)
US-11-096-706-56
       TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                       |||:
SNRI 6
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SNRI 6
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US-11-096-706-168
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US-11-096-706-62
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RESULT 15
US-11-096-706-200
; Sequence 200, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; TITLE OF INVENTION: USPERS. US-008220US
; FILE REFERENCE: 019496-008220US
; CURRENT FILING DATE: 2005-04-01
; PRIOR PLING DATE: 2004-04-08
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial
FRATURE:
OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding OTHER INFORMATION: domain)
US-11-096-706-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                  0; Gaps
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48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels
Query Match 48.6%; Score 17; DB 7; Length 7; Best Local Similarity 75.0%; Pred. No. 4.3e+04; Matches 3; Conservative 1; Mismatches 0; Indels
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Job time : 16 secs
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3 SNRI 6
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3 SNRI 6
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100.0%; Score 56; DB 1; Length 112; 100.0%; Pred. No. 0.0084; Pred. o. Mismatches 0; Indels
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQGSHVPWT
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883.9
883.9
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883.9
883.9
883.9
882.1
882.1
882.1
882.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-752-844-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                        December 30, 2005, 13:14:26; Search time 20.1774 Seconds (without alignments) 36.877 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                 lssued_Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-752-844-15
US-08-591-196-15
US-08-591-196-15
US-08-591-196-2
US-09-192-844-2
US-09-192-818B-2
US-09-192-818B-2
US-09-293-533-6
US-09-293-533-6
US-09-102-101-2
US-08-102-101-2
US-08-102-101-2
US-08-102-930B-72
US-08-102-930B-72
US-08-102-930B-11
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                       572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 - protein search, using sw model
                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                        US-10-735-916A-6
56
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Match Length DB
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100.0
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Perfect score:
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                                                                                                                                                                         Sequence:
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                                                                                            Run on:
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US-08-72-444.155

1 Gequence 15, Application US/08752844

1 Patent No. 5935821

2 GARRAAL INFORMATION

2 GARRAAL INFORMATION: Malaya

APPLICANT: Chatterjee, Malaya

APPLICANT: Chatterjee, Malaya

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOWA AND SWALL CELL. CARCINOMA

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSER: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

COMPUTER: BATOLIA FORM:

MEDIUM TYPE: PLOPS/MS-DOS

SOFTWARE: BATOLIA FORM:

MEDIUM TYPE: CACOMPATION:

MEDIUM TYPE: ANTI-ARTION DATA:

APPLICATION NUMBER: US/08/752,844

ATTORNEY AGENT INFORMATION:

MAME: SCALIFÉ, D. Michael

REGISTRATION NUMBER: 30414-2002.21

TELECHMONICATION NUMBER: 30414-2002.21

TELECHMONICATION INFORMATION:

TELECHMONICATION NUMBER: 30414-2002.21

TELECHMONICATION NUMBER: 30414-2002.21

TELECHMONICATION PROPRATION:

TELECH
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Sequence
Sequence
Sequence
Sequence
Sequence
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Sequence
Sequence
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Sequence
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US-09-232-290-15
US-08-560-558E-27
US-09-217-268B-35
US-08-497-312-14
US-08-134-346A-50
US-08-134-346A-50
US-08-134-346A-95
US-08-134-346A-95
US-09-76-228A-95
US-09-76-228A-95
US-09-646-028-14
US-09-646-028-14
US-08-653-171-29
US-08-053-171-15
US-08-053-171-15
US-08-033-171-15
US-08-331-398A-48
US-08-331-398A-50
US-08-331-398A-50
US-08-331-398A-50
US-08-331-398A-50
US-08-331-398A-50
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US-08-331-398A-50
US-08-331-398A-50
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Gaps

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FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FOGSHVPWT 9
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RESULT 2
US-08-591-196-15

US-08-591-196-15

Sequence 15, Application US/08591196

PARENT INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Malaya
APPLICANT: Chatterjee, Sunil K.
TITLB OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
CUMTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARLICATION DATA:
APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCHIFF, U. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TYPE: AMIND ACCIDENTIAL AND ACIDENTIAL AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 FQGSHVPWT 102
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US-09-293-533-15
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Sequence 2, Application US/08752844

Sequence 2, Application US/08752844

Sequence 2, Application US/08752844

Sequence 2, Application US/08752844

Sequence 3, Application US/08752844

APPLICANT: Chatterjee, Malaya

APPLICANT: Chatterjee, Malaya

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCICONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SWALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66

CORRESPONDENCES: MERISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 30414-20002.21
TELECOMMUNICATION NUMBER: 30414-2002.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (412, TELEFAX: 706141
| INFORMATION: FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 112 amino acids TVPE: amino acids TVPE: amino acids TVPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide US-09-293-533-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 FOGSHVPWT 102
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us-10-735-916a-6.rai

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APPLICANT: FOON, Kenneth A.
APPLICANT: FOON, Kenneth A.
APPLICANT: CLATTERALEE, Malaya
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000500
CURRENT APPLICATION NUMBER: US/09/192,838B
CURRENT APPLICATION NUMBER: 60/065,774
PRIOR PILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 2
LENGTH: 149
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: TYPE
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Sequence 2, Application US/09293533

Sequence 2, Application US/09293533

Patent No. 6509016

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Chatterjee, Malaya

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCIONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOWA

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533 FILING DATE:
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844 FILING DATE:
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STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTOLING DAILS
ATTOLING DAILS
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFRENCE/DOCKET NUMBER: 3041
TELECOMMUNICATION INFORMATION:
TELEPHONE: ~(415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELBEAX: (41...
TELERAX: (41...
TELER : 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
""PE: amino acids
""PE: amino acids
""PE: amino acids
""PE: amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.

Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             쉱
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Patent No. 5977316

APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 56; DB 1; Length 149; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 56; DB 1; Length 149; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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CITY: PAL

STATE: CA

STATE: USA

ZIP: 94304-1018

ZOMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/591,196

FILING DATE: 16-JAN-1996

CLASSIPICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: SCALIFF, J. Michael

REGISTRATION NUMBER: 40,253

REFERENCE/DOCKET NUMBER: 30414-20002.20

TELECOMMUNICATION INFORMATION:

THE TELEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: WORKISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-192-838B-2
; Sequence 2, Application US/09192838B
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                       TOPICGY: 11-21
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-752-844-2
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 PQGSHVPWT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 FOGSHVPWT 121
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Sequence 66, Application US/09293533
Patent No. 6509016
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCIONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      Query Match 100.0%; Score 56; DB 1; Length 263; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.021;
Artive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

CIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION NUMBER: US/09/293,533

FILING DATE:

APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40, 253
REGISCOMMUNICATION NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 6SEQUENCE CHARACTERISTICS: LENGTH: 263 amino acida TYPE: amino acid
    (415) 494-0792
                                                                                                    263 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                        TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         ; TÖPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-844-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear; MOLECULE TYPE: protein US-09-293-533-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 POGSHVPWT 253
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                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
    TELEFAX:
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                                                                                                                                                                                                                                                                                              APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
APPLICANT: CHATTERIES, Malaya
APPLICANT: FOON, Kenneth A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000540
CURRENT APPLICATION NUMBER: 1090424,191
CURRENT FILING DATE: 1990-06-02
EARLIER PILLING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chotterjee, Sunil K.
APPLICANT: Chotterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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Query Match
100.0%; Score 56; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 943104-1018
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/752,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/08752844
Patent No. 5935821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 3041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                            Sequence 2, Application US/09324191
Patent No. 6562798
                                                                                                                            113 FQGSHVPWT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-324-191-2
                                                                                               1 FQGSHVPWT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-752-844-66
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Gaps

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GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Beduardo A.
ITILE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit a
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCES: 96
CORRESPONDENCES: ADDRESS:
ADDRESSER: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTONEY/AGENT INFORMATION:
NAME: AMZEL Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFRENCE/DOCKET NUMBER: 30,930
RETERRENCE/DOCKET NUMBER: 30,930
TELEROMMUNICATION INFORMATION:
TELEROMMUNICATION INFORMATION:
TELEROMM SECOND SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A

FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rred. No. 4.6e+05;
1; Mismatches 0
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No. 6315997ember 16, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oequence 72, Application US/08976288A
Patent No. 6315997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.6%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: n.a.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
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STATE: California
COUNTRY: USA
ZIP: 90071
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                 Sequence 72, Application US/0797696C
Patent No. 5792852
GENERAL INFORMATION:
APPLICANT: Geriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Pedian Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: and Therapeutic Methods.
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSTING DATE: 11-16-92
CLASSIFICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38227
TELEFHONE: (510) 748-6868
TELEFRANE: (510) 748-6868
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APPLICANT: do Couto Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Bduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: V. AMZEL & ASSOC.
: 2055 No. 5804187th Broadway, Suite 201
Walnut Creek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 1; I Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI STREET: 444 South Flower Street, Suite 2000 CITY: LOS Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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Patent No. 5804187
GENERAL INFORMATION:
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INPORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
'TOWATH: 9 amino acids
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TITLE OF INVENTION: Diag
TITLE OF INVENTION: DIAG
TITLE OF INVENTION: Ther
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL &
STREET: 2055 NO. 58041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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1 FQGTHVPWT
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Gaps

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Indels

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Mismatches

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8; Conservative
                                                                                                      1 FOGTHVPWT 9
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US-07-977-696C-11
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   Matches
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APPLICANT: do Couto, Roberto L.

Peterson Dr., Jerry A.

Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Specificity
for Carcinomas and Kit and Diagnostic Vaccination and Therapeutic Methods.
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COMPUTATIONS
COMPUTATIONS
COMPUTATIONS
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTATE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,839B
FILING DATE: 06-Sep-2001
CLASSIFICATION: cUnknown>
ATTORNEY/AGENT INPORMATION:
NAME: AMZEI VIVIAN
NAME: AMZEI VIVIANS
TELERRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 30,930
TELERRANICATION INPORMATION:
TELEBRANICATION INPORMATION:
TELEBRANICATION INPORMATION:
TELEBRANICATION INPORMATION:
TELEBRANICATION INFORMATION:
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Pred. No. 4.6e+05;
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Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-947-839B-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. Amzel & Assoc.
STREET: P.O.Box 159
                                                                                                      P6639938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-947-839B-72
; Sequence 72, Application US/09947839B
; Patent No. 6936706
; GENERAL INFORMATION:
                            NAME: VIVAGNA ANZEL Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P663
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELERAX: (213) 489-4210
TELERAX: n.a.
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                      30,930
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Gladwyne
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.6%;
88.9%;
   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
HOLECULE TYPE: peptide
US-08-976-288A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:|||||
1 FQGTHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity
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RESULT 15

108-07-97-696C-11

109-07-97-696C-11

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December 30, 2005, 13:02:01; Search time 79.9839 Seconds (without alignments) 49.440 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                           2443163
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       2443163 segs, 439378781 residues
                                                                     sw model
                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                       - protein search, using
                                                                                                                                                                            US-10-735-916A-6
56
1 FQGSHVPWT 9
                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                    score:
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Listing first 45 summaries geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* Post-processing: Minimum Match 0% Maximum Match 100% geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:* A_Geneseq_21:* Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:* geneseqp2005s:*

Fv region Mouse HUI CDR seque Murine in Fv region Light cha Mouse mon Peptide f Anti-idio Mouse HUI Anti-IGF-Anti-IGF-Anti-IGF-Murine an Hybrid hu WO9932630 Mouse mon Mouse mon Mouse mon Anti-IGF-Hybrid Murine Description Abp52345 F Add94151 N Adj76840 C Adz67010 N Abp52310 F Aay49217 I Aae15711 N Aae15713 N Aae15704 N Aae15712 N Add35319 Add35319 Add76899 Add76899 Add76899 Add76899 Add76899 Add76899 Add76899 Add76899 Add768919 RAdd80419 RAdd80421 Add80421 A SUMMARIES ADZ67010 ABP52310 AAY49217 AAY25397 AAE15711 AAE15713 AAE15704 AAE15712 ADA14777 ADC35319 ADD94125 ADJ76888 ADJ76890 ADJ76899 ADJ76895 ADJ80422 ADJ80420 ADJ80419 ADZ67058 ADZ67069 ADJ76840 Query Match Length DB 100.0 100.0 100.0 100.0 0 0 100. 90 8 Score No. Result

Adz67060 Mouse ant Adz67065 Human ant	_		Aap81364 Light cha		Aap81366 Light cha	Aab62303 Chimeric	_		Adj76901 Anti-IGF-	Adj76897 Anti-IGF-	Adz67071 Human ant	Adz67067 Human ant	Aaw03199 Anti-idio	Aay49209 MAD 1A7 1	Aay28468 Light cha	Aay21545 Monoclona	Ada14768 Mouse ant	Adc35310 Monoclona	Aap80154 Biosynthe	
9 ADZ67060	. ~	00	1 AAP81364	1 AAB62301	1 AAP81366	1 AAB62303	7	9 ADZ67053	7	7	9 ADZ67071	6		2 AAY49209		N			1	
100.0 112	100.0 114				_					100.0 131		100.0 131				14	14	14	100.0 249	•
25 56	27 56	28 56	29 56		31 56	32 56	33 56	34 56	35 56	36 56	37 56	38 29	39 56	40 56	41 56	42 56	43 56	44 56	45	) )

## ALIGNMENTS

Cytotoxic T lymphocyte; CTL; T helper; MAGB3; cytotoxic T cell response; tumour; immune response; cancer; vaccine; antibody. Fv region SC100 antibody CDR-L3 amino acid sequence. ABP52345 standard; peptide; 9 AA. 28-JAN-2002; 2002WO-GB000354. 26-JAN-2001; 2001GB-00002145. (first entry) WO200258728-A2. Mus musculus. 17-0CT-2002 01-AUG-2002. Synthetic ABP52345; RESULT 1 ABP52345 

(SCAN-) SCANCELL LTD. (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

Use of polypeptides and nucleic acids encoding the polypeptides, in manufacturing medicament for stimulating a cytotoxic T cell response for preventing or treating cancer, e.g. colorectal, lung, breast or WPI; 2002-608418/65.

Robins A;

Durrant LG, Parsons T,

and

Example 11; Page 46; 87pp; English.

ovarian cancer

The present invention describes the use of a polypeptide (1) in the manufacture of a medicament for stimulating a cytotoxic T cell response, where (I) comprises a first portion comprishing the part of human Pc that binds to CD64 and a second portion comprishing one or more heterologous T cell epitopes. Also described is a method of stimulating a cytotoxic T cell response in a patient such as a mammal, preferably human, by administering (I) to the patient. (I) has cytostatic activity and can be used in vaccine production. (I) and the nucleic acid encoding (I) are useful in the manufacture of a medicament for stimulating cytotoxic T

Human ant

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preventing and/or treating
                cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The medicament stimulates cytotoxic and helper T call responses. The antibodies are useful as vaccines to stimulate helper and cytotoxic T cell responses. The polypeptides and nucleic acids are useful in optimisation schedules for enhancing a protective immune response against cancer. The present sequence represents an Fv region SC100 antibody CDR-L3 amino acid sequence which is used in an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agonist; collagen antagonist; concer metastasis; anti-cryptic collagen; antibody; HUI77; variable region light chain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
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                                                                                                                                                                                                                                 Score 56; DB 5; Length 9; Pred. No. 2e+06;
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100.0%; Score 56; DE
Best Local Similarity 100.0%; Pred. No. 2e+
Matches 9; Conservative 0; Mismatches
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The medicament is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 36; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD94151 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2002; 2002WO-US038147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
                                                                                                                                                      from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CELL-) CELL MATRIX INC
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N-PSDB; ADD94150.
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    response.
                                                                                                                                                                                             Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD94151;
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF-I and/or -2; and/or (ii) inhibit specifically tyrosine (IGF-IR) and/or -2; and/or (ii) inhibit specifically tyrosine (IGF-IR) and/or -2; and/or (iii) inhibit specifically tyrosine (IGF-IR) and/or epidermal growth factor receptor (EGRR) and/or with or expectation of these receptors with their ligands. Especially they inhibit (IGF-IR) and/or for these receptors with their ligands. Especially they inhibit (IGF-IR) and or for the control of normal cells to tumor cells, inhibit growth and/or prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psortlasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGRR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; antipsoriatic; antibody; idf-1R, tyrosine kinase activity; insulin-like growth factor-1 receptor; IGF-1R, tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                            Gaps
site antibody HUI77 variable region light chain CDR to the invention.
                                                                                                                            ő
                                                                                          100.0%; Score 56; DB 7; Length 9; 100.0%; Pred. No. 2e+06;
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                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        CDR sequence for anti-IGF-1R antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 6; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                    ADJ76840 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leger 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-2002; 2002FR-00000653
18-JAN-2002; 2002FR-00000654
07-MAY-2002; 2002FR-00005753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                            9; Conservative
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                                                                                                                                                              σ
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N-PSDB; ADJ76839.
                                                                                                                                                                                     1 FOGSHVPWT
                                                                                                                                                              1 FQGSHVPWT
                                                                                                          lest Local Similarity
        cryptic collagen
which is related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003059951-A2
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                                                            Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goetsch L,
                                                                                                                                                                                                                                                                                                                      ADJ76840;
                                                                                            Query Match
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                                                                                                                                Matches
                                                                                                                                                                                                                                                    RESULT 3
ADJ76840
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The invention relates to a novel isolated anti-insulin-like growth factor capable of inding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CRR) consisting at least one complementary capable of an edge and absoluted the invention is useful in the preparation of a medicament intended for the prevention is useful in the preparation of a medicament intended for the prevention or treatment of an ilness connected with an overexpression and/or an abnormal cativation of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGFR with EGFR, where interaction of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended
                                ö
                                                                                                                                                                                                                                                                                                                        Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lump tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                              Gaps
                                                                                                                                                                                                                                                                                      Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:6.
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                                Indels
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Pred. No. 2e+06;
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                                                                                                                                                                                      ADZ67010 standard; peptide; 9 AA.
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2002FR-00005753.
                 100.08;
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11-JUL-2003; 2003FR-00008538
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                                                                                                                                                                                                                                                           30-JUN-2005 (first entry)
                                   Conservative
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CORVAIA N.
LEGER O.
                                                                  FOGSHVPWT
                                                                                                  FOGSHVPWT
                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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07-MAY-2002;
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(HAEU/)
(BECK/)
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(LEGE/)
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                                     Matches
                                                                                                                                                    RESULT 4
ADZ67010
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containing the transformation or normal cetts into cetts with cumulation character, preferably IGF-dependent, especially IGF1 and/or IGF2.

dependent and/or EGF-dependent, especially IGF1 and/or IGF2.

cuseful for preparation of amedicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cancer the specific targeting of a biologically active compound to intended for the specific targeting of a biologically active compound to search service and an endicament of propersion or an underexpression of the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an overappression or an underexpression of the IGF-IR and/or EGFR receptor is and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an overappression or an underexpression of the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an overappression or an underexpression of the invention. EGFR receptor is supperted, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of polypeptides and nucleic acids encoding the polypeptides, in manufacturing medicament for stimulating a cytotoxic T cell response and for preventing or treating cancer, e.g. colorectal, lung, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes the use of a polypeptide (I) in the manufacture of a medicament for stimulating a cytotoxic T cell response, where (I) comprises a first portion comprising the part of human FC that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytotoxic T lymphocyte, CTL; T helper; MAGE3; cytotoxic T cell response; tumour; immune response; cancer; vaccine; antibody.
inhibit the transformation of normal cells into cells with tumoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 56; DB 9; Length 9; 100.0%; Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCAN-) SCANCELL LTD.
(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP52310 standard; peptide; 109 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-2002; 2002WO-GB000354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-608418/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FQGSHVPWT
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les 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2002
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Matches
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ABP52310
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Gaps

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100.0%; Score 56; DB 2; Length 112; 100.0%; Pred. No. 0.066; cive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 9; Conservative

Sequence 112 AA;

94 FOGSHVPWT 102

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1 FOGSHVPWT

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binds to CD64 and a second portion comprising one or more heterologous T cell epitopee. Also described is a method of stimulating a cytotoxic T cell response in a patient such as a mammal, preferably human, by administering (I) to the patient. (I) has cytostatic activity and can used in vaccine production. (I) and the nucleic acid encoding (I) are useful in the manufacture of a medicament for stimulating cytotoxic T cell response. The medicament is useful for preventing and/or treating cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The medicament stimulates cytotoxic and helper T cell responses. The antibodies are useful as vaccines to esimulate helper and cytotoxic T cell responses. The polypeptides and nucleic acids are useful in oppinishing immunisation schedules for enhancing a protective immune response against cancer. The present sequence represents an Fy region SC100 antibody light chain related amino acid sequence which is used in
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; MAb; 11A7; GD2; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen.
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                                                                                                                                                                                                                                                                 Score 56; DB 5; Length 109;
Pred. No. 0.064;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain variable region consensus sequence.
                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                            an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                              AAY49217 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                 100.0%;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                            1 FOGSHVPWT 9
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                                                                                                                                                                                                                                         Sequence 109 AA;
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Paraquat; antibody; light chain; herbicide; resistant; crop plant; weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I; free radical; lipid peroxidation; electron transport; photosystem II; vacuole; cell surface; cytotoxic; sensitive.

98WO-GB003760.

15-DEC-1998;

01-JUL-1999.

19-DEC-1997;

WO9932630-A1.

Unidentified

(ZENE ) ZENECA LTD. Holt DC, Jones PG;

AAY25397 standard; protein; 112 AA.

RESULT 7 AAY25397 07-SEP-1999 (first entry)

AAY25397;

WO9932630 Seg ID 36.

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This invention describes a novel herbicide binding protein which can confer herbicide resistance activity. Crop plants, such as soybean, cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower, potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas, barley, oat, turf grass, forage grass, sugar cane, pea, field bean, rice, pine, poplar, apple, grape, citrus or nut plants, transformed with a herbicide binding protein gene are resistant to the herbicides. Hence, weeds can be selectively controlled in a field of the transformed crops. The plants are substantially resistant or tolerant to herbicides, such as paraquat or diquat, that inhibit photosynthesis by accepting electrons from photosystem I thus generating free radicals which cause lipid proteins advantageously sequester the herbicide, e.g. cat the cell surface or in the vacuolse of a treated plant. Sequestration at the cell surface prevents the entry of the herbicide into the cell so that the herbicide cannot reach its intracellular target and exert any significant cyctoxic effect. The herbicide binding protein inhibits the mobility of the herbicide from the application site to the whole plant preventing the herbicide reaching particularly sensitive organs.

Additionally, tolerant plants can be produced against herbicides that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 2; Length 112;
Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herbicide binding proteins and related polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 44-45; 60pp; English.
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Best Local Similarity
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The invention provides a monoclonal antibody (WAb) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. WAb 1A7 has defined light and heavy chain variable region sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2 - associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence represents the light chain variable region consensus sequence

Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)

Disclosure, Fig 3C, 74pp, English.

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region variant, 340VKb
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                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                     FOGSHVPWT
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                                                                                                                                          Sequence 112 AA;
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24-AUG-2000;
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Synthetic.
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                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
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                                                                                                                                                           Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; inhibitor; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a humanised form of the antibody 340 mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line
 Gaps
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                                                                                                                                           Mouse monoclonal antibody alpha 340 Vk region variant, 340VKb.
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                                                                                                                                                                                                                                                             note= "Wild type Thr substituted with Ser"
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 Mismatches
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                                                                                     AAE15711 standard; protein; 112 AA.
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24-AUG-2000; 2000GB-00020794
                                                                                                                          (first entry)
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Durrant LG;
                                FQGSHVPWT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCAN-) SCANCELL LTD.
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                     1 PQGSHVPWT
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Synthetic.
                                                                                                       AAE15711;
   Matches
                                                                   RESULT
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deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF immunogenicity, as the original murine antibody and has increased ability to inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; inhibitor; mutent; mutein; variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 56; DB 5; 100.0%; Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Matches
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                                                                                                                                                         The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (EGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF immunogenicity but shows similar binding to cells expressing EGF inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                             New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; humanised form; monoclonal antibody alpha 340; gene therapy; epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast; gastric; ovarian; immune response; cytostatic; cell growth; apoptosis; inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse monoclonal antibody alpha 340 light chain variable (VK) region.
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/label= CDR3
/note= "Complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 56; DB 5; Length 112; 100.0%; Pred. No. 0.066;
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                                                                                                                                    Example 2; Fig 7; 53pp; English
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                          Ellis JRM, Durrant LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 FQGSHVPWT 102
                                                                                                                                                                                                                                                                                                                                                                               region variant, 340VKd
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(SCAN-) SCANCELL LTD.
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                                                     WPI; 2002-062384/08.
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 112 AA;
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Region
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Matches
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mouse monoclonal antibody which binds to epidermal growth factor (BGF)
receptor and inhibits binding of BGF), obtainable from the cell line
deposited with the ECACC under accession number 97021428. The humanised
form of the antibody 340 is useful in gene therapy, medicine and in the
manufacture of a medicament for treatment or prophylaxis of cancer. The
invention is useful for treatment or prophylaxis of cancer. The
invention is useful for treatment or prophylaxis of cancer. The
covarian cancers or also for preventing the recurrence of ancer after
covarian cancers or also for preventing the recurrence of ancer after
covarian teatment or surgery. The invention is also useful for enhancing
a protective immune response against cancer by optimised immunisation
cochedules. The humanised form of the antibody 340 has reduced
immunogenicity but shows similar binding to cells expressing EGF
immunogenicity but shows similar binding to cells expressing EGF
immunogenicity but shows similar binding to cells expressing EGF
immunogenicity but shows similar binding to cells expressing EGF
indibit the growth of EGF receptor expressing cells. The invention is
used as cell growth and apoptosis inhibitor. The present sequence is
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                                                                                                                                                                                                                                                                                                                                                   New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 56; DB 5; Length 112; 100.0%; Pred. No. 0.066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used as cell growth and apoptosis inhibitor. The present mouse monoclonal antibody alpha 340 light chain variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 2; 53pp; English.
21-MAY-2001; 2001WO-GB002226
                                                       19-MAY-2000; 2000GB-00011981
24-AUG-2000; 2000GB-00020794
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                                                                                                                                                                                                        Ellis JRM, Durrant LG;
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Best Local Similarity
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Synthetic.
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The present invention relates to a humanised form of the antibody 340 (a mouse monoclonal antibody which binds to epidermal growth factor (BGF) receptor and inhibits binding of EGF), obtainable from the cell line deposited with the ECACC under accession number 97021428. The humanised form of the antibody 340 is useful in gene therapy, medicine and in the manufacture of a medicament for treatment or prophylaxis of cancer. The invention is useful for treating colorectal, lung, breast, gastric or ovarian cancers or also for preventing the recurrence of cancer after initial treatment or surgery. The invention is also useful for enhancing a protective immune response against cancer by optimised immunisation schedules. The humanised form of the antibody 340 has reduced immunogenicity but shows similar binding to cells expressing EGF immunogenicity but shows similar binding to cells expressing EGF inhibit the growth of EGF receptor expressing cells. The invention is used as cell growth and apoptosis inhibitor. The present sequence is mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanized form of mouse monoclonal antibody 340 which binds to epidermal growth factor receptor and inhibits binding of growth factor, useful for treating colorectal, lung, breast, gastric and ovarian cancer.
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                                                                                                                                                                                            /note= "Wild type Asn substituted with Lys"
                                               'note= "Wild type Lys substituted with Gln"
                                                                                                                      'note= "Wild type Ile substituted with Val"
                                                                                                                                                        'note= "Wild type Leu substituted with Val"
               /note= "Wild type Gln substituted with Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide from antibody heavy chain resembling 1A7 #6.
                                                                                    Leu substituted
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                                                                                note= "Wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 7; 53pp; English.
                                                                                                                                                                                                                                                                                                         21-MAY-2001; 2001WO-GB002226
                                                                                                                                                                                                                                                                                                                                            19-MAY-2000; 2000GB-00011981
24-AUG-2000; 2000GB-00020794
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Durrant LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region variant, 340VKc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-062384/08.
                                                                                                                                                                            Misc-difference 112
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Misc-difference 18
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                               Misc-difference
                                                                   Misc-difference
                                                                                                       Misc-difference
                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                 WO200188138-A1.
                                                                                                                                                                                                                                                                     22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ellis JRM,
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The invention relates to the recurrence and/or development of a ganglioside GD2-associated tumour, e.g. melanoma, in an individual which is delayed by administration of an antibody comprising light and heavy chain variable region sequences of the anti-idiotype monoclonal antibody 1A7. The antibody is used for delaying recurrence and/or development of GD2-associated tumour. e.g. melanoma, neuroblastoma, glioma, sarcoma, or small cell lung cancer, in individual, and for treating individual with GD2-associated tumour. The present sequence is a unique peptide region from an antibody sequence resembling the anti-idiotype antibody 1A7 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; monoclonal antibody; 1A7; anti-idiotype antibody; ganglioside GD2; cytostatic; melanoma; neuroblastoma; small cell lung cancer; tumour; antibody; variable region; VH; VL; glioma; soft tissue sarcoma; vaccine.
                                                                                                                                                                                                                                                                                                                                                heavy
                                                                                                                                                                                                                                                                                                                            Delaying recurrence and/or development of ganglioside GD2-associated tumor in individual, by administering antibody containing light and heavy chain variable region sequences contained in sequence of specified amino
heavy chain variable region; mouse; ganglioside GD2-associated tumour; melanoma; antibody; anti-idiotype; monoclonal antibody; 1A7; neuroblastoma; glioma; sarcoma; small cell lung cancer.
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                                                                                                                                                                                                                                                                        Chatterjee SK;
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                                                                                                                                                                               95US-00372676.
96US-00591196.
96US-00752844.
                                                                                                                                                    99US-00293533.
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Best Local Similarity 100...
9; Conservative
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                                                                                                                                                                                                                                                                         Chatterjee M,
                                                                                          US6509016-B1
                                                                                                                                                    15-APR-1999;
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                                                                                                                                                                                  17-JAN-1995;
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21-MAY-2002; 2002US-00153401.

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This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the partial amino acid sequence of the mouse anticryptic collagen site antibody HU177 variable region light chain used during the creation of the antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; antipsoriatic; antibody; IGF-1R; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; or epiderma; cancer; osteosarcoma; complementarity determining region;
anti-cryptic collagen; antibody; HUI77; variable region light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determining regions, useful for diagnosing and treating disorders associated with anglogenesis, tumor growth and/or cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cryptic collagen antibody with one or more complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 56; DB 7; Length 112; 100.0%; Pred. No. 0.066; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   Brooks PC;
                                                                                                                                                                                                                                                                                                                                                     Broek D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 10; 232pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-IGF-1R related protein #5.
                                                                                                                                                                                                                                                                                                                                                       Tang Y,
                                                                                                                                                                                               26-NOV-2002; 2002WO-US038147.
                                                                                                                                                                                                                                        26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112 AA;
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                                                                                                             WO2003046204-A2
                         mouse; murine.
                                                                  Mus musculus.
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    $XXCCCCCCCCCX8X47474XBXXBXXBXXBXXBXXBXXBXXBXX8XX8XX8XX8X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      under conditions where the region were not total a sequence appearing as ADC35321 - ADC35370, a host cell comprising the polymuclectide, a fusion polymetic cell comprising the polymuclectide, a fusion polymetic comprising 1A7, a humanised antibody comprising 5 consecutive amino acids from the 1A7 variable regions and a vaccine comprising the antibodies. The antibodies are useful for associated disease in an individual. The GD2-associated diseases is chosen from melanoma, neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma. The individual has a clinically detectable tumour, and the method is for palliating the GD2-associated disease. 1A7 is preferably useful for treating a tumour that was previously detected in the individual and has been treated and is clinically undetectable at the time of the administering of 1A7, or for reducing the risk of recurrence of a clinically detectable tumour. The under time of the administering of 1A7, and the humanised antibody are useful for detecting the presence of an anti-GD2 antibody bound to a time of the administering construction of the humanised antibody are useful for detecting the presence of an anti-GD2 antibody bound to a time of the administering the presence of an anti-GD2 antibody bound to a time of the administering the presence of an anti-GD2 antibody bound to a time of the administering the presence of an anti-GD2 antibody bound to a time of the administering the presence of an anti-GD2 antibody bound sequence for the time.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a monoclonal antibody 1A7 (an anti-idiotype antibody eliciting an anti-GD2(ganglioside) response). Also included are an antibody producing cell deposited under ATCC Accession No. HB-11786 (or its progeny), a polynucleotide comprising a sequence encoding a polypeptide with immunological activity of 1A7 (where the polypeptide comprises at least 5 consecutive amino acids from a variable region of 1A7), an isolated polynucleotide comprising a region of at least 20 consecutive nucleotides that is capable of forming a stable duplex with a polynucleotide encoding the light or heavy chain variable region of 1A7 under conditions where the region of form a stable hybrid with a
                                                                                                                                                                                                                                                                                   Novel anti-idiotypic monoclonal antibody 1A7, that is capable of recruiting a tumor-specific response against glycosphingolipid GD2, useful for treating a GD2-associated disease e.g., melanoma, glioma, soft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agonist; cancer metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                   Chatterjee SK;
                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 15; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD94125 standard; protein; 112 AA.
                                           96US-00591196.
99US-00293533.
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                                                                                                             CHATTERJEE M.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                    FOON K
                                                                                                                                                                                                   Chatterjee M,
                                                                                                                                                                                                                                                                                                                                                            tissue sarcoma
                      17-JAN-1995;
16-JAN-1996;
15-APR-1999;
                                                                                                             (CHAT/)
                                                                                                                                    FOON/)
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Gaps

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(FABR ) FABRE MEDICAMENT SA PIERRE.
                                          Goetsch L, Corvaia N, Leger O;
             18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
    20-JAN-2003; 2003WO-FR000178.
                                                    WPI; 2003-569653/53.
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New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 54; 164pp; French

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or creat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with a comparation of hyperactivity of signal transduction pathways mediated by interaction of hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.

Sequence 112 AA;

Gaps ö Query Match 100.0%; Score 56; DB 7; Length 112; Best Local Similarity 100.0%; Pred. No. 0.066; Matches 9; Conservative 0; Mismatches 0; Indels

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1 FOGSHVPWT 9

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94 FQGSHVPWT 102

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Ig light chain V r Ig kappa chain BrB Ig kappa chain V r Ig light chain V r Ig kappa chai
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                                                                                               December 30, 2005, 13:11:41; Search time 12.7742 Seconds (without alignments) 67.789 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
                                                                   - protein search, using sw model
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PL0203
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Gapop 10.0 , Gapext 0.5
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H28840
B31485
A27887
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Maximum DB seq length: 200000000
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Match Length DB
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2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                     Run on:
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Ig kappa chain V r	anti-peptide Fab'	Ig kappa chain V r	Ig kappa chain pre	Ig kappa chain V r	Ig kappa chain pre	Ig kappa chain - m	Ig kappa chain pre	Ig kappa chain V r	Ig light chain V r	Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain V r	Ig light chain V r	Ig light chain V r	Iq light chain V r
E30560	A34353	PT0359	B34904	S52449	C34904	852028	JL0029	855366	PH1035	A49032	S15673	C27887	PH1034	PH1038	PH1037
~	0	7	7	~	0	N	N	~	~	N	7	~	N	N	N
13	114	118	131	131	131	219	225	96	102	119	111	112	103	103	103
Н.														_	_
73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	71.4	71.4	71.4	9.69	9.69	67.9	67.9	67.5

## **ALIGNMENTS**

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PH1043
Ig light chain V region (clone 111.68) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #text_change 09-Jul-2004
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Date: BPH1043
C;Accession: PH1043
C;Accession: PH1043
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Status: mRNA A;Molecule type: mRNA A;Molecu
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σ 1 FOGSHVPWT ઠે 셤

94 FOGSHVPWT 102

RESULT 2

Grappa chain BrE-3 - mouse (fragment)

Ig kappa chain BrE-3 - mouse (fragment)

Ig kappa chain BrE-3 - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Accession: 867944

R; Couto, J.R.; Blank, E.W.; Peterson, J.A.; Ceriani, R.L.

Hybridoma 12, 15-23, 1933

A; Title: Cloning of cDNAs encoding the variable domains of antibody BrE-3 and construct A; Reference number: 867944

A; Reference number: 867944

A; Residua: preliminary

A; Molecule: UNA

A; Residues: 1-121 < COU>
A; Residues: 1-121 < COU>
A; Residues: 1-121 < COU>
A; COU
A; COU
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Gaps ö Length 121; 0; Indels 94.6%; Score 53; DB 2; 88.9%; Pred. No. 0.022; tive 1; Mismatches Query Match Best Local Similarity 88.9³

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1 FOGSHVPWT 9

Gaps

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Indels

Length 102;

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A,Cross-references: UNIPARC:UP10000115F42; EMED:X58664; NID:g52931; PIDN:CAA41521.1; PIL C,Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UP10001115F43; EMBL:X58665; NID:952933; PIDN:CAA41522.1; PIC;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S14593
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH A;Reference number: S14484
A;Accession: S14593
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
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88.9%; Pred. No. 0.21;
                                                                                                                                                                               83.9%; Score 47; DB 2;
88.9%; Pred. No. 0.21;
iive 1; Mismatches
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Matches 8; Conservative
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Matches 8, Conservative
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Best Local Similarity
8; Conserv?
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A; Residues: 1-102 < CHE>
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                                                                                                                                                                                                                 Jackson Learning (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
R;Aschano 0, 5 tenzel-Poorte, M.; Rittenberg, M.B.
R;Apscription: Natural polyreactive antibodies differ from Ag-induced antibodies in VH C A;Pescription: Natural polyreactive antibodies differ from Ag-induced antibodies in VH C A;Accession: S14590
A;Accession: S14590
A;Accession: S14590
A;Accession: S14590
A;Accession: S14590
A;Accession: Jun Agenty C;Apscription: Jun A;Accession: Jul A;Accession: Jun A;Accession: Jul A;Accession: Jun A;Accession: Jul A;Accession: Jul A;Accession: Jul A;Accessi
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R;Chan, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH
A;Reference number: S14484
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R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in A;Reference number: S14484
A;Reference number: S14594
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
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Pred. No. 0.21;
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Pred. No. 0.21;
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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FQGTHVPWT 111
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Best Local Similarity
'... 8; Conserv?
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A;Molecule type: mRNA
A;Residues: 1-102 <CHE>
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A;Molecule type: mRNA
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Gaps

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RESULT 7
E28195
E19195
E198195
E198195
E198195
E198195
E198196
E198196
E198196
E2986168: Wus musculus (house mouse)
E298196
E2986168: Wus musculus (house mouse)
E298196
E298196
E298196
E298196
E298197
E298197
E298198
E29818

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A,Residues: 1-102 <SHE>
A,Residues: 1-102 <SHE>
A,Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B1B; EMBL:M29770
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F,6-85/Domain: immunoglobulin homology <IMM>
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PH1042

g light chain V region (clone 202.838) - mouse (fragment)

G;Species: Mus musculus (house mouse)

G;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

G;Accession: PH1042

R;Tillnan, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A;Reference number: PH0971; MUID: 92381444; PMID:1512540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0203
B;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from A;Reference number: PL0198; MUID:90309768; PMID:2114528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-113 <SMT.3 <SMT.3 <SMT.4)
A;Cross-references: UNIPARC:UPI0000113786; GB:X53643; NID:G50196; PIDN:CAA37694.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V-II region TE33 - mouse
C;Species: Mus musculus (house mouse)
C;Dacies 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
C;Accession: A2367
R;Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglister, J.
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Gaps
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CjSuperfamily: immunoglobulin V region; immunoglobulin homology
CjKeywords: immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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Indels
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A;Molecule type: mRNA
A;Residues: 1-103 <TIL>
A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176AA4
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88.9%; Pred. No. 0.33;
tive 1; Mismatches (
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  Mismatches
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Best Local Similarity 88.9*
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Matches 8; Conservative
8; Conservative
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94 FOGSHVPFT 102
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Matches
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
           C,Accession: D28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. Com. 253, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid shacession: D28195
A;Accession: D28195
A;Accession: D28195
A;Molecule type: mRNA
A;Residues: 1-112 <SHE>
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C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.28;
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88.9%; Pred. No. 0.23;
ive 1; Mismatches
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88.9%; Pred. No.
C;Species: Mus musculus (house mouse)
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Matches 8, Conservative
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-131 <REI>
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Search completed: December 30, 2005, 13:34:54 Job time : 13.7742 secs
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PH1040
C;Accession: Immunoglobulin
C;Accession: Immuno
Biochemistry 28, 7168-7175, 1989
A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predi A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predi A;Reference number: A32967; MUD:90057406; PMID:2819059
A;Accession: A32967
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra A;Molecule type: mRNA
A;Residues: 1-114 < LEV>
A;Cross-references: UNIPARC:UPI0000114F5D; GB:M30481; NID:g197157; PIDN:AA38935.1; PID:C;Superfamally: immunoglobulin immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology < LMM>
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A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-112 <07T7-
A;Cross-references: UNIPARC:UPI0000115509; GB:U01240; NID:g402265; PIDN:AAD10617.1; PID:
A;A;Dets: authors translated the codon CTT for residue 99 as Val
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.4%; Score 45; DB 2; Length 114; Best Local Similarity 77.8%; Pred. No. 0.54; Matches 7; Conservative 2; Mismatches 0; Indels
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MEDLINE-92020904; PubMed=1924323;

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MEDLINE-92020904; PubMed=1924323;

MEDLINE-92020904; PubMed=1924323;

MEDLINE-92020904; PubMed=1924323;

MEDLINE-92020904; Patalogue in mice.";

MEDLINE-92020904; Medd. Sci. U.S.A. 88:8616-8620(1991).

MEDLINE-92090359; Medl. Medl. Acad. Sci. U.S.A. 88:8616-8620(1991).

MEDLINE-920; PRO03599; J. G. J. MENA.

MEDLINE-920; PRO03599; J. G. J. MENA.

MEDLINE-920; PRO03599; J. G. J. MENA.

MEDLINE-920; PRO0406; J. G. J. J. MENA.

MEDLINE-920; PRO0406; J. G. J. J. MENA.

MEDLINE-920835; J. G. LIKE; 2.

MEDLINE-920835; J. G. LIKE; 2.

MEDLINE-920835; J. G. LIKE; 2.

MEDLINE-920835; J. G. LIKE; 2.
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus
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Last sequence update)
Last annotation update)
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Last sequence update)
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Q850Y4_ORYSA
Q6LNP1_PHOPR
Q5MB05_MICTO
Q8ZBA0_YERPE
G6F83_YERPE
G5GF83_YERPE
G51B0_CAMAC
G33X81_STRRO
G53PM9_ORYSA
Q5MB06_MICTO
Q5MB06_MICTO
Q5MB06_MICTO
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Q8H8E2_ORYSA
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065207;

25-OCT-2004 (TEMBLEEL 28, C

25-OCT-2004 (TEMBLEEL 28, L

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B3(FY)-PB40 (Fragment).
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091YR3;
01-DEC-2001 (TrEMBLrel. 19, C.
01-DEC-2001 (TrEMBLrel. 19, L.
01-MRA-2004 (TrEMBLrel. 26, L.
Phfl protein
Name=Phfl;
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FQGSHVPFT
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mycobacteri
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sulfolobus
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                                                                                                                                    December 30, 2005, 13:11:26; Search time 81 Seconds (without alignments) 78.392 Million cell updates/sec
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090x19
040x68
0845y7
0845y7
0845y7
0981x8
0931x1
0931x1
0931x2
0050x2
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                2166443 seqs, 705528306 residues
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05JZY2_MAGGR
07WRQ4_9N0ST
082DC5_STRAW
05C219_SCHJA
YB71_SCHPO
055HW6_MAGGR
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091YR3_MOUSE
09C1EF_1EACLA
09C1EF_1EACLA
04HV68_G1BZE
053VP8_MOUSE
0845Y7_9CHRO
0845Y7_9CHRO
0845Y7_9CHRO
0845Y7_9CHRO
0845Y7_MICAE
0931RR1_MICAE
0931RR2_MICAE
0931RR2_MICAE
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Q6Z5V6_ORYSA
Q4 IQD3_GIBZE
Q4J838_SULAC
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O51MF7 MAGGR
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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56
1 PQGSHVPWT 9
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Match Length DB
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Perfect score:
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us-10-735-916a-6.rup

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Pfam; PF02378; PTS EIIC; 1.
TIGREAMS; TIGRO0410; lacE; 1.
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Q4HV68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                 RC TISSUE-Amamary tumor metastatized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.;

Expression driven by an MMTV-LTR enhancer.;

Expression driven by an MMTV-LTR enhancer.;

RABDINE=22388257; PubMed=12477932; DOI=10.173/pnas.242603899;

Strausberg R.L., Feligold E.A., Groues L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.E., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Altechnis R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Altechnis R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Robkins R.F., Jordan H., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robkins S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Mhting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rhesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rherfield Y.S.N., Krzzwinski M.I., Skalska U., Smailus D.E.,

Rhemeration and initial analysis of more than 15,000 full-length human
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
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Ensembl; ENSMUSG0000024193; Mus musculus.
Ensembl; ENSMUSG0000024193; Mus musculus.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001965; Znf_PHD.
Pf00628; PHD; 2.
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0
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TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
Expression driven by an MMTV-LTR enhancer.;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cellobiose-specific PTS system IIC component (EC 2.7.1.69).
Name=ptcC; OrderedLocusNames=LL0416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%; Score 42; DB 2; Length 375; 85.7%; Pred. No. 53;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
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SMART; SM00333; TUDOR; 1.
PROSITE; PS01359; ZF PHD_1; UNKNOWN_1.
PROSITE; PS0016; ZF PHD_2; 1.
SEQUENCE 375 AA; 41146 MW; 57D88E19A5BBB729 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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STRAIN=IL1403;
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                                        NUCLEOTIDE SEQUENCE.
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  NCBI_TaxID=10090;
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Matches
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RESULT 3

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RA BILTON B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Birten B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguelavkiy L., Boukhgilter B., Butler J., Calvo S.E., Camarata J., Chang J., Cooke P., Corum B., DeArellano K., Ander B., Daza J.S., Dooley K., Dooris L., Elkins T., Engels R., Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J., Radion D., Hagos B., Hall J., Horton L., Hulme W., Iliev I., R., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A., Rahle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A., R., Malle T., Macroan C., Macdonald P., Major J., Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L., Manda V., Murphy T., Naylor J., Nguyen C., Nigyen C., Nigyen C., Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D., A Rachupka A., Ramasamy U., Raymond C., Retter R., Rise C., Rogov P., R. Roman J., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Alander B., Mander B., Zamen S., Sewery P., Simrnow R., Lalames M., Young G., Zainoun J., Zembek L., Zimmer A., Zody M., Mander M., Arman J., Sonday R., Lander R., Rander R., Samen R., Zimmer A., Zody M., Rander R., Rander R., Rander R., Samen R., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008982; P:protein-N(PI)-phosphohistidine-sugar phosph. . .; IEA.
GO; GO:0005351; F:sugar porter activity; IEA.
GO; GO:000540; F:transferase activity; IEA.
GO; GO:0005401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR004352; Ptrans_EIIC.
InterPro; IPR004501; Pts lac.
BEA.
GO:0006810; Pts lac.
MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.GR-1697R; Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weiseenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403."; Genome Res. II:731-753(2001). EMBL; AR006278; AAK04514.1; -; Genomic_DNA.
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Submitted (FB2-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2; Length 389;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.0%; Score 42; 66.7%; Pred. No. 55;
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108678 MW; 37F77CFD87F5FCB4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Match
Best Local Similarity 66.7.,
6; Conservative
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Q845Y8;
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862 FKGSHLSWT 870
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                                                                                                                                                                                                                                                                                                                                                                                             962 AA;
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NON TER
SEQUENCE
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ID Q845Y8 M
AC Q845Y8 M
AC Q845Y8 M
AC Q1-JUN-2\
DT Q1-JU
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MEDLIFFS.66136012; PubMed=3937730;

MEDLIFFS.66136012; PubMed=3937730;

Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;

The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";

EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                            Gaps
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Yoshida T., Shi R., Chinen H., Yuki Y., Yoshida M., Kondo R.,
                                                                                                      Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.2%; Score 41; DB 2; Length 112; 77.8%; Pred. No. 24;
                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03386; CAA27113.1; -; mRNA.
preliminary data.

EMBL; AACM01000459; EAA74791.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 504 AA; 55160 MW; 26098EA86A332C2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 AA; 12266 MW; C844B7881A89C18A CRC64;
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NCBI_TaxID=44822;
                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Kappa chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Microcystin synthetase (Fragment).
                                                                                                  75.0%; Score 42; DB 2; 66.7%; Pred. No. 72; ative 2; Mismatches
                                                                                                                                                                                                                                                                                                                              112 AA.
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                                                                                                                                                                                                                                                                                                     9 MOUSE
Q53VP8 MOUSE PRELIMINARY;
Q53VP8;
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Q845Y7;
                                                                                                Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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les 7; Conservative
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94 FQGIHVPYT 102
                                                                                                                                                                                                         72 FVGSHLPWS 80
                                                                                                                                                                                1 FQGSHVPWT 9
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Microcystis viridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     73.2%; Score 41; DB 2; Length 962; 66.7%; Pred. No. 2.1e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   108980 MW; 2510459A5CCD484F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microcystis aeruginosa.
Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBI_TaxID=1126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
EMBL; AB092807; BAC57997.1; -; Genomic_DNA.
HSSP; P14687; 1AMU.
GO; GO:0048037; F:cofactor binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; F:metabolism; IEA.
InterPro; IPR010071; AA_adenyl_dom.
InterPro; IPR0100913; ARP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR001242; Condensatn.
InterPro; IPR001242; Condensatn.
Pfam; PF00560; Phebinding; 1.
Pfam; PF00560; Pe-binding; 1.
Pfam; PF00550; PP-binding; 1.
Pfam; PR00550; PP-binding; 1.
Pfam; PR00550; PP-binding; 1.
Pfam; PR00550; PP-binding; 1.
Pfam; PR00550; PP-binding; 1.
PRINTS; PR00154; AMPBINING; 1.
PROSITE; PS00075; ACP_DOMAIN; 1.
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TICKFAMB; TICRO1733; AA-adenyl-dom; 1.
PROSITE; PSCO075; ACP_DOWAIN; 1.
PROSITE; PSCO0455; AMP_BINDING; 1.
PROSITE; PSCO141; ASP_PROTEASE; UNKNOWN_1.
NOW TER 962 962
SEQÜBNCE 962 AA; 108678 MW; 37F77CFD87F5
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R GO; GO: 0016874; F:10fage activity; IEA.

R GO; GO: 0016874; F:11gage activity; IEA.

R GO; GO: 0016874; F:11gage activity; IEA.

R GO; GO: 0018177; F:phosphopantetheline binding; IEA.

GO; GO: 0008152; P:metabolism; IEA.

InterPro; IPR001071; AA_adenyl_dom.

InterPro; IPR001242; Condensatn.

InterPro; IPR00134; AMP-bind.

InterPro; IPR001673; AMP-bind.

InterPro; IPR001673; AMP-bind.

InterPro; IPR001673; Phantne S.

IN Pfam; PF00560; PP-binding; 2.

IN Pfam; PF00560; PP-binding; 2.

IN PR0SITE; PS00455; AMP BINDING; 2.

IN PROSITE; PS00455; AMP BINDING; 2.

IN PROSITE; PS00045; PHOSPHOPANTETHEINE; 1.

IN ROSITE; PS00045; PHOSPHOPANTETHEINE; 1.
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66.7%; Pred. No. 4.6e+02;
ive 2; Mismatches 1; Indels
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY034602; AAK61391.1; -; Genomic_DNA.
HSSP; 030409; IDNY.
                                                                                                                                                                                                                                   Raps S., Miller D., Ratner S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF458094; AAL82383.1; -; Genomic_DNA.
HSSP; 303409; IDNY.
                                                                                                                        Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBL_TaxID=1126;
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Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBI_TaxID=1126;
            (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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GG) GG:0016874; F:ligase activity; IEA.
GG) GG:001177; F:phosphopantetheine binding; IEA.
GG) GG:0008152; F:metabolism; IEA.
InterPro; IPR010071; AA_adenyl_dom.
InterPro; IPR009081; ACP_like.
InterPro; IPR0010873; AMP-bind.
InterPro; IPR001242; Condensatn.
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nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1267 FKGSHLSWT 1275
                                                                                                                    Microcystis aeruginosa.
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              01-JUN-2002 (
01-JUN-2002 (
01-MAR-2004 (
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STRAIN=HUB 5-2-4;
MEDLINE=96162875; PubWed=8595871; DOI=10.1016/0378-1097(95)00469-6;
Meisener K., Dittmann E., Borner T.; orange of the cyanobacterium Microcystis aeruginosa contain sequences homologous to peptide synthetase genes."; FEMS Microbiol. Lett. 135:295-303(1996).
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                                                          Gaps
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Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
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                Score 41; DB 2; Length 962;
Pred. No. 2.1e+02;
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66.7%; Pred. No. 2.18+02;
tive 2; Mismatches 1; Indels
                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Cyanobacteria, Chroococcales, Microcystis NCBI_TaxID=1126;
                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Peptide synthetase module (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2114 AA.
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GO; GO:0048037; F:cofactor binding; IEA.

GO; GO:001874; F:lagase activity; IEA.

GO; GO:001874; F:lagase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR001071; AA_adenyl_dom.

InterPro; IPR0010873; AMP-bind.

InterPro; IPR001242; Condensatn.

InterPro; IPR001243; Condensatn.

InterPro; IPR001663; Pheppanteth_bind.

Pfam; PF00501; AMP-binding; 1.

Pfam; PF00568; Condensation; 1.

Pfam; PF00569; Condensation; 1.
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00550; PP-binding; 1.
PRINTS; PR00154; AMPBINDING.
TIGRPAMS; TIGR01733; AA-adenyl-dom; 1.
PROSITE; PS0075; ACP DOWAIN; 1.
PROSITE; PS00155; AMP BINDING; 1.
PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 228338; CAA82192.1; -; Genomic_DNA.
PIR; S49111; S49111.
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                                                                                                                                                                                           RESULT 8
048915 MICAE PRELIMINARY;
AC 048915;
DC 01-NOV-1996 (TYEMBLEE]. 01,
DT 01-NOV-1996 (TYEMBLEE]. 02,
DT 01-NOV-1996 (TYEMBLEE]. 01,
DT 02 STRAIN-HUB 5-2-4;
DT 03 SSOUGHS1; PRODAINS AD-DINGING;
DT 02 STRAIN-HUB 5-2-4;
DT 03 STRAIN-HUB 5-2-4;
DT 03 STRAIN-HUB 5-2-4;
DT 04 STREE, PSOUGHS1; AMPBINDING
DT 04 STREE 993 AA; 112326 M
                  73.2%;
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QBRTG4 MICAE
ID QBRTG4 MICAE PRELIMINARY;
AC QBRTG4;
Query Match
Best Local Similarity 66.7
Local 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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874 FKGSHLSWT 882
                                                                                                                    |:|||: ||
862 FKGSHLSWT 870
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Gaps

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Length 2114;

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CREATURE STREAM 
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TIGRFAMB; TIGR01733; AA-adenyl-dom; 1...
PROSITE; PSS0075; AMP BINDING; 2.
PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
PROSITE; PS00121; POSPEROPERSEABI, UNKNOWN 1.
PROSITE; PS0012; POSPEROPERSEABI, 1.
SEQUENCE 2126 AA; 242242 MW; DTFFCGC9F6F43AB3 CRC64;
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Bukaryota, Alveolata, Apicomplexa, Coccidia, Bimeriida, Cryptosporidiidae, Cryptosporidium.

NCBI_TaxIb=237895;
                                                                                                                                                                                                                                                                              Microcystis aeruginosa.
Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBI_TaxID=1126;
                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                            PRT; 2126 AA
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                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26, MCyB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, Hypothetical protein. ORFNames=Chro.70128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSCFU2_CRYHO PRELIMINARY;
QSCFU2;
                                                                                                         Q9S1A8_MICAE PRELIMINARY;
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Best Local Similarity 66.77
6, Conservative
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
STRAIN=TU502;
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                                                                                                                                                                                                                                                                   Name=mcyB;
                                                                                 MICAE
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                                                   RESULT 12
Q9S1A8 MIC
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                  InterPro; IPRO06163; Phappaneth_bind.
InterPro; IPRO06163; Phaptne S.
Pfam, PRO0668; Condensation; 2.
Pfam; PRO0668; Condensation; 2.
PRAM; PRO0154; AMPBINDING; 2.
PRINTS; PRO16154; AMPBINDING; 2.
PROSITE; PS00455; AMP BINDING; 1.
PROSITE; PS00455; AMP BINDING; 1.
PROSITE; PS00697; DNA_LIGASE A1; UNKNOWN I.
PROSITE; PS00615; PHOSPHOPANTETHRINE; 1.
SEQUENCE 2126 A4; 242439 MW; 6DB575F2A49B1933 CRC64;
                                                                                                                                                                                                                                                                                                                                                               73.2%; Score 41; DB 2; Length 2126;
66.7%; Pred. No. 4.6e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2126;
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TIGREAMS; TIGRO1733; AA-adenyl-dom; 1.
PROSITE; PSS0075; ACP_DOMAIN; 2.
PROSITE; PS00145; AMP_BINDING; 2.
PROSITE; PS00697; DNA_LIGAGE_AI, UNKNOWN 1.
PROSITE; PS00697; DNA_LIGAGE_AI, UNKNOWN 1.
PROSITE; PS006012; PROFPLOFANTETHEINE; 1.
SEQUENCE 2126 AA; 242247 WW; 2A8438725198E85C CRC64;
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66.7%; Pred. No. 4.6e+02;
ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microcyštis aeruginosa.
Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBI_TaxID=1126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO: 0048037; F: cofactor binding; IEA.
GO; GO: 0016874; F: ligase activity; IEA.
GO; GO: 0011177; F: Phosphopantetheine binding; IEA.
GO; GO: 00008152; P: metabolism; IEA.
InterPro; IPR010071; AA_adenyl_dom.
InterPro; IPR0090873; APP-bind.
InterPro; IPR0090873; APP-bind.
InterPro; IPR001242; Condensatn.
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HSSP; 030409; 1DNY.
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InterPro; IPR001969; Pept Asp AS.
InterPro; IPR006163; Phsppanteth bind.
InterPro; IPR006162; Ppantne S.
Pfam; PF00501; AMP-binding; Z.
Pfam; PF00560; PP-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
InterPro; IPR000977; DNA_ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q93LR2_MICAE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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les 6; Conservative
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1279 FKGSHLSWT 1287
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1279 FKGSHLSWT 1287
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STRAIN=PCC 7813;
                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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RATAINS—10-15;

Birren B., Nusbeum C., Abebe A., Abouelleil A., Adekoya E.,

RA Ait-zahra M., Allen T., An P., Anderson M., Anderson S.,

RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,

Rayol T., Biltehsteyn B., Bloom T., Blye J., Boguslavekiy L.,

Borowsky M., Boukhgalter B., Brunache A., Buller J., Claixte N.,

Borowsky M., Boukhgalter B., Brunache A., Buller J., Claixe N.,

RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,

Collymore A., Considing T., Cooke P., Cooke P., Cooke P.,

Cooke P., Cooke P., Cooke P., Cooke P.,

Bayol R., Dawoe T., Deffey N., Dupes A., Elkins T., Engels R.,

Brickson J., Farins A., Faro S., Petreira P., Fischer H., Gagls R.,

Erickson J., Farins A., Faro S., Ferreira P., Fischer H., Hafez N.,

RA Dorjee K., Douris L., Duffey N., Dupes A., Elkins T., Engels R.,

RA Dorjee K., Douris L., Duffey N., Dupes A., Elkins T., Engels R.,

RA Dorjee K., Douris L., Duffey N., Dupes A., Elkins T., Engels R.,

RA Dorjee K., Douris L., Luis C., Galagan J., Gearin G., Gnerre S.,

RA Honan T., Houde N., Hughes L., Hallme W., Husby E., Iliev I.,

Radls C., Kieu A., Kianer P., Kodira C., Kulbokas E., Labutti K.,

Ralls C., Kieu A., Kianer P., Kodira C., Mancells B.,

Radls C., Marabella R., Maru K., Marchas D., Lewis T.,

Indiblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,

Lui A., Marabella R., Maru K., Matches C., Malcell C.,

Marabella R., Marabella R., Maru K., Malches C., Malcel L.,

Mostorough S., Michowa T., Michowa T., Michowa E.,

Mostorough S., Michowa T., Michowa T., Michowa T., Marman S.,

Rad Retta R., Richardson S., Rochews O., O'Leary S.,

Rutman M., Schupbach R., Seamen C., Settipalli S., Sharpe T.,

Ruman M., Schupbach R., Seamen C., Settipalli S., Sharpe T.,

Ruman M., Schupbach R., Seamen C., Stertipalli S., Sharpe T.,

Ruman M., Schupbach R., Stange-thomann N., Sterson K., Stone C., Stone S., Thecopere J., Phulman B.,

Rock S., Thecele D., Wasaliew H., Topham R.,

Towey S., Teamla T., Topon J., Vo A., Wade C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G., Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H., Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S., Buck G.A.;
"The genome of Cryptosporidium hominis.";
"The genome of Cryptospor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%; Score 40; DB 2; Length 201; 85.7%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Last annotation update)
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORRNames=MG05904.4;
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Best Local Similarity 85.،
المالية 6; Conservative 6; Conservative
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051272 MAG
051272 MAG
051272 AAG
051273 AAG
051274 AAG
051274 AAG
0713 
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Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S., Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L., Zimmer A., Zody M., Lander E., "The genome sequence of Manaporthe grisea."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rouhiainen L., Vakkilainen T., Siemer B.L., Buikema W., Haselkorn R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A Rouhiainen L., Vakkilainen T., Lumbye-Siemer B., Buikema W.,
A Haselkorn R., Sivonen K.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
B Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL, AJ21249; AAO62587.1; -; Genomic_DNA.
R EMBL, AJ236156; CAD60102.1; -; Genomic_DNA.
R GO; GO:001687; F:cofactor binding; IEA.
R GO; GO:00187; F:cofactor binding; IEA.
R GO; GO:00187; F:ligase activity; IEA.
R GO; GO:001177; F:phosphopantetheine binding; IEA.
R InterPro; IPR010071; AA adenyl_dom.
InterPro; IPR010981; AGP_like.
R InterPro; IPR000873; MAP-bind.
R InterPro; IPR000873; Phospanteth_bind.
R InterPro; IPR006163; Phospanteth_bind.
R InterPro; IPR006163; Phospanteth_bind.
R InterPro; IPR006163; Phospanteth_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, AACUO100839; EAA52776.1; -; Genomic_DNA.

InterPro; IPR012351; Cytokine 4 hlx.

InterPro; IPR012340; NA-bind_OB_sub.

InterPro; IPR012340; NA-bind_OB_sub.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBL_TaxID=46234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=70-15;
Zhu H., Blackmon B.;
Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2003)
                                                                                                                                                                                                                                                                          STRAIN=70-15;
Dean R., Mitchell T., Brown D., Pan H., Thon M.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ll protein.
982 AA; 106107 MW; EC7E86B1E6911520 CRC64;
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PubMed=14766543; DOI=10.1128/AEM.70.2.686-692.2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Q7WRQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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554 GEHIPWT 560
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DR Pfam; PP00501; AMP-binding; 2.

DR Pfam; PP00668; Condensation; 2.

DR PETAM; PP00560; PP-binding; 2.

DR PRINTS; PR00154; AMPBINDING; 2.

DR PROSITE; PS000154; ACP_DOMAIN; 2.

DR PROSITE; PS00455; AMP_BINDING; 2.

DR PROSITE; PS00455; AMP_BINDING; 2.

DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.

SQ SEQUENCE 2133 AA; 243072 MW; AF806DB0P9372FF7 CRC64;

QUETY MATCH

Best Local Similarity 66.7%; Pred. No. 76+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps

QY 1 FQGSHVPWT 9

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Db 1286 FNGSHLSWT 1294

Search completed: December 30, 2005, 13:33:26

Job time: 84 secs
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TYPE: PRT
ORGANISM: Mus musculus
US-09-995-529-36
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                                               ; Search time 66.9194 Seconds (without alignments) 56.194 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-470-045-94
US-09-995-529-10
US-10-153-401-15
US-10-308-817-172
US-10-308-817-179
US-10-308-817-181
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US-10-735-916A-56
US-10-735-916A-61
US-10-735-916A-65
                                                                                                                                               Total number of hits satisfying chosen parameters:
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-10-258-728-26
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                                                                                                                                  1867569 segs, 417829326 residues
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                                                December 30, 2005, 13:33:42
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Maximum Match 100%
Listing first 45 summaries
                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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US-10-735-916A-63

US-10-135-916A-67

US-09-990-205-2

US-10-153-401-2

US-10-153-401-66

US-10-153-401-66

US-09-947-839-72

US-09-995-529-138

US-09-995-529-128

US-09-995-529-138

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US-09-95-529-36

Squence 36, Application US/0995529

Publication No. US2003009655A1

GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
APPLICANT: Huse, Ying
TITLE OF INVENTION: Related Methods
FILE OF INVENTION: Related Methods
GURRENT APPLICATION NUMBER: US/09/995,529
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT PALING DATE: 2001-11-26

NUMBER OF SEQ ID NOS: 358

SOFTWARRE: FastSEQ for Windows Version 4.0

SECONDANT OF SEQ ID NOS: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 56; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
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Sequence 36, Application US/09995529
; Bequence 36, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION, Jeffry D.
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Tang, Ying
TITLE OF INVENTION: Related Methods
; TITLE OF INVENTION: Related Methods
; TITLE OF INVENTION: Related Methods
; TITLE OF INVENTION: NUMBER: US/09/995,529
; CURRENT APPLICATION NUMBER: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: RM mus musculus
US-09-995-529-36

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Length 9;

us-10-735-916a-6.rapbm

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Query Match 100.0%; Score 56; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                  US-10-470-045-94

US-10-470-045-94

Sequence 94, Application US/10470045

Publication No. US20040146505A1

GENERAL INFORMATION:

APPLICANT: Scancell Limited

APPLICANT: Durrant, Linda Gillian

APPLICANT: Parsons, Tina

TITLE NEFERENCE: P32181WO/NJL

CURRENT APPLICATION NUMBER: US/10/470,045

CURRENT FILING DATE: 2003-07-24

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 101

SCOFTWARE: Patentin version 3.1

SEQ ID NO 94

LENGTH: 49
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Best Local Similarity 100...
Lac 9, Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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CRGANISM: Mus musculus
US-09-995-529-10
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ORGANISM: Mus musculus
US-10-470-045-94
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US-09-995-529-10
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Publication No. US20050084906A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CORVAIA, Nathalie
APPLICANT: LIGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
APPLICANT: HAEUW, Jean-Francois
APPLICANT: HAEUW, Jean-Francois
APPLICANT: HAEUW, Jean-Francois
FILE REFERENCE: 017753-183
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           Length 9;
100.0%; Score 56; DB 3; I
llarity 100.0%; Pred. No. 1.7e+06;
Conservative 0; Mismatchem n.
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CURRENT FILING DATE: 2003-12-16

PRIOR APPLICATION WUMBER: FR 03/08 538

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-20

PRIOR APPLICATION WUMBER: PR 02/00 653

PRIOR PILING DATE: 2002-01-18

SROFTWARE: PREMEMBER: PR 02/05 753

NUMBER OF SEQ ID NOS: 156

SOFTWARE: PATENTIN VOY: 2.1

SEQ TING BATE: 2002-05-07
                                                                                                                                                                                             US-10-470-045-48

US-10-470-045-48

Sequence 48, Application US/10470045

PUDIcation No. US20040146505A1

GENERAL INFORMATION:
APPLICANT: Borrant, Linda Gillian
APPLICANT: Purrant, Linda Gillian
APPLICANT: Parsons, Tina
TITLE OF INVENTION: Substances
FILE REPERENCE: P32181WO/MJL
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: US/10/470,045
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 48

SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
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ORGANISM: Homo sapiens
                                                                                                                                       1 FOGSHVPWT 9
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      Query Match
Best Local Similarity
Matches 9; Conserv
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100.0%; Score 56; DB 4; Length 49; 100.0%; Pred. No. 0.077; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 Sequence 10, Application US/09995529
Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Withins, Joffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Related Methods
TITLE OF INVENTION: Related Methods
FILE REFERRENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT APPLICATION NUMBER: US/09/995,529
SOFTWARE: FALLING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SEQ ID NO 10
LENGTH: 112
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Gaps

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100.0%; Score 56; DB 4; Length 112; 100.0%; Pred. No. 0.16; ative 0; Mismatches 0; Indels
                                                                                                                                                                Query Match 100.0%; Score 56; DB 4; Length 112; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 9; Conservative 0; Mismatches 0; Indels
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// OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Security Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SEQ ID NO 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYERID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
                      STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 179, Application US/10308817; Publication No. US20030219861A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 100.
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-10-308-817-172
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LENGTH: 112
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Publication No. US20030114398A1
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
Chatterjee, Sunil K.
Chatterjee, Sunil R.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 56; DB 3; Length 112; 100.0%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: STATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: CURKNOWN>
Sequence 10, Application US/09995529
Publication No. US20040091482A9
GENERAL INFORMATION
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
ITLE OP INVENTION: Humanized Collagen Antibodies and
ITLE OP INVENTION: Humanized Methods
ITLE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1966-01-16
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 FQGSHVPWT 102
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US-09-995-529-10
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COUNTRY: USA
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US-10-153-401-15
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Query Match
100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.16;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-453-699-179

Sequence 179, Application US/10453698

Sequence 179, Application US/10453698

Publication No. US20040038308A1

GENERAL INFORMATION:

APPLICANT: Rother, Russell

TITLE OF INVENTION: HYBRID ANTIBODIES

FILE REFERENCE: 82 CIP (1087-37 CIP)

CURRENT APPLICATION NUMBER: US/10/453,698

CURRENT FILING DATE: 2003-06-03

NUMBER OF SEQ ID NOS: 196

SEQ ID NO 179

LENGTH: 112
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 172, Application US/10453698
| Publication No. US20040038308A1
| GENERAL INFORMATION:
| APPLICATION SOCIETY ROCHET, RUSSELL
| TITLE OF INVENTION: HYBRID ANTIBODIES
| FILE REFERENCE: 82 CIP (1087-37 CIP)
| CURRENT APPLICATION NUMBER: US/10/453,698
| CURRENT FILING DATE: 2003-06-03
| NUMBER OF SEQ ID NOS: 196
| SOFTWARE: Patentin version 3.2
| ENGITH: 112
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SOFTWARE: Patentin version 3.1
SEQ ID NO 182
LENGTH: 112
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Best Local Similarity 100...
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                 ) ORGANISM: human
US-10-308-817-182
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ORGANISM: mouse
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US-10-453-698-172
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                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: hybrid humanized antibody light chain US-10-308-817-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: hybrid humanized antibody light chain US-10-308-817-181
                                                    Sequence 180, Application US/10308917
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFRENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 180
LENGTH: 112
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Publication No. US20030219861A1
GENERAL INPORMATTON:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 181
LENGTH: 112
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APPLICANT: Wu, Dayang
TITLE OF INVENTON: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT PELLICATION NUMBER: US/10/308,817
CURRENT FILING ADATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 9, Conservative
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US-10-308-817-181
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Appl Appl Appl Appl

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US-10-932-334-62
US-10-932-334-6
US-10-932-334-10
US-10-932-334-11
US-10-932-334-11
US-10-932-334-12
US-10-932-334-63
US-10-932-334-64
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US-10-932-334-85
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US-10-932-334-86
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US-11-125-837-15
; Sequence 15, Application US/11125837
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9; Conservative
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ORGANISM: Mus musculus
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                                                                                                                                  December 30, 2005, 13:35:07 ; Search time 3.33871 Seconds (without alignments) 20.187 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                    GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-125-837-15
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US-10-932-334-61
US-10-512-184-67
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Perfect score:
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Maximum DB
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Application US/11012353
                                               US20050249730A
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SOFTWARE: Patentin Ver. 3.3
       Sequence 54, Application US/:
Publication No. US2005024973
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 FOGSHVPWT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Mus musculus
US-11-012-353-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGSHVPWT 9
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SEQ ID NO 54
LENGTH: 112
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APPLICANT: Freimark, Bruce
APPLICANT: Van Epps, Dennis
APPLICANT: Uan Epps, Dennis
FILE REFERENCE: 30797-704.501
CURRENT APPLICATION NUMBER: Us/11/105,708
CURRENT APPLICATION NUMBER: 09/478,977
PRIOR APPLICATION NUMBER: 60/152,496
PRIOR APPLICATION NUMBER: 60/152,496
PRIOR APPLICATION NUMBER: 60/143,534
PRIOR PILING DATE: 1999-09-02
PRIOR PLILNG DATE: 1999-01-06
PRIOR PLILNG DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
PRIOR PLING DATE: 1999-01-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
Publication No. US20050266003A1
GENERAL INFORMATION:
APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-diun
APPLICANT: Huang, Chiu-Chen
TITLE OF INVENTION: ANTIBODIES
TILE REPERENCE: 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT APPLICATION NUMBER: US 60/569,892
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR PILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Synthetic peptide US-11-105-708-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/11105708 Publication No. US:0050281821A1 GENERAL INFORMATION: APPLICANT: Pernasetti, Flavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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RESULT 4 US-11-012-353-54

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APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, DISAN-FRANCOIS
APPLICANT: HAEUW, DISAN-FRANCOIS
APPLICANT: HEGEK, OLIVIER
APPLICANT: EGEK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVELE: US/11/012,353
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT PILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
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100.0%; Score 56; DB 7; I
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-012-353-56;
Sequence 56, Application US/11012353;
Sublication No. US20050249730A1;
GENERAL INFORMATION: LILIANE;
APPLICANT: CORPAG, LILIANE;
APPLICANT: CORVAG, NATHALIE;
APPLICANT: DUFLOS, ALAIN;
APPLICANT: HEAUW, JEAN FRANCOIS;
APPLICANT: HEGER, OLIVIER;
APPLICANT: BECK, ALAIN
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GENERAL INVENDATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: GOETSCH, MATHALIE

APPLICANT: CORVATA, NATHALIE

APPLICANT: OFFICANT: DIFLOS, ALAIN

APPLICANT: HAEUW, JEAA-FRANCOIS

APPLICANT: HERW, JEAA-FRANCOIS

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REPERENCE: 017753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT APPLICATION NUMBER: 10/735,916

PRIOR APPLICATION NUMBER: RR 0308538

PRIOR PILING DATE: 2003-01-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-01-20

PRIOR PILING DATE: 2003-01-20

PRIOR PLING DATE: 2003-01-18

PRIOR PLING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 0200653

PRIOR PLING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 0200654

PRIOR FILING DATE: 2002-01-18

PRIOR PLING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 0200654

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SSOF ID NO 49

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100.0%; Score 56; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                       CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-01-20
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 020653
PRIOR PILING DATE: 2002-01-18
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Publication No. US20050249730A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Mus musculus
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US-11-012-353-65
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WESTLY '0.2-353-61

Sequence 61, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: HARLY

APPLICANT: NUMBER: US/11/012,353

CURRENT APPLICATION NUMBER: PR 0308538

FRIOR PILING DATE: 2003-01-16

FRIOR PILING DATE: 2003-01-16

FRIOR PILING DATE: 2003-01-10

FRIOR PILING DATE: 2003-01-10

FRIOR PILING DATE: 2003-01-10

FRIOR PILING DATE: 2002-01-18

FRIOR PIL
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Sequence 65, Application US/20050249730A1
GENERAL INFORMATION:
APPLICANT: CORVAIA, INTHALIE
APPLICANT: UCRUALAIN
APPLICANT: HABUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: HABUW, ABAN-FRANCOIS
APPLICANT: HABUW, ABAN-FRANCOIS
APPLICANT: RECER, ALIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                     Query Match 100.0%; Score 56; DB 7; Length 112; Best Local Similarity 100.0%; Pred. No. 0.00059; Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 9; Conservative
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                                                               TYPE: PRT
CORGANISM: Mus musculus
US-11-012-353-56
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US-11-012-353-61
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SEQ ID NO 56
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Length 131; 0; Indels

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 59, Application US/10932334

Publication No. US20050249728A1

GENERAL INFORMATION:

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY

CURRENT APPLICATION NUMBER: US/10/729,441

PRIOR APPLICATION NUMBER: US/10/729,441

PRIOR FILING DATE: 2003-12-08

PRIOR FILING DATE: 2003-16-14

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 59

LENGTHA: 113
                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 56; DB 7; I
100.0%; Pred. No. 0.00068;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/11125837

Sequence 23, Application US/11125837

publication No. US20050266003A1

GENERAL INFORMATION:
APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
TITLE NOF INVENTION: NATIBODIES
TITLE REFERENCE: 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2005-05-10
PRIOR PILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SEQ ID NO 23
LENGTH: 131

LENGTH: 131
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 67
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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US-11-125-837-23
                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-012-353-67
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US-11-125-837-23
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                                                                                                                                                             US-11-U1Z-353-63

Sequence 63, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, OLIVIER

APPLICANT: BECK, OLIVIER

APPLICANT: BECK, OLIVIER

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEE ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEER ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEER: 2001-12-16

FILE REFRENCE: 017753-196

FRIOR APPLICATION NUMBER: PC7/FR03/00178

PRIOR PELING DATE: 2003-12-16

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR PELING DATE: 2003-01-20

PRIOR PELING DATE: 2003-01-20

PRIOR PELING DATE: 2003-01-20

PRIOR PELING DATE: 2002-05-07

PRIOR FILING DATE: 2002-05-07

PRIOR PELING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PELING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PELING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORVAIA, NATHALIE
APPLICANT: GORVAIA, NATHALIE
APPLICANT: GORVAIA, NATHALIE
APPLICANT: BUFLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVER ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-0-11
PRIOR FILING DATE: 2003-0-11
PRIOR FILING DATE: 2003-0-11
PRIOR FILING DATE: 2003-0-12
PRIOR FILING DATE: 2003-0-12
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Matches 9; Conservative
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   104 PQGSHVPWT 112
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CRGANISM: Homo sapiens
US-11-012-353-63
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Gaps

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Search completed: December 30, 2005, 14:15:21 Job time: 4.33871 secs
                                                                                                                                                                 ; Sequence 67, Application US/10512184; Publication No. US20050244901A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 8; Conservative
                                           231 FQGSHVPYT 239
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US-10-512-184-67
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TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistence against fungi
FILE REPRENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SSGTWARE: Patentin Ver. 2.1
SSG ID NO 30
LENGTH: 251
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                                                                                   Length 113;
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                                                                            83.9%; Score 47; DB 6; Length 113
88.9%; Pred. No. 0.027;
ative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      Sequence 61, Application US/10932334
Publication No. US2050249728A1
GENERAL INFORMATION:
APPLICANT: Immunoden, Inc.
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILLE REFRENCE: A868 BBBBR: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR PLILING DATE: 2003-12-08
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR APPLICATION NUMBER: US/10/739,691
PRIOR PLILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.2
      ; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: synthetic antibody structure US-10-932-334-61
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88.9%; Pred. No. 0.056;
vative 1; Mismatches
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; Sequence 30, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
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                                                         Query Match
Best Local Similarity 88.3.
Best Local Similarity 88.3.
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Best Local Similarity 88.99
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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94 FQGSHVPYT 102
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                                                                                                                                                                                                                                                                                RESULT 13
US-10-932-334-61
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FEATURE:
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PAPELICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V. TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.010501
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 67
LENGTH: 320
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88.9%; Pred. No. 0.07;
tive 1; Mismatches 0; Indels
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Complemen Murine 5B Mouse HUI Mouse HUI Human SJB Human SJB Human SJB Murine de Mouse ant

Ade36488 Ad135324 Ad135324 Abd0942710 Abd094251 Add94289 Add94289 Adm78125 Adm78125 Adm78131 Adm78131

Mouse ant Murine an

Mouse HUI Human ant EphA2-spe EphA2 ant Murine mo

Scoring table:

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score:

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Sequence:

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Abp58278 | Adh61994 | Adr19274 | Aaw70922 | Aea42984

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Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response; tumour; immune response; cancer; vaccine; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of polypeptides and nucleic acids encoding the polypeptides, in manufacturing medicament for stimulating a cytotoxic T cell response and for preventing or treating cancer, e.g. colorectal, lung, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes the use of a polypeptide (I) in the manufacture of a medicament for stimulating a cytotoxic T cell response, where (I) comprises a first portion comprising the part of human Fc that binds to CD64 and a second portion comprising one or more heterologous T cell epitopes. Also described is a method of stimulating a cytotoxic T cell response in a patient such as a mammal, preferably human, by administering (I) to the patient. (I) has cytostatic activity and can be used in vaccine production. (I) and the nucleic acid encoding (I) are useful in the manufacture of a medicament for stimulating cytotoxic T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fv region SC100 antibody CDR-L3 amino acid sequence.
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                                                              ADP84870
ABB03714
ADD94251
ADD94249
ADM78107
ADM78107
ADM78107
ADM78125
ADM78126
ADM78131
ADM94473
ADM94747
ADM9474
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ABP58278
ADH61994
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WO200258728-A2
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  Synthetic
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  Fv region
Mouse HUI
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                                                                                                                                                 December 30, 2005, 14:52:54 ; Search time 182 Seconds (without alignments) 21.728 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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cell response. The medicament is useful for preventing and/or treating cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The medicament stimulates cytotoxic and helper T cell responses. The antibodies are useful as vaccines to stimulate helper and cytotoxic T cell responses. The polypeptides and nucleic acids are useful in optimising immunisation schedules for enhancing a protective immune response against cancer. The present sequence represents an Fv region SC100 antibody CDR-L3 amino acid sequence represents an Fv region from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               grafted antibody, complementarity determining region, CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agonist; cancer metastasis; anti-cryptic collagen; antibody; HUI77; variable region light chain;
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                    100.0%; Score 56; DB 5; Length 9; 100.0%; Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 36; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD94151 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2002; 2002WO-US038147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                 9; Conservative
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N-PSDB; ADD94150.
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                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                              Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse; murine.
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                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                   Matches
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proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriabile. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-18) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-18. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-18 and/or prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-18 and/or prevent or hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or transformation of normal cells to tumor cells, inhibit growth and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                       insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                           Gapa
cryptic collagen site antibody HUI77 variable region light chain CDR which is related to the invention.
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                                                                                                                         0; Indels
                                                                                      Length
                                                                                      Score 56; DB 7;
Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                          CDR sequence for anti-IGF-1R antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 6; 164pp; French.
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07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                         Local Similarity 100.
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                                                      Sequence 9 AA;
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Query Match

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inhibit the transformation of normal cells into cells with tumoral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated anti-insulin-like growth factor receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (GDR) consisting of one of two fully defined 16 amino acids (ADS67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of a milness connected with an overexpression and/or an abnormal coffination of the IGF-IR and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended
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                                                                                                                                                                                                                                        neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipporiatic; psoriasis; dermatological disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                       Gaps
                                                                                                                                                                                                     Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:6.
                                                                                                                                                                                                                              Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
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Pred. No. 2e+06;
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                                                                                                                             ADZ67010 standard; peptide; 9 AA.
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07-MAY-2002; 2002FR-00005753.
20-JANY-2003; 2003WO-FR00178.
11-JUL-2003; 2003FR-00008538.
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                                                           1 FOGSHVPWT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corvaia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating
           Similarity
                                             FOGSHVPWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUFLOS A. HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADZ67009.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BECK A.
                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                               21-APR-2005
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                                                                                                                                                     ADZ67010;
          Best Local
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(LEGE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DUFL/)
(HAEU/)
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                      Matches
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character, preferably IGF-dependent, especially IGF1 and/or IGR2.

Character, preferably IGF-dependent and/or HER2/neu-dependent cells. (I) is dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, and/or the proliferation of tumor cells, preferably IGF-dependent, cells, (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriaals. (I) is useful in preparation of a medicament content of psoriaals. (I) is useful in preparation of a medicament content of psoriaals. (I) is useful in preparation of a medicament content of psoriaals. (I) is useful in preparation of a medicament content of psoriaals. (I) is useful in preparation of a medicament content of psoriaals. (I) is useful in preparation of a medicament of intended for the specific targeting of a biologically and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor is suspected, which involves contacting the contacting the biological sample with (I), which is optionally labeled. The present contacting the sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody against the G glycoprotein of RSV with a variable region having a first and second domain from a VL and VH region, respectively, useful for treating respiratory syncytial virus (RSV) infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 56; DB 9; Length 9; 100.0%; Pred. No. 2e+06; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mekseepralard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 3; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS88735 standard; peptide; 9 AA.
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Best Local Similarity luv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-2004
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Length 9;

92.98;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth, angiogenesis; tumour growth, cytostatic; collagen agonist; collagen anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
             eyncytial virus (RSV). The present sequence represents a complementarity determining region (CDR) derived from the variable light chain (VL) region of an antibody directed against the G glycoprotein of RSV. This peptide is used to construct antibodies of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cryptic collagen site antibody HUI77 variable region light chain CDR which may be used during the creation of an antibody of the invention.
                                                                                                                                                                                      Gaps
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of infections caused by the respiratory
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                                                                                                                                               Length 9;
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                                                                                                                                               DB 8;
                                                                                                                                           Score 55; DB 8;
Pred. No. 2e+06;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          ADD94253 standard; peptide; 9 AA.
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                                                                                                                                               98.2%;
88.9%;
 preventing the development
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                                                                                                                                                                                    8; Conservative
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                                                                                                                                                                                                                       1 FOGSHVPWT
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Best Local Similarity
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                                                                                                          Sequence 9 AA;
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                                                                                                                                                                                    Matches
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ប្រក្តប្តប្តវន្តន្ត
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                                                                                                                                                                                                                                                                                                                                  grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agoniet; collagen anti-cryptic collagen atti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
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                                 Gape
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                                                                                                                                                                                                                                                                                                  Mouse HUI77 mutant light chain CDR amino acid sequence SeqID128.
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                                 1; Indels
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Score 52; DB
Pred. No. 2e+0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 24; SEQ ID NO 128; 232pp; English
                                                                                                                                                                                            ADD94243 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-2002; 2002WO-US038147.
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06-DEC-2001; 2001US-00011250.
                88.98;
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Best Local Similarity 88.9
Matches 8; Conservative
                                     8; Conservative
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Query Match
Best Local Similarity
                                                                                                     FOGSHTPWT
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                                                                                                                                                                                                                                ADD94243;
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                                     Matches
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1 FOGSHVPWT 9

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Sequence 9 AA;

Mouse HUI77 mutant light chain CDR amino acid sequence SeqID145.

(first entry)

29-JAN-2004

ADD94260;

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fragment comprising one or more complementarity determining regions cCDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of antagonist. The invention activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anti-cryptic collagen site antibody HU177 variable region light chain CDR which may be used during the creation of an antibody of the invention.
                                                                                                                                                                                                                     grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agonist; collagen anti-cryptic collagen anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel grafted antibody or its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
                                                                                                                                                                                      Mouse HUI77 mutant light chain CDR amino acid sequence SeqID132.
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Pred. No. 2e+06;
); Mismatches
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                                                                                  ADD94247 standard; peptide; 9 AA.
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06-DEC-2001; 2001US-00011250.
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88.9%;
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FRGSHVPWT
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                  mutant; mutein.
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                                                                                                                                                   29-JAN-2004
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                                                                                                                    ADD94247;
                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                               RESULT 8
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                                                                            prafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen antagonist; cancer metastasis; anti-cryptic collagen; HUI77; variable region light chain; mouse; murine; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (as) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, anglogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cryostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with anglogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anticryptic collagen site antibody HUI77 variable region light chain CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which may be used during the creation of an antibody of the invention.
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Pred. No. 2e+06;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Huse WD,
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8; Conserv
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                                                                                                                                                                                                                          Mus musculus.
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                                                                                                                                                                                                         Synthetic
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Best Local
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This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anticryptic collagen site antibody HUI77 variable region light chain CDR
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heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; angiogenesis; tumour growth; cytostatic; collagen agonist; collagen antagonist; cancer metastasis; anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cryptic collagen site antibody HUI77 variable region light chain CDR which may be used during the creation of an antibody of the invention.
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                                                                                                                                                                                                                                                    26-NOV-2002; 2002WO-US038147.
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06-DEC-2001; 2001US-00011250.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                        Mus musculus.
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                                                                                                                  Synthetic
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New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with anglogenesis, tumor growth and/or cancer metastasis.

Brooks

Broek D,

Tang Y,

(CELL-) CELL MATRIX INC. Watking JD, Huse WD, WPI; 2003-513649/48.

26-NOV-2002; 2002WO-US038147. 26-NOV-2001; 2001US-00995529. 06-DEC-2001; 2001US-00011250.

WO2003046204-A2

05-JUN-2003

Mus musculus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; heavy CDR growth; anglogenesis; tumour growth; cytostatic; collagen agonist; collagen arti-cryptic collagen, HUI77; variable region light chain; mouse; murine;
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100.0%; Pred. No. 2e+06;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   Claim 24; SEQ ID NO 139; 232pp; English.
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ADD94258
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Synthetic

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CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention growth and/or cancer metastasis. The associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse antiperprise collagen site antibody HUIT? variable region light chain CDR which may be used during the creation of an antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           grafted antibody, complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth; anglogenesis; tumour growth; cytostatic; collagen agoniat; collagen antisoniat; cancer metastasis; anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
                                                          New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
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hes 0; Indels
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                                                                                                                                                   Claim 24; SEQ ID NO 142; 232pp; English
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06-DEC-2001; 2001US-00011250.
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                  WPI; 2003-513649/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth, angiogenesis; tumour growth; cytostatic; collagen agonist; collagen anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
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                                                                                                                                                                                                                New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
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                                                                                                                            Brooks PC;
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                                                                                                                                                                                                                                                                                                       Claim 24; SEQ ID NO 143; 232pp; English.
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                26-NOV-2001; 2001US-00995529.
06-DEC-2001; 2001US-00011250.
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06-DEC-2001; 2001US-00011250.
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                                                                               (CELL-) CELL MATRIX INC.
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                                                                                                                         Watking JD, Huse WD,
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                                                                                                                                                                      WPI; 2003-513649/48.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
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Matches

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RESULT 13 ADD94257

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Gaps

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                                             fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (las) substitution where the antibody has specific binding activity for a cryptic collagen epicope. The growth of all solid tumours requires new blood vessel growth, anglogenesis, inhibition of which is an approach the amour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with anglogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anti-cryptic collagen site antibody HU177 variable region light chain CDR which may be used during the creation of an antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour; new blood vessel growth, angiogenesis; tumour growth; cytostatic; collagen agonist; collagen anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
                                    This invention relates to a novel grafted antibody or its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse HUI77 mutant light chain CDR amino acid sequence SeqID127.
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                                                                                                                                                                                                                                                                                                                  91.1%; Score 51; DB 7; Length 9; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 24; SEQ ID NO 127; 232pp; English.
 Claim 24; SEQ ID NO 140; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD94242 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-2002; 2002WO-US038147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-2001; 2001US-00995529
06-DEC-2001; 2001US-00011250
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               FQGSHVPW
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CC to limiting tumour growth, angiogenesis, inhibition of which is an approach continiting tumour growth. The invention may allow development of the integration with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the amino acid sequence of a mutant mouse anti-cryptic collagen site antibody MINT7 variable region light chain CDR cryptic collagen site antibody MINT7 variable region light chain CDR which may be used during the creation of an antibody of the invention.

XX

Sequence 9 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 QGSHVPWT 9

2 Dob time: 183 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

December 30, 2005, 15:05:21; Search time 37 Seconds (without alignments)
23.404 Million cell updates/sec

US-10-735-916A-6 56 Perfect score: Title:

1 FOGSHVPWT 9 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

185 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 9 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:* 1: pirl:* 2: pir2:* 3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	ים מי	d U	ote	rec	Ω, Di	adhe	b-A	ida	iti	car	В	ch	В.	tic	hes	۷r	ga		(BC	(EC	пп	48.7K	ida	- pi	uo	цр	rmo	- Au	Austra
tion	xenopsin-related	xenopsin-related	hypothetical prote	growth hormone rec	sperm-activating	rface ad	neuropeptide Grb-A	cytochrome-c oxida	locustamyoinhibiti	estrin,	fibrinopeptide	fibrinogen beta	fibrinopeptide B	gastrin - domestic	pyrimidine synthes	Ig heavy chain V	receptor	peptidylglycine	dolase		locustamyotropin		D-amino-acid oxida	factor -	n - common	thymocyte growth p	adipokinetic hormo	2-G]n	I - Aue
Description	xenopsi	xenopsi	hypothe	growth	sperm-a	cell surface	neurope	cytochr	locusta	calsequestrin,	fibrino	fibrino	fibrino	gastrin	pyrimid	Ig heav	T-cell	peptidy	transaldolase	transaldolase	locusta	unidentified	D-amino	thymic	isotocin -	thymocy	adipoki	litorin	litorin
EI CI	JS0302	A60320	T31612	146023	A60522	A43848	D57444	S77984	AKLOIM	A61230	D28854	C24180	E28854	C60070	865913	836850	G41946	A42266	A12872	A11497	A61620	PC7078	839437	YFPG	A61364	A60957	A24244	807205	807204
DB	7	~	~	~	~	~	~	~	-	~	7	~	N	7	~	N	~	~	~	N	7	~	~	-	~	~	~	7	7
% Query Match Length DB	6	σ	σ	σ	σ	6	σ	σ	σ	0	σ	σ	0	Đ	σ	0	6	σ	σ	0	σ	0	0	6	9	Q	6	6	6
% Query Match	32.1	32.1	32.1	32.1	32.1	28.6	28.6	26.8	23.2	23.2	23.2	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	19.6		19.6	19.6	19.6	19.6
Score	18	18	18	18	18	16	16	15	13	13	13	12	12	12	12	12	12	12	12	12	12	12	12	11	11	11	11	11	11
Result No.	-	7	e	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

litorin - Rohde's	phyllocaerulein -	endosperm protein,	cardioactive pepti	Ig heavy chain CDR	heavy chain	Ig heavy chain CRD	heavy chain	Ig heavy chain CRD	heavy chain	Ig H chain V-D-J r	T-cell receptor be	T-cell receptor be	gene c-mpl protein	52.5K protein - sp	cardioactive pepti
807241	A61357	S70334	839766	PT0231	PT0270	PT0272	PT0288	PT0299	PT0324	PH1591	PT0634	PT0562	I58350	878426	839767
~	0	7	~	~	0	~	~	7	7	7	N	~	~	N	0
σ	0	0	0	σ	0	0	σ	σ	0	o	6	o,	σ	9	σ
9.	9.6	9.6	9.6	19.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.	9.6	9.6	9.
15	ä	ñ	ä	15	51	5	ä	ä	ä	2	ä	5	5	5	7
11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	<b>4</b> .

## ALIGNMENTS

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venopain-related peptide 2 - turkey
N;Contains: xenopsin-related peptide 1
C;Species Melegaris gallopavo (common turkey)
C;Species Melegaris gallopavo (common turkey)
C;Species Melegaris gallopavo (common turkey)
C;Accession: JS0302
R;Carraway, R.E.; Cochrane, D.E.; Mitra, S.P.
R;Carraway, R.E.;
A;Title: Xenopsin-related peptide generated in avian gastric extracts.
A;Reference: JS0302
A;Molecule type: protein
A;Residues: 1-9 «CAR»
A;Carraway
A;Carraway, R.E.;
A;Residues: 1-9 «CAR»
A;Carraway, R.E.;
A;Carraw
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Gaps ; 0 32.1%; Score 18; DB 2; Length 9; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels Query Match Best Local Similarity 100...

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PW 7 7 PW 8

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RESULT 2

xenopsin-related peptide 2 - rat

xenopsin-related peptide 1
C;Species: Rattus norvegicus (Norway rat)
C;Species: A60320
R;Carraway, R.E.; Mitra, S.P.; Muraki, K.
R;Carraway, R.E.; Mitra, S.P.; Muraki, F.
R;Carraway, R.E.; Mitra, S.P.; Muraki, R.
R;Carraway, R.E.; Mitra, S.P.; Muraki, R;Carraway, R;Carraway,

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neuropeptide Grb-AST B4 - two-spotted cricket
Cispecies: Grylus bimaculatus (two-spotted cricket)
Cjate: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
CjAccession: D57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
R;Lorenz, Chem. 270, 21103-22108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr
A;Reference number: A57444; MUID:95403341; PMID:7673141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytochrome-c oxidase (EC 1.9.3.1) chain VIa - bigeye tuna (fragment)
C;Species: Thumus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: 877984
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Staphylococcus aureus
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Infect. Immun. 60, 899-906, 1992
A;Title: Binding of heparan sulfate to Staphylococcus aureus.
A;Reference number: A43848; MUID:92176005; PMID:1541563
A;Accession: A43848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-9 <LIA>
A;Cross-references: UNIPROT:Q9R5M1; UNIPARC:UPI00000B9726
A;Note: sequence extracted from NCBI backbone (NCBIP:85442)
A;Accession: A60522
A;Molecule type: protein
A;Residues: 1-9 <705.
A;Cross-references: UNIPARC:UPI000017A4D9
P;2-9/Disulfide bonds: #status experimental
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-9 <LOR>
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Best Local Similarity
Matches 2; Conserv
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C;Species: Diadema setosum
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
C;Accession: A60522
R;Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuk
Comp. Blochem. Physiol. B 95, 422-429, 1990
A;Title: A species = Specific sperm-activating peptide from the egg jelly of the sea urchi
A;Reference number: A60522; MUID:90227916; PMID:2158412
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A;Cross-references: UNIPROT:Q28121; UNIPARC:UPI000086CAB; EMBL:U24113; NID:g775221; PIC
C;Genetics:
A;Gene: GHR
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A;Experimental source: clone Y50E8A
C;Genetics:
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R;Hauser, S.D.; McGrath, M.F.; Collier, R.J.; Krivi, G.G.
Mol. Cell. Endocrinol. 72, 187-200, 1990
A;Telle: Cloning and in vivo expression of bovine growth hormone receptor mRNA.
A;Reference number: 146023; MUID:91146804; PMID:2289631
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Cispecies: Caenorhabditis elegans
Cispate: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
Ciscession: T31612
Risteward, C.
Submitted to the EMBL Data Library, September 1999
Aireference number: 221047
Aireference number: 221047
Aireference number: translated from GB/EMBL/DDBJ
Aireference DNA
Ai
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C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug_1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
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    DB 2; Length 9; 2.8e+05; Indels
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0;
        Query Match 32.1%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 2.8 Matches 2; Conservative 0; Mismatches
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fibrinopeptide B - olive baboon
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accessions D: 7 Takenaka, O.; Takahashi, K.
R;Nakamura, S: 7 Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropi
A;Reference number: A91973; MUID:84161822; PMID:6423621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
Ksesidues: 1-9 - NAK>
A;Cross-references: UNIPROT:P19344; UNIPARC:UPI000012A77F
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
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J. Biochem. 97, 1487-1492, 1985
A; Biochem. 97, 1487-1492, 1985
A; Title: Ribrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (ucnons, and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Reference number: protein
A;Reference protein
A;Residues: 1-9 cNAKs
A;Cross-references: UNIPROT:P19345; UNIPARC:UPI000012A77B
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
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CjSpecies Papio hamadryas (hamadryas baboon)
CjDate: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
CjAccession: B28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
A;Nakamura, S.; Takenaka, O.; Takahashi, K.
A;Pitle: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropi A;Reference number: A91973; MUD:84161822; PMID:6423621
A;Accession: B28854
A;Molecule type: protein
A;Residues: 1-9 <NAK>
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N;Contains: fibrinopeptide B
C;Species: Macacca fuscata (Japanese macaque)
C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: C24180
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Pred. No. 2.8e+05;
1; Mismatches 0; Indels
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Pred. No. 2.8e+05;
2; Mismatches 2
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Best Local Similarity 66.7%;
Matches 2; Conservative
     33.3%;
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les 2; Conservative
Best Local Similarity 33.3
Matches 2; Conservative
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2 EGLNFP 7
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                                A.Reference number: $77980
A.Reference number: $77980
A.Accession: $77994
A.Accession:
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C;Species: Locusta migratoria (migratory locust)
C;Species: Locusta migratoria (migratory locust)
C;Species: Locusta migratoria (migratory locust)
C;Accession: A60065
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
A;Title: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MI A;Reference number: A60065; MUID:92179466; PMID:1796179
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A;Reference number: Description of the control of con
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Nylternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-C;Species: Rana pipiens (northern leopard frog)
C;Date: 03-May-1994 #equence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A61230
C;Accession: A61230
A;Circ. Res. 69, 344-359, 1991
A;Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A60065
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Ross-references: UNIPROT:P31799; UNIPARC:UP1000012E77A
C;Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and C;Superfamily: locustamyoinhibiting peptide
C;Superfamily: locustamyoinhibiting peptide
C;Keywords: amidated carboxyl end; hormone
F;9/Modified site: amidated carboxyl end (Trp) #status experimental
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submitted to the Protein Sequence Database, June 1997
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Matches 3; Conservative
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gastrin - domestic ferret (fragment)
C;Species: Mustela putorius furo (domestic ferret)
C;Species: Mustela putorius furo (domestic ferret)
C;Species: O1-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 18-Jun-1993
C;Accession: C60070
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
A;Accession: C60070
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A;Ac
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C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 14-Reb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: 565913 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
R;Hemmens, B.; Carrey, B.A.
Bur. J. Biochem. 231, 220-225, 1995
Eur. J. Biochem. 231, 220-225, 1995
A;Fitlen: Mammallan dihydroorotase; secondary structure, and interactions with other prot A;Reference number: 565913; MUID:95354692; PMID:7628474
A;Accession: 565913
A;Accession: S65913
A;Accession: 
А,Стовв-references: UNIPROT:P19343; UNIPARC:UP1000012A780
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
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21.4%; Score 12; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 3; Indels
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=92129337; PubMed=1733949;

MEDLINE=92129337; PubMed=1733949;

Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,

Schiffmann E., Liotta L.A.;

"Identification, purification, and partial sequence analysis of
autocaxin, a novel motility-stimulating protein.";

J. Biol. Chem. 267:2524-2529(1992).

GO; GO:0006528; P:cell motility; NAS.
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.larity 100.0%; Pred. No. 2.2e+06;
Conservative 0; Mismatches 0; Indels
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QGQF45;
QGQF45;
O5_UUL_2004 (TrEMBLrel. 27, Created)
O5_UUL_2004 (TrEMBLrel. 27, Last sequence update)
O1_FEB-2005 (TrEMBLrel. 29, Last annotation update)
C4_COLTONE P450 4F12 (Fragment).
Name=CYP46112;
Homo sapiens (Human).
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Last annotation update)
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0673X7_9CORV
0673X9_9CORV
0673X9_9CORV
0673X1_9CORV
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01-MAY-2000 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
AUTOTAXIN (Fragment).
         Homo sapiens (Human)
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                                                                                                                                                       ; Search time 230 Seconds (without alignments) 27.608 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Homo sapiens (Human)
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Q9UMF3_HU
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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MEDLINE=21547785; PubMed=11688995; DOI=10.1006/bbrc.2001.5833;
Massilia G.R., Schinina M.E., Ascenzi P., Polticelli F.;
"Contryphan-Vn: a novel peptide from the venom of the Mediterranean snail Conus ventricosus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE, SYNTHESIS, DISULFIDE BONDS, AND MASS SPECTROMETRY
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Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conlae; Conus.
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                                                                                                                                                                                                Score 19; DB 2; Length 9; Pred. No. 2.2e+06; 1; Mismatches 0; Indels
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Gevry N.Y., Lacroix D.A., Murphy B.D.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF184964; AAK83683.1; -; Genomic_DNA.
NON TER
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SEQÜENCE 9 AA; 890 MW; 2C4E2DC761E1EDD8 CRC64;
                                        EMBL/GenBank/DDBJ databases.
                                                                                                                                                            9 AA; 1059 MW; 970A676735B72735 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ)R EMBL; AY544783; AAS49384.1; -; Genomic_DNA.
R EMBL; AY544784; AAS49385.1; -; Genomic_DNA.
R EMBL; AY544782; AAS49386.1; -; Genomic_DNA.
R EMBL; AY544782; AAS49383.1; -; Genomic_DNA.
S EMBL; AY544782; AAS49383.1; -; Genomic_DNA.
S EMBL; AY544782; AAS49383.1; -; Genomic_DNA.
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16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
Niemann Pick type C1 protein (Fragment).
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Similarity 66.7%;
2; Conservative
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Q924N8 MOUSE PRELIMINARY;
Q924N8;
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6 LPW 8
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ID _ COW_CONVE
AC P83047;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Placenta;
MEDIATE=9743511; PubMed=9332365; DOI=10.1016/S0378-1119(97)00260-6;
Pringer L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
Burrows P.D., Billips L.D.;
"The human Pb.1 gene: complete cDNA, genomic organization, and
developmentally regulated expression in B cell progenitors.";
Gene 197:177-187(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 1NXN; NWR; A=1-9.
3D-structure; Amidation; D-amino acid; Direct protein sequencing;
Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
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Last annotation update)
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Cysteine amide.
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Q9UMF3;
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Best Local Similarity 100.
Matches 2; Conservative
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Matches 2; Conservative
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Name=PD-1;
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NUCLEOTIDE SEQUENCE.
MEDLINE=96043217; PubMed=7486254;
Moody D.E., Pomp D.., Barendse W., Womack J.E.;
Massignment of the growth hormone receptor gene to bovine chromosome 20 using linkage analysis and somatic cell mapping.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE.
MEDLINE=91146804; PUDMed=2289631; DOI=10.1016/0303-7207(90)90143-V;
MEDLINE=91146804; PUDMed=2289631; DOI=10.1016/0303-7207(90)90143-V;
MEDLINE=91146804; MCGrath M.F., Collier R.J., Krivi G.G.;
"Cloning and in vivo expression of bovine growth hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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                                                                              Indels
                                         Length 9;
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Submitted (APR-1955) to the EMBL/GenBank/DDBJ databases.
EMBL, 124113; AAA91014.1; -; Genomic_DNA.
PIR; 146023; 146023.
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24, Last annotation update)
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Last annotation update)
  849 MW; 9639CDD87863676E CRC64;
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                                       32.1%; Score 18; DB 2; Le
100.0%; Pred. No. 2.2e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                           9 AA.
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                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                        Growth hormone receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anim. Genet. 26:341-343(1995).
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Q28121;
                                                                                Conservative
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                  NUCLEOTIDE SEQUENCE.
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9 AA;
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  SEQUENCE
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                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUCLEOTIDE SEQUENCE.
MEDLINE=93076813; PubMed=1332868;
Peers B., Nalda A.M., Monget P., Voz M.L., Belayew A., Martial J.A.;
Peers B., Nalda A.M., Monget P., Voz M.L., Belayew A., Martial J.A.;
Binding of aquivcha ubiquitous factor to the human prolactin
promocer is required for its basal and hormone-regulated activity.";
Eur. J. Biochem. 210:53-58(1992).
EMBL; X00368; CAA25108.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sperm-activating peptide SAP-IV.
Jadema serosum (Sea urchin).
Bukaryota, Metazca, Echinodermata, Eleutherozoa, Echinozoa, Echinoidea, Ethinoidea, Diadematacea, Diadematoida, Diadematidae,
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                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and characterization of the human prolactin gene."; EMBO J. 3:429-437(1984).
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                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Prolatin precursor (Fragment).
Homo sapiens (Human).
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                              9 AA.
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MEDLINE=84182507; PubMed=6325171;
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                                                                            QSUQWO HUMAN PRELIMINARY;
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Q51LX3 MAG
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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PIR; JS0302; JS0302.
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MEDLINE=91018491; PubMed=2217904; DOI=10.1016/0167-0115(90)90085-B;
Carraway R.E., Mitra S.P., Muraki K.;
Carraway R.E., Mitra S.P., Muraki K.;
Isolation and structures of xenopsin-related peptides from rat stomach, liver and brain.";
Regul. Pept. 29:229-239(1990).
PR. A60320; A60320. ... momental and structures to the structure of the structu
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
NCBL_TaxID=9103;
MEDLINE=88118956; PubMed=2963134;
Buckley K.J., Hayashi M.;
Buckley K.J., Hayashi M.;
Ryole of premature translational termination in the regulation of expression of the phi X174 lysis gene.";
J. Mol. Biol. 198:599-607(1987).
EMBL; X07809; CAA30668.1; -; Genomic_DNA.
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Pred. No. 2.2e+06;
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Pred. No. 2.2e+06;
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Q7L266.
Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
U-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Xenopsin-related peptide 2.
Meleagris gallopavo (Common turkey).
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Xenopsin-related peptide 2.
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100.0%;
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75.0%;
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Best Local Similarity 75.v.
3; Conservative
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
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Q7M078_RAT
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Q7LZ66_MEI
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MESULY 12

GENERAL AMOONE PREINTIANAY, PRT, 9 AA.

GELLAS, MACARE PREINTIANAY, PRT, 9 AA.

DESILYS AMOONE PREINTIANAY, PRT, 9 AA.

MACHINEL AND AMOONE PREINTIANAY, PRT, 9 AA.

MACHINEL AND CONTRACT CONTRACT AND AMOONE AN
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Gaps

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25-OCT-2004 (TYEMBLrel. 28, Created)
25-OCT-2004 (TYEMBLrel. 28, Last sequence update)
25-OCT-2004 (TYEMBLrel. 28, Last annotation update)
25-OCT-2004 (TYEMBLrel. 28, Last annotation update)
MHC class II antigen (Fragment).
Name=HLA-DPB1;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                  Length 9;
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Wood J.M., Simons M.J., Ashdown M.L.;
"HLA-DPB1 3' intron 1.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX375792; AAQ88086.1; -; Genomic_DNA.
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       30.4%; Score 17; DB 2; Le
100.0%; Pred. No. 2.2e+06;
tive 0; Mismatches 0;
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Q67AR7;
          Query Match
Best Local Similarity 100.
Matches 3; Conservative
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Matches 3; Conservative
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SEQUENCE
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                       Gaps
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-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/AACUOIO01555; EAA47525.1; -; Genomic_DNA.

Hypothetical protein.

SEQUENCE 9 AA; 1003 MW; DF9FC5A6D1F5BDC6 CRC64;
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WOOD J.M., Simons M.J., Ashdown M.L.;

"HLA-DPB1 3' intron 1.";

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; XY37795; AAQ8889.1; -; Genomic_DNA.
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"HLA-DBB13" interon 1.";
Submitted (1007-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AX375793; AAQ88087.1; -; Genomic_DNA.
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NON TER 1 5
SEQÜENCE 9 AA; 1154 MW; 1AF0C40866D9C73B CRC64;
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SEQUENCE 9 AA; 1154 MW; 1AF0C40866D9C73B CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
MHC class II antigen (Fragment).
Name-HLA-DPB1;
Homo sapiens (Human).
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
MHC class II antigen (Fragment).
Name-HLA-DPB1;
Homo sapiens (Human).
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Best Local Similarity 100.
Matches 3; Conservative
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QETARE;
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Matches 3; Conserv
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Gaps

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TELEX: n.a. INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TRNGTH: 9 amino acids
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-07-977-696C-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQGSHVPWT
ZIP: 90071
                                                                                                                                                                                                                                       US-07-977-696C-72
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                                                               December 30, 2005, 15:02:40; Search time 50 Seconds (without alignments)
14.882 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-947-298A-72
US-09-947-696C-34
US-08-129-930B-34
US-08-129-930B-34
US-08-129-930B-34
US-08-134-346A-21
US-09-217-268B-31
US-09-217-268B-31
US-09-947-839B-34
US-09-724-409-5
US-09-724-795-30
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                           572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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56
1 FQGSHVPWT 9
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Match Length
                   Copyright
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seg length: 9
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Perfect score:
Sequence:
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APPLICANT: do Couto, Fernando J.R.
APPLICANT: do Couto, Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
TITLE OF INVENTION: and Therapeutic Methods.
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: PERTTY, SCHHOEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
CITT: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Plan PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ameel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
US-09-996-265-61
US-08-846-561-39
US-09-440-781-25
US-09-771-415-5
US-09-771-415-16
US-09-996-286-6
US-09-996-286-6
US-08-908-468-10
US-08-908-468-10
US-08-908-448-425
US-09-104-337A-364
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
TELEFAX: (510) 748-6688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 72, Application US/07977696C Patent No. 5792852 GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
    CORRESPONDENCE ADDRESS:
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US-08-976-288A-72
is Sequence 72, Application US/08976288A
is Patent No. 6315997
is GENERAL INFORMATION:
is APPLICANT: do Couto Dr., Fernando J.R.
is APPLICANT: Peterson Dr., Jorry A.
is APPLICANT: Peterson Dr., Gauardo A.
is APPLICANT: Peterson Dr., Gauardo A.
is TITLE OF INVENTION: Carcinoma Specificity, and Kit and TITLE OF INVENTION: Diagnostic Vaccination and it TITLE OF INVENTION: Diagnostic Vaccination and it ITLE OF INVENTION: Therapeutic Methods
is NUMBER OF SEQUENCES: 96
                                                                                                                       gequence 72, Application US/08129930B

Patent No. 7804187

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.

APPLICANT: Peterson Dr., Jeiry A.

APPLICANT: Padian Dr., Roberto L.

APPLICANT: Padian Dr., Guardo A.

APPLICANT: Padian Dr., Balando J.R.

TITLE OF INVENTION: Analogue Peptides With Broad

TITLE OF INVENTION: Carcinoma Specificity, and Kit and

TITLE OF INVENTION: Therapeutic Methods

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.6%; Score 53; DB 1; Length 9; 88.9%; Pred. No. 4.6e+05; ative 1; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ISP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/POCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
                                                                                                                                                                                                                                                                                                                                                                  STREET: 2055 No. 5804187th Broadway, Suite 201 CITY: Walnut Greek STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (510) 521-3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-129-930B-72
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Query Match
Best Local Similarity
                                                                                                                     US-08-129-930B-72
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Sequence 72, Application US/09947839B

Patent No. 6936706

GENERAL INFORMATION:

APPLICANT: do Couto, Fernando J.R.

Ceriani Dr., Roberto L.

Peterson Dr., Jerry A.

Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Specificity

for Carcinomas and Kit and Diagnostic Vaccination
and Therapeutic Methods.
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
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COMPUTER: TBM PC Compatible
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COMPUTER: TBM PC COMPATIBLE
COMPUTER: PATER: PC-DCS/MS-DOS 5.0
SOFTWARE: PATERIN DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION DATE: No. 6315997ember 16, 1992
ATTORNEY/AGBNT INPORMATION:
NAME: VIVIAINA AMERIE: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: BC639938
TELEPHONE: (213) 622-7700
TELEFRAN: CALLO
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: V. Amzel & Assoc.
STREET: P.O.Box 159
CITY: Gladwyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19035
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: n.a.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
XX: linear
                                               CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FOGSHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQGTHVPWT 9
                                                                                                                         90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-947-839B-72
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US-08-129-930B-34
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TELEX: n.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/07977696C
Fatent No. 5792652
GENERAL INFORMATION:
APPLICANT: do Couto, Fernando J.R.
APPLICANT: do Couto, Fernando J.R.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Jerry A.
APPLICANT: Padlan Dr., Jerry A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: and Therapeutic Methods.
TITLE OF INVENTION: and Therapeutic Methods.
MUMBER OF SEQUENCES:
ADDRESSE: PRETTY, SCHROEDER & POPLAWSKI
STREET: A44 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                               94.6%; Score 53; DB 2; Length 9; 88.9%; Pred. No. 4.6e+05; rative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: I Ploppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 415-92
CLASSIFICATION: Viviana
REASISTRATION WUMBER: 96 38227
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAK: (510) 748-6688
                    FILING DATE: 06-Sep-2001
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INPORMATION:
NAME: Amzel Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRPC-083
TELECOMUNICATION INPORMATION:
TELEPHONE: 610-649-0609
APPLICATION NUMBER: US/09/947,839B
                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear;

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-947-839B-72
                                                                                                                                                                                                            TELEX: n.a.
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                             TELEFAX: 240-359-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: n.a. INPORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / MOLECULE TYPE: peptide US-07-977-696C-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FOGTHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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US-07-977-696C-34
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Humanized and chimeric monoclonal antibodies that recognize epidermal growth factor receptor
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                                                                                                                                                                                                                                  Sequence 34, Application US/08129930B
; Batent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: detiani Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Bduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and TITLE OF INVENTION: Therapeutic Methods
; TITLE OF INVENTION: Therapeutic Methods
; CORRESPONDENCE ADDRESS:
ADDRESSER: V. AMZEL & ASSOC.
                                               0; Indels
  Score 47; DB 1; Length 9;
Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.9%; Score 47; DB 1; Length 9; 88.9%; Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: California

COUNTRY: USA

ZIP: 94596

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATYONREY/AGENT INFORMATION:
NAME: Ameel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REPRENCE/DOCKET NUMBER: 30,930
REPRENCE/DOCKET NUMBER: 30,930
REPRENCE/DOCKET NUMBER: CRECC-008A
TELERPRAN: (510) 521-1333
TELERPAX: (510) 521-1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEB: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/08560558E Patent No. 5891996
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Humanized and TITLE OF INVENTION: antibodies tha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: n.a.
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
    83.9%;
Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9°
"---hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                   1 FQGSHVPYT 9
                                                                                            1 FOGSHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOGSHVPWT 9
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Gaps
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APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: de Catani Dr., Roberto L.
APPLICANT: Pactani Dr., Jerry A.
APPLICANT: Pactani Dr., Jerry A.
APPLICANT: Pactani Dr., Jerry A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2; Length 9; Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Calliornia
CUUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUW TYEE: FOLDEY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING APPLICATION ATA:
APPLICATION NUMBER: 08/129,930
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING APPLICATION NUMBER: 08/129,930
FILING APPLICATION NUMBER: 08/129,930
RICHARY AGENT INFORMATION:
ATTCRNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 20,930
REGISTRATION NUMBER: 20,930
REGISTRATION NUMBER: 20,930
RELEPRAK: (213) 489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                   CLT 149,608
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US-08-976-288A-34
; Sequence 34, Application US/08976288A
; Patent No. 6315997
     REGISTRATION NUMBER: 34,889
REFERENCE/DOCKET UNMBER: CL'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-826-6565
                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.9%;
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                          TELEFAX: 212-826-5909
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: n.a.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-134-346A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FOGSHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FOGSHVPYT 9
                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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Sequence 21, Application US/0813436A

Patent No. 6213135

Patent No. 6213135

APPLICANT: Ceriani, R.L.C.

APPLICANT: Ceriani, R.L.C.

APPLICANT: PRESENT JA.

TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ostrager, Chong & Flaherty

STREET: 300 Park Avenue

CITY: New York

STREET: 300 Park Avenue

CITY: New York

STREET: 300 Park Avenue

COUNTRY: US

COUNTRY: US

COUNTRY: US

COUNTRY: ISBA PC compatible

COMPUTER: ISBA PC compatible

COMPUTER: ISBA PC compatible

COMPUTER: Datast IT Delease #1 0 Varsion #1 30
TITLE OF INVENTION: EGF-R); diagnostic and therapeutic use.

NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
STREET: P.O. Box 2250
CITY: Salt Lake City
STATE: Utah tee City
STATE: Utah tee City
COUNTRY: United States of America
ZIP: 84110
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS95
SOFTWARE: WORDER: AINDOWS95
SOFTWARE: WORDER: 11/5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,558E
FILING DATE: Union S891996ember 17, 1995
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 31,041
REFERENCE/CRETERISTICS:
TELEFOAK: (801) 532-1968
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.9%; Score 47; DB 1; Length 9; 88.9%; Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/134,346A PILING DATE: 08-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Onofrio, Dara L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.9
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FQYSHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOGSHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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US-08-560-558E-31
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US-08-053-171-29
is Sequence 29, Application US/08053171
is Patent No. 5562903
is GENERAL INFORMATION:
is APPLICANT: Co. Loibner
it TITLE OF INVENTION: Antibody Derivatives
inther OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
is ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP.
                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 1; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFFCATION: 44
ATTOMATON NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELEPONE: (415) 326-2400
TELEPONE: (415) 326-2400
TELEPAX: (415) 326-2400
TELEPAX: (415) 326-2402
TELEPAX: (415) 326-2402
TELEPAX: (415) 326-2402
TELEPAX: 9 amino acids
                                                                                                                                                                                                                                                                                                                                            Score 47; DB 2;
Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-947-839B-34
                  NAME: Amzel Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-649-0609
TELEFAX: 240-359-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Third
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                    TELEX: n.a.
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                              83.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.1%;
                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAMBY KEY: Peptide
LOCATION: 1.9
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-053-171-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriquez, Rolando P
APPLICANT: Frias, Ennesto M
TITLE OF INVERTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
TITLE OF INVERTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
CURRENT APPLICATION NUMBER: US/09/217,268B
CURRENT APPLICATION NUMBER: 1938-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/09947839B
Patent No. 6936706
GENERAL INFORMATION:
APPLICANT: do Couto, Fernando J.R.
Ceriani Dr., Roberto L.
Peterson Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
for Carcinomas and Kit and Diagnostic Vaccination and Therapeutic Methods.
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,839B
FILING DATE: 06-Sep-2001
CLASSIFICATION: <Unknown>
                                     Score 47; DB 2; Length 9;
Pred. No. 4.6e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 2; Length 9;
Pred. No. 4.6e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSE: V. Amzel & Assoc.
STREET: P.O.Box 159
CITY: Gladwyne
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                       US-09-217-268B-31
; Sequence 31, Application US/09217268B
; Patent No. 6506883
                                     83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.9%;
88.9%;
                                   Query Match 83.9
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                         1 FOGSHVPYT
                                                                                                                   1 FQGSHVPWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Murine
US-08-976-288A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-947-839B-34
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Sequence 5, Application US/09724530

Sequence 5, Application US/09724530

GENERAL INFORMATION:
SEQUENCE 5, Application US/09724530

GENERAL INFORMATION:
SECONDER 5, APPLICANT: Wahl, Alan
SAPPLICANT: Francisco, Joseph
SAPPLICANT: Francisco, Joseph
TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REFERENCE: 9622-005

CURRENT APPLICATION NUMBER: US/09/724,530

CURRENT FILING DATE: CURRENT FILING DATE: 1999-06-08

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATOR PATOR NUMBER: CURRENT FILING DATE: 1999-06-08

SEQ ID NO 5

LENGTH: 9

LENGTH: 9
                                                                                                                                                                                                                                                     APPLICANT: Siegall, Clay
APPLICANT: Siegall, Clay
APPLICANT: Wahl, Alan
APPLICANT: Fancisco, Joseph
APPLICANT: Francisco, Joseph
APPLICANT: Fell, H. Perry
TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REFERENCE: 9632-005
CURRENT APPLICATION NUMBER: US/09/724,409
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 9
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Best Local Similarity 88.9%; Pred. No. 4.6e+05; Matches 8; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 2; L
Pred. No. 4.6e+05;
1; Mismatches 1;
                                                                                                                                                                            US-09-724-409-5
; Sequence 5, Application US/09724409
; Patent No. 683851
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.6%;
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Best Local Similarity 75.07
6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Mus musculus
US-09-724-409-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Mus musculus
US-09-724-530-5
                                                                                   1 FQGSHVPFT 9
                                                            1 FQGSHVPWT 9
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2 QTTHVPWT 9
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RESULT 15

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US-09-328-296-5
; Sequence 5, Application US/09328296
; Patent No. 69461201
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TILLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 963-2065
; CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 5
; SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: MUS musculus US-09-328-296-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QGSHVPWT 9
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2 QTTHVPWT 9
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137, App 31, Appl 135, App 34, Appl 135, App

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 2 Sequence 1 Sequence 6

OM protein

Run on:

Sequence:

Searched:

Database

Result

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Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/09995529

Sequence 36, Application WS/09995529

Publication No. US20030099655A1

GENERAL INFORMATION:

APPLICANT: Watkins, Jeffry D.

APPLICANT: Tang, Xing

TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Walated Methods

FILE REPREBUCE: P.IX 4976

CURRENT FILING DATE: 2001-11-26

NUMBER OF SEQ ID NOS: 358

SEQ ID NOS: 358

LENGTHARE: PASLEEQ for Windows Version 4.0

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/0995529
; Sequence 36, Application US/0995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Related Methods
; TITLE OF INVENTION: Related Methods
; TITLE OF INVENTION: Related Methods
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PastSEQ for Windows Version 4.0
; LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 56; DB 3; L
llarity 100.0%; Pred. No. 1.7e+06;
Conservative 0; Mismatches 0;
US-09-995-529-127
US-09-995-529-131
US-09-995-529-131
US-09-995-529-131
US-09-995-529-131
US-09-995-529-137
US-09-995-529-137
US-09-995-529-137
US-09-2947-68B-31
US-09-2947-68B-31
US-09-947-68B-31
US-09-947-68B-31
US-10-482-105-10
US-10-482-105-10
US-10-409-611-81
US-10-409-611-81
US-10-409-611-81
US-10-409-611-81
US-10-409-611-81
US-10-409-611-81
US-10-409-611-81
                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mus musculus
US-09-995-529-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Mus musculus
US-09-995-529-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FQGSHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
   RESULT 2
US-09-995-529-36
                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-09-995-529-36
    TYPE: PRT
    Sequence 36, Appl
Sequence 48, Appl
Sequence 6, Appl
Sequence 72, Appl
Sequence 128, App
Sequence 138, App
Sequence 139, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                         December 30, 2005, 15:12:47 ; Search time 160 Seconds (without alignments) 23.503 Million cell updates/sec
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Sequence 140,
Sequence 141,
Sequence 142,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA Main: * /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: * : /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * : /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * : /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: * : /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep: * : /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: * : /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-995-529-36
US-10-47-48
US-10-735-916A-6
US-09-995-529-128
US-09-995-529-132
US-09-995-529-138
US-09-995-529-138
US-09-995-529-138
US-09-995-529-138
US-09-995-529-140
US-09-995-529-141
US-09-995-529-141
US-09-995-529-142
US-09-995-529-143
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
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                                                                                                                                                                        US-10-735-916A-6
56
1 PQGSHVPWT 9
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Match Length
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Perfect score:
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                       Sequence 72, Application US/09947839
Publication No. US20030138428A1
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
Fernando T., Techeron Dr., Jerry A.
Padlan Dr., Jerry A.
Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
Diagnostic Vaccination and
Therapeutic Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071

COMPUTER READABLE FORM:
    MEDLUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
    SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRINT APPLICATION DATE: US/09/947,839
    FILING DATE: 06-Sep-2001
    CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,288
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/977,696
FILING DATE: NO. US20030138428Alember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Yiviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.6%; Score 53; DB 3; Length 9;
88.9%; Pred. No. 1.7e+06;
"...matrhes 0; Indels
                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSER: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
                        Query Match
100.0%; Score 56; DB 5; I
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-947-839-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (213) 489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.>
8, Conservative
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US-09-995-529-128
                                                                                                                                                                                                                                                                                          RESULT 5
US-09-947-839-72
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Sequence 6, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GORYALA, Nathalie
APPLICANT: GORYALA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION NOVER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/308 538
FRIOR APPLICATION NUMBER: FR 03/08 538
FRIOR APPLICATION NUMBER: FR 02/00 653
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
                                                                                       Gaps
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                              100.0%; Score 56; DB 3; Length 9; 100.0%; Pred. No. 1.7e+06;
                                                                                 0; Indels
                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                       Sequence 48, Application US/10470045
| Publication No. US20040146505A1
| GENERAL INFORMATION:
| APPLICANT: Scancell Limited
| APPLICANT: Burrant, Linda Gillian
| APPLICANT: Parsons, Tina
| CURRENT APPLICATION NUMBER: US/10/470,045
| CURRENT PILING DATE: 2003-07-24
| PRIOR APPLICATION NUMBER: GB 0102145.0
| PRIOR APPLICATION NUMBER: GB 0102145.0
| PRIOR PLING DATE: 2001-01-26
| NUMBER OF SEQ ID NOS: 101
| SOFTWARE: Patentin version 3.1
Query Match
Best Local Similarity 100..
-.a 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Mus musculus
US-10-735-916A-6
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US-10-470-045-48
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LENGTH: 9
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Gaps
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                                                                                                                                                                                                                                                                           Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 128, Application US/0995529
Publication No. US20040091482A9
GENERAL INFORMATION:
APPLICANT: Wathins, Jeffry D.
APPLICANT: Wathins, Jeffry D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 128
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 132, Application US/09995529
Publication No. US20040091482A9
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
                                                                                                                                                                                                                                                                        Score 52; DB 3; ]
Pred. No. 1.7e+06; 0; Mismatches 1
                                                                                                                                                                                                       ; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-138
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CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 132
LENGTH: 9
         CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SUFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 138
LENGTH: 9
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.5
Matches 8; Conservative
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Matches 8; Conservative
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Pred. No. 1.7e+06;
1; Mismatches 0; Indels
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Sequence 128, Application US/09995529
Publication No. US200300996581
GENERAL INFORMATION:
APPLICANT: Watting, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
APPLICANT: Huse, William D.
TITLE OF INVENTION: Related Methods
TITLE OF INVENTION: Related Methods
FILE REPERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 132, Application US/09995529
Fublication No. US20030099655A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT APPLICATION NUMBER: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOOTWARE: FastSEQ for Windows Version 4.0
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Sequence 138, Application US/09995529
Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Warkine, Jeffry D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REPERENCE: P-IX 4976
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                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: synthetic antibody mutation US-09-995-529-128
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Best Local Similarity 88.9%;
Matches 8; Conservative C
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Best Local Similarity 88.9
Matches 8; Conservative
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1 FRGSHVPWT 9
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100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0; Indels
                                                                                                   Sequence 140, Application US/0895529;
Publication No. US20030099655A1;
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Hase, William D.
APPLICANT: Tang, Xing
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976;
CURRENT PRILIG DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 141, Application US/09995529
; Publication No. US200300995551
; Publication No. US200300995551
; GENERAL INFORMATION:
; APPLICANT: Week, William D.
; APPLICANT: Tang, Ying
TITLE OF INVENTION: Related Methods
; TITLE OF INVENTION: Related Methods
; TITLE OF INVENTION: Related Methods
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: synthetic antibody mutation US-09-995-529-140
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 8; Conservative
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1 FQGSHVPW 8
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US-09-995-529-142
                                                                    RESULT 13
US-09-995-529-140
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US-09-995-529-141
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                                                                    Score 52; DB 3; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                               Sequence 138, Application US/0995529;
Publication No. US20040031482A9;
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOUTHARE PRACESOR FOR Windows Version 4.0
SEQ ID NO 138
LENGTH: 9
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Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Methods
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICANTON NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1;
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    i OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-132
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ORGANISM: Artificial Sequence
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                                                                      Query Match 92.9%;
Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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LENGTH: 9
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; ORGANISM: Mus musculus
US-11-012-353-6
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US-11-125-837-15
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Sequence 15, Appl
Sequence 6, Appli
Sequence 7, Appli
Sequence 196, Appl
Sequence 196, Appl
Sequence 196, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 1355, Appl
Sequence 371, Appl
Sequence 6971, Appl
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                                                                                       December 30, 2005, 15:13:42; Search time 13 Seconds (without alignments) 5.185 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-125-837-15
US-11-105-708-19
US-10-932-334-6
US-11-102-743-5
US-11-102-743-5
US-11-102-743-6
US-11-097-812-196
US-11-097-812-196
US-11-097-812-196
US-11-097-62-59
US-11-043-037-62-59
US-11-045-024-7048
US-11-045-024-13595
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US-11-045-024-6971
US-11-045-024-7067
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                             57103 seqs, 7488799 residues
                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                      US-10-735-916A-6
56
                                                                                                                                                                                          1 FQGSHVPWT 9
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Match Length
                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 9 Maximum DB seq length: 9
                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein
                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                             Run on:
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No.
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301, App
302, App
305, App
306, App
10563, A
11335, A
1135, Ap
4056, A
4056, Ap
12607, A
                                                                                                                  13630, A
13638, A
                                                                                       Sequence
Seq
                                                            Sequence
                     US-11-045-024-13594

US-11-045-024-13597

US-11-045-024-13604

US-11-045-024-13604

US-11-045-024-13638

US-11-103-12-45

US-11-101-748A-301

US-11-010-748A-305

US-11-010-748A-305

US-11-010-748A-305

US-11-045-024-10563

US-11-045-024-10563

US-11-045-024-4058

US-11-045-024-4058

US-11-045-024-4058

US-11-045-024-4058

US-11-045-024-4058

US-11-045-024-4058

US-11-045-024-4058

US-11-045-024-1336

US-11-045-024-1336

US-11-045-024-1336
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## ALIGNMENTS

```
Sequence 6, Application US/11012353
| Sequence 6, Application US/11012353
| Publication No. US20050249730A1
| GENERAL INFORMATION:
| APPLICANT: GOESTETH, LILIANE
| APPLICANT: CORTAIA, NATHALIE
| APPLICANT: CORTAIA, NETHALIE
| APPLICANT: BECR, ALAIN
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
| TITLE OF INVENTION: NOVER: 2004-12-16
| PRIOR EDILICATION NUMBER: PROSESSE OF THE OF INVENTION NUMBER: PROSESSE OF THE OF ILLING DATE: 2003-07-11
| PRIOR PLILING DATE: 2003-07-21
| PRIOR PLILING DATE: 2003-01-20
| PRIOR PLILING DATE: 2003-01-20
| PRIOR PLILING DATE: 2003-01-20
| PRIOR PLILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Score 56; DB 7; L
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0;
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Sequence 15, Application US/11125837

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1 FOGSHVPWT 9
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2 QTTHVPWT 9
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Matches 6; Conserv
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US-11-125-837-3
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WESULT:

WESULT:

Sequence 19, Application US/11105708

Publication No. US20050281821A1

GENERAL INFORMATION:

APPLICANT: Perhasetti, Flavia

APPLICANT: Preinark, Burce

APPLICANT: Preinark, Burce

APPLICANT: Wan Epps, Dennis

APPLICANT: Wan Epps, Dennis

APPLICANT: Wan Epps, Dennis

APPLICANT: Wan Epps, Dennis

APPLICANT: Brooks, Peter C

TITLE OF INFORMATION: Method and Composition for Angiogenesis Inhibition

FILE REFERENCE: 30797-704.501

CURRENT APPLICATION NUMBER: 05/478,977

PRIOR PPLICATION NUMBER: 60/152,496

PRIOR APPLICATION NUMBER: 60/122,496

PRIOR PPLING DATE: 1999-09-02

PRIOR PPLING DATE: 1999-09-02

PRIOR APPLICATION NUMBER: 60/114,878

PRIOR PLING DATE: 1999-01-06

PRIOR APPLICATION NUMBER: 60/114,877

PRIOR PLING DATE: 1999-01-06

PRIOR PLING DATE: 1999-01-06

PRIOR PRIOR APPLICATION NUMBER: 60/114,877

PRIOR PLING DATE: 1999-01-06

PRIOR PLING DATE: 1999-01-06

PRIOR PLING DATE: 1999-01-06

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Version 3.2
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100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 56; DB 7; L
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0;
                 GENERAL INFORMATION:
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
TITLE NEPERNOLES:
TITLE REFERENCE: 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2005-05-10
PRIOR PILING DATE: 2006-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PASLESQ for Windows Version 4.0
SERIOTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Synthetic peptide
Publication No. US20050266003A1
                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FQGSHVPWT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-105-708-19
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RESULT 4 US-10-932-334-6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wahl, Alan
APPLICANT: Francisco, Joseph
APPLICANT: Fell, H. Perry
TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
FILE REFERENCE: 9632-005
CURRENT APPLICATION NUMBER: US/11/102,743
CURRENT PILING DATE: 2005-04-08
PRIOR PPLICATION NUMBER: US/99/328,296
PRIOR FILING DATE: 1999-06-08
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Sequence 6, Application US/10932334
Publication No. US20050249728A1
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR PELING DATE: 2003-12-08
PRIOR PLING DATE: 2003-12-08
PRIOR PLING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/11102743; Publication No. US20050266002A1; GENERAL INFORMATION: APPLICANT: Siegall, Clay
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.2
Best Local Similarity 88.9
Matches 8; Conservative
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Gaps
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NAME: Lawrence, 111, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, Nobuo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Huma
Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-Aug-2005
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DĀTA:
APPLICATION NUMBER: US/11/193,512
PRIOR FILING DATE: 2004-02-28
PRIOR APPLICATION NUMBER: US 60/529,500
PRIOR FILING DATE: 2003-12-15
PRIOR PILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin version 3.2
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasteSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT: 9
US-11-193-512-39
US-11-193-512-39
; Sequence 39, Application US/11193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURIYA, Akiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                         57.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 OGSHVPWT 9
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                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                     US-11-097-812-196
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| Publication No. US20050281828A1 |
| Publication No. US20050281828A1 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Bowdish, Katherine S. |
| APPLICANT: Bowdish, Naveen |
| TITLE OF INVENTION: | METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN |
| TITLE OF INVENTION: | PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS |
| CURRENT APPLICATION NUMBER: US/11/097,812 |
| CURRENT APPLICATION NUMBER: US/11/097,812 |
| PRIOR FILING DATE: 2004-12-17 |
| PRIOR FILING DATE: 2004-12-17 |
| PRIOR FILING DATE: 2004-03-04 |
| PRIOR APPLICATION NUMBER: US 60/548,385
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US-11-009-939-40

i Sequence 40, Application US/11009939
i Publication No. US20050265998A1
i GENERAL INFORMATION:
i APPLICANT: Blson, Greg Christopher Andrew
i TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
i FILE REFERENCE: 23135-402
CURRENT APPLICATION NUMBER: US/11/009,939
CURRENT FILING DATE: 2003-12-10
i PRIOR PILING DATE: 2003-12-10
i PRIOR APPLICATION NUMBER: 60/528,811
i PRIOR PILING DATE: 2003-12-10
i PRIOR FILING DATE: 2003-12-10
i RIOR FILING DATE: 2003-12-10
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                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 37; DB 7; Length 9; 77.8%; Pred. No. 4.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                               CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR FILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PASICEQ for Windows Version 4.0
SEQ ID NO 3
           FILE REFERENCE: 13062-011001
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.0-
                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus
US-11-009-939-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FQGSHVPWT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QGSHVPWT 9
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US-11-097-812-196
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##FULLWARTHON: Unducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REPERENCE: 2060-004007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 1995-10-05
FRIOR PELING DATE: 1995-10-05
FRIOR FILING DATE: 1995-10-05
FRIOR FILING DATE: 1993-03-05
FRIOR FILING DATE: 1993-03-05
FRIOR FILING DATE: 1993-06-06
FRIOR APPLICATION NUMBER: US 08/103,396
FRIOR RILING DATE: 1993-06-06
FRIOR PELING DATE: 1993-11-29
FRIOR FILING DATE: 1993-11-29
FRIOR FILING DATE: 1993-11-29
FRIOR FILING DATE: 1993-11-29
FRIOR FILING DATE: 1994-03-04
FRIOR FILING DATE: 1994-03-04
FRIOR FILING DATE: 1994-11-29
FRIOR FILING DATE: 1994-11-29
FRIOR FILING DATE: 1994-11-29
FRIOR FILING DATE: 1994-11-29
FRIOR FILING DATE: 1994-11-20
FRIOR FILING DATE: 1994-11-20
FRIOR FILING DATE: 1994-13-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT PILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FLILING DATE: 2002-03-13
PRIOR PLILING DATE: 2002-11-13
SEQUID NOS: 64
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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Pred. No. 4.3e+04;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 46, Application US/11045024; Publication No. US20050271676A1; GENERAL INFORMATION:
                                                                                                                             ; Sequence 59, Application US/10507662; Publication No. US20050255102A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Cheanut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Kibo, Ralph
APPLICANT: Krob, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-59
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6 IPWT 9
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6 VPWT 9
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US-11-045-024-46
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US-10-473-037-8
US-10-473-037-8

Sequence 8, Application US/10473037

Sequence 8, Application US/10473037

Publication No. US2050266A1

GENERAL INFORMATION:

APPLICANT: KYOWA HAKKO KOGYO CO., LTD.

TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibod

TITLE OF INVENTION: He antibody fragments

FILE REFERENCE: 11374WO1

CURRENT APPLICATION NUMBER: US/10/473,037

CURRENT FILING DATE: 2003-09-26

FRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 8

LENGTH: 9
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APPLICANT: BIOGEN, INC.
THE RECENTS OF THE UNIVERSITY OF CALIFORNIA
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT APPLICATION NUMBER: 60/364,991
PRIOR PILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PALENTI VET: 2.1
SEQ ID NO 60
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                  Query Match 55.4%; Score 31; DB 7; Length 9; Best Local Similarity 62.5%; Pred. No. 4.3e+04; Matches 5; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.8%; Score 29; DB 6; I 62.5%; Pred. No. 4.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-11-193-512-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 60, Application US/10507662; Publication No. US20050255102A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.8
Best Local Similarity 62.5
Matches 5; Conservative
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US-10-507-662-60
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US-10-507-662-60
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SOFTWARE: FastSEQ for Windows Version 4.0

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Search completed: December 30, 2005, 15:27:03 Job time : 16 secs
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                                                                                         APPLICANT:
APPLICANT:
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APPLICANT: Chesure, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT FILING DATE: 2060.0040007
CURRENT PILLING DATE: 1999-10-05
PRIOR PELICATION NUMBER: US 08/027,146
PRIOR PELING DATE: 1993-06-04
PRIOR PELING DATE: 1993-06-06
PRIOR PELING DATE: 1993-06-06
PRIOR PELING DATE: 1993-11-29
PRIOR PELING DATE: 1993-11-29
PRIOR PELING DATE: 1994-11-29
PRIOR PELING DATE: 1994-12-01
NUMBER: US 08/159,184
PRIOR PELING DATE: 1994-12-01
NUMBER: PSEQ ID NOS: 14528
SOFTWARE PRESENCE FOR WINDOW VETBION 4.0
SEQ ID NO 3770
LENGTH: 9
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                                                                                                                              42.9%; Score 24; DB 7; Length 9; 60.0%; Pred. No. 4.3e+04; ive 2; Mismatches 0; Indels
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                                            ; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS US-11-045-024-3770
                                                                                                                                                                                                                                                                                                                                                                                Sequence 3770, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
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US-11-045-024-7048
Sequence 7048, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
                                                                                                                            Query Match
Best Local Similarity 60.0°
Matches 3; Conservative
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5 TNVPW 9
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5 TNVPW 9
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US-11-045-024-3770
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APPLICANT:
APPLICANT:
; SEQ ID NO 46
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42.9%; Score 24; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
Southwood, Scott
Livingston, Brian
Chesnut, Robert
Baker, Denise Marie
Celis, Esteban
Kubo, Ralph
Grey, Howard M.
Epimmune Inc.
                                                                                                                                                                                                                                                                                                                                               4 SHVPW 8
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5 TNVPW 9
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; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12128
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Best Local Similarity
Matches 5; Conserv
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880.00
880.00
880.00
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880.00
777.50
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US-09-252-991A-19202
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14, Appl
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34, Appl
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Sequence 48720,
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                                                                                                                                     December 30, 2005, 13:14:26; Search time 13.4516 Seconds (without alignments) 36.877 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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Sequence 3
Sequence 3
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/cgn2_6/ptodata/1/iaa/f_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RR_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RR_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-583-110-2944
US-09-583-110-2944
US-09-769-781-19
US-09-107-433-4262
US-09-107-433-4262
US-09-540-236-3594
US-09-540-236-3594
US-09-913-159-13
US-09-913-159-13
US-09-328-352-7439
US-09-328-352-7439
US-09-328-352-7439
US-09-328-352-7439
US-09-328-352-7439
US-09-949-016-6846
US-09-949-018-6846
US-09-949-018-6846
US-09-949-018-6846
US-09-902-540-13914
US-09-902-540-13914
US-09-134-533-3
US-09-134-533-3
US-09-2770-767-48720
US-09-770-767-48720
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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40
1 GGYLWN 6
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Match Length DB
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Perfect score:
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FOR DIAGN(

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Itent No. 000001.
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID
TITLE OF INVENTION: THERAPEUTICS
THERAPEUTICS
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/09/107,433
PRIOR APPLICATION NUMBER: US/09/107,433
PRIOR APPLICATION DATA:
PILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
APPLICATION NUMBER: 60/05153
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
SOFTWARE: «Unknown»
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 17547, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al.
                                                                                                                       Sequence 4262, Application US/09107433 Patent No. 6800744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 290 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4262: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 5; Conserv
67 GGYYWN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 GGYYWN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGYLWN 6
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                                                                             RESULT 5
US-09-107-433-4262
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                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
CURRENT PRINCIP.
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR PLING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR PILING DATE: 1998-0-02-12
PRIOR PILING DATE: 1998-0-02-02
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                          Score 35; DB 2; Length 275;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.5%; Score 35; DB 2; Length 277; 83.3%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION

JECURE NO. 693625

GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REPRENCE: PMC/P21129WO
CURRENT FILIMG DATE: 2001-01-26
CURRENT FILIMG DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
FRIOR PILING DATE: 1999-03-19
FRIOR PILING DATE: 1999-03-19
FRIOR FILING DATE: 1909-03-19
FRIOR FILING DATE: 1909-03-19
FRIOR FILING DATE: 1908-03-19
                                                                                                                                                                                                                                                                            US-09-583-110-2944
; Sequence 2944, Application US/09583110
; Partent No. 6699703
; PRINEAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae US-09-769-787-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptococcus pneumoniae US-09-583-110-2944
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83.3%;
                          Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conservative
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SEQ ID NO 2944
LENGTH: 277
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                                                                                                                               1 GGYLWN 6
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US-09-769-787-19
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                                                       Gaps
                                                                                                                                                                       ;
0
                                                                                                                       Length 290;
                                                                                                                                                                       Indels
                                                                                                                    87.5%; Score 35; DB 2; 183.3%; Pred. No. 1.1e+02; ive 0; Mismatches 1.
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...290
SEQUENCE DESCRIPTION: SEQ ID NO: 4262:
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US-09-440-833-2
| Sequence 2, Application US/09440833
| Sequence 2, Application US/09440833
| Patent No. 6277580
| GENERAL INFORMATION:
| APPLICANT: Blingson, Jay L.E. APPLICANT: Blingson, Jay L.E. APPLICANT: Stabel, Judith R. TITLE OF INVENTION: Species-Specific Genetic Identification TITLE OF INVENTION: of Mycobacterium Paratuberculosis NUMBER OF SEQUENCES: 16
| CORRESPONDENCE ADDRESS: ADDRESSER: Curtis P. Ribando STRET: 1815 N. University Street CITY: Peoria STATE: IL COUNTY: Peoria STATE: IL COUNTY: Peoria STATE: IL COUNTY: Blink PC Compatible COMPUTER READABLE FORM: COMPUTER: IBM PC Compatible COMPUTER: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PELLICATION DATA: PELLICAT
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; Pred. No. 85;
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100.0%; Pred. No. c.
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APPLICATION NUMBER: 09/108,051
FILING DATE:
                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RAIDando, Curties P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0229.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 309/681-6513
TELEFAX: 309/681-6688
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE THARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REFRENCE/DOCKET NUMBER: 0229
TELECOMMUNICATION INFORMATION:
TELEPHONE: 399/681-6513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 144 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-09-108-051-2
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; MOLECULE TYPE: protein
US-09-440-833-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERABEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3594
LENGTH: 739
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; Sequence 2, Application US/09108051
; Patent No. 598576
; GENERAL INFORMATION:
APPLICANT: Ellingson, Jay L.E.
TITLE OF INVENTION: Species-Specific Genetic Identification
TITLE OF INVENTION: of Mycobacterium Paratuberculosis
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
CITY: Peoria
STATE: IL
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83.3%; Pred. No. 2.18+02;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTER: 105
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%; Score 35; DB 2; 1
83.3%; Pred. No. 2.8e+02;
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.33
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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US-09-540-236-3594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 GGYYWN 262
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US-09-108-051-2
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Patent No. 6610836
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE REFERENCE: 7136-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45401
LENGTH: 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 326;
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Pred. No. 1.9e+02;
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US-09-270-767-45401
US-09-270-767-670367
; Sequence 45401, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRGANISM: Drosophila melanogaster US-09-270-767-45401
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.08;
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9700
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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Sequence 7439, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: MUGHER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7439
                                                                                                                                                                                                                                                       Sequence 13, Application US/08913159
Fatent No. 6300109
GENERAL INFORMATION:
FAPLICANT:
TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
TOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,159
FILING DATE:
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100.0%; Pred. No. 1.1e+02;
Live 0; Mismatches 0;
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US-09-489-039A-9700
; Sequence 9700, Application US/09489039A
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APPLICATION NUMBER: DK 0179/95
FILLING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: 1inear
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US-09-328-352-7439
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Best Local Similarity 100.
Matches 5; Conservative
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US-08-913-159-13
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RESULT 15

US-09-949-016-6846

J Sequence 6846, Application US/09949016

J PALENT NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PPLICATION NUMBER: 60/241,755

PRIOR PPLICATION NUMBER: 60/241,755

PRIOR PPLICATION NUMBER: 60/237,768

PRIOR PPLING DATE: 2000-10-20

PRIOR PPLING DATE: 2000-10-03

PRIOR PPLING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOFTWARE: FastSEC for Windows Version 4.0

SEQ ID NO 6846

LENGTH: 609

TYPE: PRT

NEASTING: Human
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Query Match 85.0%; Score 34; DB 2; Length 516; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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COCATION: (1)...(609)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-949-016-6846
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Search completed: December 30, 2005, 13:37:18 Job time : 14.4516 secs

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Human nov Drosophil Human ORF Human ORF

Abp34716

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with
                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies that bind to human insulin-like useful for treatment, prevention and diagnosis
                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                      CDR sequence for anti-IGF-1R antibody,
                                                                                                                                ABG80748
ABB17537
AAG73998
AAM92258
AAG29147
          ADB75644
AB065611
ADK46429
AAX81519
ABU02392
ABR95627
AEA59497
AEA59497
AB068801
ADL05908
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AAU20236
ABB59022
AAB41367
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                                                                                                                                                                                                                                                ABP34716
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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Goetsch L, Corvaia N,
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N-PSDB; ADJ76841.
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ADJ76842;
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ADJ76842
Adj76842 CDR seque
Adj76903 Anti-1GF-
Adj76917 Anti-1GF-
Adj76913 Anti-1GF-
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Adj76913 Human ant
Adz67093 Human ant
Adz67097 Human ant
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Adj76886 Anti-1GF-
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                                                                          December 30, 2005, 13:02:01; Search time 53.3226 Seconds (without alignments) 49.440 Million cell updates/sec
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          GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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growth factor receptor, of cancers.

ABU05763 ADJ80377 ADP03868

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hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGFTR and/or EGFR. This sequence represents an consequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obsterincs; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                    Gaps
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WD-FR000178.
11-JUL-2003; 2003FR-00008538.
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N-PSDB; ADZ67011.
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CORVAIA N.
LEGER O.
DUFLOS A.
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Best Local Similarity
Matches 6; Conserv
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comprising a light or heavy chain having at least one complementary determining a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (AD267006 and AD267014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illiness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a horizon of the Iransduction pathway of the signal mediated by the interaction of the transduction pathway of the signal mediated by the interaction of the transformation of preparation of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral receptor. The antibody is useful for preparation of a medicament intended to inhibit the growth capendent and/or EGF-dependent, especially IGF1 and/or IGF2.

Consequence in and/or EGF-dependent and/or EGF-dependent and/or the proliferation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent of a medicament intended for prevention or for the treatment of cancer, where the cancer, endometrial cancer or colon cancer. (I) is useful in the cancer of preparation of a medicament intended for the prevention or colon cancer. (I) is useful in vitro diagnosis of illnesses induced by an overappression or an underexpression of the IGF-IR and/or EGFR receptor is useful for in vitro diagnosis of illnesses induced by an overappression or an underexpression of the halvention. The present of sequence is supported, which involves contacting the receptor is useful for in vitro diagnosis of illnesses induced or the present of is suspected, which the halvent intended for the exemplification of the invention.

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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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Best Local Similarity
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07-MAY-2002;
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(FABR ) FABRE MEDICAMENT SA PIERRE.

Disclosure; SEQ ID NO 75; 164pp; French.

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; antipsoriatic; antibody; inf-1R; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
                                                                                   New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                       Disclosure; SEQ ID NO 69; 164pp; French.
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                    Leger O;
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18-JAN-2002; 2002FR-00000554.
07-MAY-2002; 2002FR-00005753.
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                    Corvaia N,
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Best Local Similarity
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                  Goetsch L,
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                                              The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or-2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or spidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit prowth and/or proliferation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; antipsoriatic; antibody; IGF-1R; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; IGFR; signal transduction pathway: __igand; tumor; cancer; osteosarcoma; complementarity determining region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%; 6; Conservative 0
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 117 AA;
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Matches
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kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies that bind to human insulin-like growth factor receptor, iul for treatment, prevention and diagnosis of cancers.
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Best Local Similarity 10v..
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                                                                                                                                                                                                                                 Sequence 117 AA;
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prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                               Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsorlatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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                                                                                                              100.0%; Score 40; DB
100.0%; Pred. No. 21;
ive 0; Mismatches
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00006538.
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                                                                                                                                                 6; Conservative
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                GGYLWN 6
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                                                                                    Sequence 117 AA
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(HAEU/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BECK/)
                                                                                                                                                 Matches
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the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal cativation of the IGF-IR and/or EGFR, and/or connected with a chyperactivation of the IGF-IR and/or EGFR, with of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only alightly induces secondary effects connected with inhibition of the insulin control of an edicament intended to inhibit the transformation of normal calls into calls with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2.

Consecut for preparation of medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, calls, its dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent a
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Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,

Example 13; SEQ ID NO 83; 125pp; English.

useful for treating cancer.

Beck A;

Duflos A, Haeuw J,

Leger O,

Goetsch L, Corvaia N, WPI; 2005-321968/33

BECK A.

CORVAIA N. LEGER O. DUFLOS A. HAEUW J.

(DUFL/) (BECK/) (HAEU/)

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/ Match 100.0%; Score 40; DB 9; Length 117; Local Similarity 100.0%; Pred. No. 21; Osservative 0; Mismatches 0; Indels
                                                                                      1 GGYLWN 6
  Query Match
                                           Matches
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Gaps ö

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Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.
                                                                                                       ADZ67087 standard; protein; 117 AA.
                                                                                                                                                                                          30-JUN-2005 (first entry)
  31 GGYLWN 36
                                                                                                                                                   ADZ67087;
                                                                 RESULT
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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.

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2002FR-00000654.
                                                                                                        16-DEC-2003; 2003US-00735916.
                                                                                                                                 20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                  18-JAN-2002; 2002FR-00000653
                                                                                    US2005084906-A1.
                                                                           Homo sapiens.
                                                                                                                            37-MAY-2002;
                                                                                                                       18-JAN-2002;
                                                                                              21-APR-2005.
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(GOET/) GOETSCH L.

Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tynosine kinase activity of the receptor, operation of binding to heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS67014). An antibody of the invention is useful in a determining region (CDR) consisting of one of two fully defined 16 amino acids (ADS67016 and ADS67014). An antibody of the invention of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with an antibody of the signal mediated by the interaction of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where continues secondary effects connected with inhibition of the insulant receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent cells, it is useful in the preparation of a medicament intended for prevention or the preparation of a medicament intended for prevention or ancer. (I) is useful in the preparation of a medicament intended for prevention or ancer. (I) is useful in the preparation of a medicament intended for prevention or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to retarge transforment of psorialss. (I) is useful in the abnormal presence, of IGF-cells expressing or overexpression or an underexpression of the IGF-IR and/or EGFR receptor is useful in the exemplification of the invent
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IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.

useful for treating cancer. Corvaia N, BECK A. Mus musculus. 20-JAN-2003; 11-JUL-2003; 18-JAN-2002; 07-MAY-2002; .8-JAN-2002; 21-APR-2005 Soetsch L, (BECK/) GOET/) CORV/) LEGE/) HAEU/ 

Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region. 2002FR-0000654. 2002FR-00005753. 2003WO-FR000178. 2003FR-00008538. 16-DEC-2003; 2003US-00735916 GOETSCH L. CORVAIA N. LEGER O. DUFLOS A. HAEUW J. US2005084906-A1

Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, WPI; 2005-321968/33

Beck A;

Haeuw J,

Duflos A,

Leger 0,

Example 13; SEQ ID NO 69; 125pp; English.

Treceptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of gradifically inhibiting tyrosine kinase activity of the receptor.

Comprising a light or heavy chain having at least one complementary comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADEG-ONG) and ADEG-ONJ. An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of the IGF-IR and/or connected with a noverexpression and/or an abnormal activation of the IGF-IR and/or connected with a hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin conduces secondary effects connected with inhibition of the insulin conduces secondary effects connected with inhibition of the insulin conduces secondary effects connected with inhibition of the insulin conduces secondary effects connected with inhibition of the insulin conduces secondary effects connected with inhibition of the insulin conducts of intended to inhibit the transformation of normal cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, preferably IGF-dependent and/or IGF2-adependent cells, preferably IGF-dependent cells, preferably IGF-dependent cells, preferably IGF-dependent cells, preferably IGF-dependent cells in the prevention of a medicament intended for the prostate cancer, colon cancer. (I) is useful in preparation of a medicament intended for the specific targeting or overexpressing or overexpressing or overexpressing or overexpressio invention relates to a novel isolated anti-insulin-like growth factor

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                                                                                                                                                                                                                                                                                                                                                                           neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; colon tumor; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                  Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
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                                                                                   9; Length 117;
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                                                                                   BB
                                                                                    Score 40; DB
Pred. No. 21;
                                                                                                                 Mismatches
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                                                                             100.0%; Scc
100.0%; Pre
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18-JAN-2002; 2002FR-00005543.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WD-FR000178.
11-JUL-2003; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                 6; Conservative
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CORVAIA N.
LEGER O.
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                         31 GGYLWN 36
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                                                       Sequence 117 AA;
                                                                                                                                            GGYLWN
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(LEGE/)
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(HAEU/)
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or an intense counterceau with an overcoppression analysis and contracted with a citivation of the Iransduction pathway of the signal mediated by the hyperactivation of the transduction pathway of the signal mediated by the interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral chearacter, preferably IGF-dependent, especially IGF1 and/or IGF2.

Character, preferably IGF-dependent, especially IGF1 and/or IGF2.

Character, preferably IGF-dependent and/or IRRZ/hou-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth especially IGF-and/or IGF2-dependent and/or IGF-dependent and/or IGF-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to cancer seconds in vitro diagnosis of intended by an undarances of invarances of in vitro diagnosis of illnesses induced by an overcence of the cancer of intended by an undarance of invarances of intended by an undarance of invarances.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; antipsoriatic; antibody; igF-1R; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
an illness connected with an overexpression and/or an abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is used in the exemplification of the invention
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18-JAN-2002; 2002FR-0000054.
07-MAY-2002; 2002FR-00005753.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
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                                                                          The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or repidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lumg, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipporiatic; psoriasis; dermacological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.
New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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                                                                                                                                                                                                                                                                                                                         protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                               Disclosure; SEQ ID NO 52; 164pp; French.
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/note= "leader peptide"
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/note= "CDR2"
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/note= "CDR3"
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07-MAY-2002; 2002FR-00005753
20-JAN-2003; 2003WO-FR000178
11-JUL-2003; 2003FR-00008538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;

cytostatic, antipsoriatic, antibody;

Anti-IGF-1R related protein #23

06-MAY-2004 (first entry)

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The invention relates to a novel isolated anti-insulin-like growth factor
                                                           Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                    Beck A;
                                    Haeuw J,
                                    Leger O, Duflos A,
                                                                                   Example 8; SEQ ID NO 52; 125pp; English.
                                                                          useful for treating cancer.
                                    Goetsch L, Corvaia N,
                                             WPI; 2005-321968/33.
N-PSDB; ADZ67055.
    GOETSCH L.
CORVAIA N.
                 DUFLOS A.
                                                                                                                                                                                                                                                                     Sequence 127 AA;
             LEGER O.
                           BECK A.
                           BECK/)
    GOET/)
             LEGE/)
                  DUFL/)
                       HAEU/)
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New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

(FABR ) FABRE MEDICAMENT SA PIERRE.

20-JAN-2003; 2003WO-FR000178. 18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-0000654.

WO2003059951-A2. Homo sapiens.

24-JUL-2003

Leger 0;

Corvaia N,

Goetsch L,

WPI; 2003-569653/53.

Disclosure; SEQ ID NO 77; 164pp; French

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway;
                                                                                                                        Gaps
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                                                                                 100.0%; Score 40; DB 7; Length 135; 100.0%; Pred. No. 24;
protein sequence used to generate the Ab of the invention.
                                                                                                                          0; Indels
                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                           ADJ76919 standard; protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-IGF-1R related protein #27.
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                              Query Match
Best Local Similarity lvv..
6; Conservative
                                                                                                                                                                                                         49 GGYLWN 54
                                                                                                                                                                  1 GGYLWN 6
                                           Sequence 135 AA;
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GGYLWN 46 1 GGYLWN 6

Best Local Similarity

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Query Match

100.0%; Score 40; DB 9; Length 127; 100.0%; Pred. No. 22;

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ADJ76911 standard; protein; 135 AA.

RESULT 13 ADJ76911 ADJ76911;

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or read diseases associated with overexpression and/or abnormal activity of IGF-1R and/or eceptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit prowth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-1R and/or EGFR. This sequence represents a

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New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 81; 164pp; French.
                                                                                                            (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                    18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                           20-JAN-2003; 2003WO-FR000178.
                                                                                                                                                                     WPI; 2003-569653/53
24-JUL-2003
                                                                                                                                         Goetsch L,
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                                                                                                                                                                                                                                                                                                                                                                                    fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinas diseases associated with order fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or profiteration of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                    New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated antibody (Ab), and its functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein sequence used to generate the Ab of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ76915 standard; protein; 135 AA.
                                                                                                                                                                                                              (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-IGF-1R related protein #25.
                                                                                                                                                     18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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                                                                                                                                                                                                                                            Corvaia N,
                                                                                                                                                                                                                                                                         WPI; 2003-569653/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 135 AA;
                                                                  WO2003059951-A2
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                                        Homo sapiens.
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                                                                                                                                                                                                                                            Goetsch L,
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ADJ76915
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-18) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF.1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or proliferation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
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Local Similarity 100.0%; Pred. No. 24;
les 6; Conservative 0; Mismatches 0; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein December 30, 2005, 13:11:41; Search time 8.51613 Seconds (without alignments) 67.789 Million cell updates/sec Run on:

US-10-735-916A-8 40 1 GGYLWN 6 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	membrane protein M	D-rhamnose synthes	phosphomannose iso	chlorophyll a/b-bi	transposase as1724	probable membrane	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote	sugar ABC transpor	hypothetical prote	mannose-6-phosphat	phosphomannose iso	hypothetical prote	late embryogenesis	perlucin - Halioti	hypothetical prote		hypothetical prote	_	hypothetical prote	hypothetical prote	signal-transducing	hypothetical prote		hypothetical prote		mannose-1-phosphat
SUMMAKIES	ID	D42400	T44446	F82964	S01430	AF2508	AD0615	C90754	G64831	A85618	D98085	E95221	F69322	A38598	B83201	AG1979	H84839	S78774	AB2051	G71548	B95912	T22354	T05587	AI1945	P69454	T26536	AD3140	H98147	590	C97265
	Length DB	277 2	479 2	479 2	530 2			259 2											159 2				304 2					ı,		9
æ	Query Match Le	90.06	0.06	0.06	0.06	•	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	Š.	'n.	85.0	85.0
	Score	36	36	36	36	32	35	35	35	32	32	32	35	32	32	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34
	Result No.		8	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25		27	28	

probable aminotran	hypothetical prote	MAF1 protein - yea	hydroxyneurosporen	mannose-1-phosphat	mannose-6-phosphat	mannose-1-phosphat	mannose-1-phosphat	mannose-6-phosphat	ba-type ubiquinol	cytochrome O ubiqu	hypoxia inducible	N-acetylmuramoyl-L	cationic amino aci	100K protein - fow	hypothetical prote
D81289	AB1870	S50986	T50894	H87697	H69386	AH2968	C98314	S30187	A97376	AG2593	JC7771	A41322	C69451	JN0878	T34010
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390	394	395	406	436	448	476	476	494	667	667	667	705	736	798	1482
85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0
34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34

## ALIGNMENTS

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C;Species: Streptococcus mutans
C;Species: Streptococcus mutans
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Paccession: D42400
A;Fulse: A binding protein-dependent transport system in Streptococcus mutans responsib
A;Reference number: A42400; MUID:92165821; PMID:1537846
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-277 <RUS>
A;Residues: 1-277 <RUS>
A;Crose-references: UNIPROT:Q00751; UNIPARC:UPI000012F61F; GB:M77351; GB:M19349; GB:M30
A;Note: sequence extracted from NCBI backbone (NCBIN:83895, NCBIP:83891)
C;Superfamily: maltose transport protein malG
C;Keywords: transmembrane protein
                                        membrane protein MsmG - Streptococcus mutans
D42400
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Gaps ö 90.0%; Score 36; DB 2; Length 277; 83.3%; Pred. No. 18; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 83.3
Matches 5; Conservative

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GGYFWN 71 1 GGYLWN 6 ઠે 셤

D-rhamnose synthesis protein wbpW [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Accession: T44446
R;Rocchetta, H.L.; Pacan, J.C.; Lam, J.S.
M;Rocchetta, H.L.; Pacan, J.C.; Lam, J.S.
A;Title: Synthesis of the A-band polysaccharide sugar D-rhamnose requires Rmd and WbpW:
A;Roccession: T44446
A;Roccession: T44446
A;Roccession: T44446
A;Roccession: T44446
A;Roccession: T44446
A;Roccession: T4446
A;Roccession: T4466
A;Roccession: T44

ô Gaps ö Query Match 90.0%; Score 36; DB 2; Length 479; Best Local Similarity 83.3%; Pred. No. 32; Matches 5; Conservative 1; Mismatches 0; Indels

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DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anc A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2508
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:Q8YKP7; UNIPARC:UPI0000CEF4C; GB:BA000020; PIDN:BAB78330.1;
A,Bxperimental source: strain PCC 7120
C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ciggocies Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-Jul-2004
C;Accession: Abolis
C;Accession: Abolis
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron A;Accession: Abolis
A;Accession: Abolis
A;Accession: Abolis
A;Accession: DAA
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 12-Jul-2004
C;Accession: C90754
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DAR Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <HAX>
A;Crosa-references: UNIPROT:P36565; UNIPARC:UPI000013A5A1; GB:BA000007; PIDN:BAB34426.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-258 <PAR>
A;Cross-references: UNIPARC:UP1000005A069; GB:AL513382; PIDN:CAD05390.1; PID:916502152;
Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein BCs1003 [imported] - Escherichia coli (strain 0157:H7, substrain
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A;Gene: STY0992
C;Superfamily: conserved hypothetical protein HI1262
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Pred. No. 6.7;
1; Mismatches
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83.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: as17246
A;Genome: plasmid
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N.Alternate names: light-harvesting complex I apoprotein
C.Species: Euglena gracilis
C.Species: Euglena gracilis
C.Species: Euglena gracilis
C.Species: Suglena gracilis
C.Species: Suglena gracilis
C.Species: A: Schantz, R.
Mollow, G.; Schantz, G.; Suglena gracilis: The A; Reference number: S01430
A; Rocession: S01430
A; Rocession: Sold, G.
Mollow, G.; Schantz, G.;
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Matches 5; Conservative
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193 GGFLWN 198
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hypothetical protein memG (imported) - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: D98085
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D98085
A;Accession: D98085
A;Actesion: D98085
A;Residues: 1-277 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q8DNI0; UNIPARC:UPI00000B36DD; GB:AE007317; PIDN:AAL00513.1
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Rifettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heison, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001  
A;Authors: Loftuble, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule: 1-278 <KUR>
A,FCross-references: UNIPROT:Q97NM4; UNIPARC:UPI0000C9CFA; GB:AE005672; PIDN:AAK75966.1
A,Experimental source: strain TIGR4
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69322
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso.; Riklenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
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Pred. No. 28;
0; Mismatches 1; Indels
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Pred. No. 28;
0; Mismatches
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C;Superfamily: maltose transport protein malG
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llarity 83.3%;
Conservative
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Best Local Similarity 83.3%;
---- 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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A;Gene: SP1895
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                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bscherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 12-Jul-2004
C;Accession: G64831
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A,Residues: 1-259 <BLAT>
A;Cross-references: UNIPROT:P36565; UNIPARC:UP1000013A5A1; GB:AE000194; GB:U00096; NID:g
A;Experimental source: strain K-12, substrain MG1655
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A,Residues: 1-259 <STO>
A,Cross-references: UNIPROT:P36565; UNIPARC:UPI000013A5A1; GB:AE005174; NID:g12514089; A,Experimental source: strain 0157:H7, substrain BDL933
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A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein ycbC - Escherichia coli (strain K-12)
C;Species: Bscherichia coli
                                                                                    Length 259;
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F;13-29/Domain: transmembrane #status predicted <TM1>
F;39-55/Domain: transmembrane #status predicted <TM2>
A;Gene: ECs1003
C;Superfamily: conserved hypothetical protein H11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: conserved hypothetical protein H11262
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C;Superfamily: conserved hypothetical protein HI1262
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83.3%; Pred. No. 26;
iive 0; Mismatches
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83.3%; Pred. No. 26;
iive 0; Mismatches
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Las 5; Conserv?
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Search completed: December 30, 2005, 13:34:55 Job time : 9.51613 secs
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AG1979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mannose-6-phosphate isomerase (EC 5.3.1.8) / mannose-1-phosphate guanylyltransferase (GD N;Alternate names: phosphomannose isomerase
N;Alternate names: phosphomannose aeruginosa
C;Species: Beeudomonas aeruginosa
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-Jul-2004
C;Accession: A38598; A25638
R;Shinabarger, D.; Berry, A.; May, T.B.; Rothmel, R.; Fialho, A.; Chakrabarty, A.M.
J; Biol. Chem. 266, 2080-2088, 1991
A;Title: Purification and characterization of phosphomannose isomerase-guanosine diphosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA A;Residues: 1-25, FL', 28-39, LL',41-57, A',59-106,108-114, I',116-358, EV',361-478, A',48 A;Residues: 1-25, FL', 28-39, LL',41-57, A',59-106,108-114, I',116-358, EV',361-478, A',48 A;Cross-references: UNIPARC:UPI0000176197 A;Note: the nucleotide sequence given predicts 26-Leu, 27-Val, 115-Leu, 359-Asp, and 360 C;Superfamily: Helicobacter mannose-6-phosphate isomerase C;Reywords: intramolecular oxidoreductase; isomerase; nucleotidyltransferase
A;Status: preliminary
A;Molecule type: DNA
A;Residuae: 1-481 < SHI>
A;Cross-references: UNIPROT: P07874; UNIPARC: UPI000016FCF0; GB:M14037; NID:g151503; PIDN:
R;Darzins, A.; Frantz, B.; Vanags, R.I.; Chakrabarty, A.M.
R;Darzins, A.; Frantz, B.; Vanags, R.I.; Chakrabarty, A.M.
A;Title: Nucleotide sequence analysis of the phosphomannose isomerase gene (pmi) of Pseu A;Reference number: A25638; MUID:86276004; PMID:3089876
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Pred. No. 49;
0; Mismatches 1; Indels
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A;Accession: A38598
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0; Mismatches
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Best Local Similarity
5; Conserve
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A;Molecule type: DNA
A;Residues: 1-481 «STO»
A;Residues: 1-481 «STO»
A;Residues: 1-481 «STO»
A;Residues: 1-481 «STO»
A;Experimental source: strain PAO1
A;Experimental source: strain PAO1
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: a,JQA; PA3551
C;Superfamily: Helicobacter mannose-6-phosphate isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Nostoc sp. PCC 7120
A; Note: Nostoc sp. PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Accession: AG1979
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, FDNA Res: 9, 205-213, 2001
A; Ttle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A; Reference number: AB1807; MUD:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1001 «KUR»
A;Cross-references: UNIPROT:Q8YX32; UNIPARC:UPI0000CE0A1; GB:BA000019; PIDN:BAB73343.1,
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1386
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Pred. No. 1.18+02;
1; Mismatches 0; Indels
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Pred. No. 49;
0; Mismatches 1; Indels
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.5.
Loca 5; Conservative
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clostridium gluconobact azotobacter pseudomonas pseudomonas

bacteroides nocardia fa chromobacte

salmonella salmonella

salmonella salmonella

escherichia escherichia

Perfect score: Sequence: Scoring table:

Searched:

Database

OM protein

Run on:

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Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1811_TaxID=562;
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MEDLINE-21135136; PubMed=11238967;
Jensen S.O., Reeves P.R.;
"Molecular evolution of the GDP-mannose pathway genes (manB and in Salmonella enterica.").
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in Salmonolla enterica.";

Microbiology 147:599-610(2001).

Microbiology 15. kinase activity; IEA.

Microbiology 15. kinanose-1-phosphate guanylyltransferase (GD. GO:000958).

Microbiology 15. kinanose-1-phosphate guanylyltransferase.

Microbiology 15. kinanose-1-phosphate guanylyltransferase.

Microbiology 16. kinanose-1-phosphate guaneril; 1.

Microbiolo
                      QSfn84
Q4ivk8
Q4kab9
Q880d2
Q880d2
Q5ymi3
Q7nwt8
Q57r07
Q5ggf7
Q8zd28
P36565
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Last annotation update)
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                    OSFN84_GLUOX
Q41X4B9 PSBFS
Q80D2_PSBFS
Q80D2_PSBFS
Q8AD13 MOCFA
Q5YM13 WOCFA
Q5YM13 WOCFA
Q5YM13 WOCFA
Q5YM13 WOCFA
Q5YM13 WOCFA
Q5PGF7 SALCH
Q8ZQB8 SALTY
Q8ZQB8 SALTY
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Q8ZQB8 SALTY
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01-WAR-2001 (TrEMBLrel. 16, La
01-WIN-2003 (TrEMBLrel. 24, La
GDP-mannose pyrophosphorylase.
Name=manC;
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031278 ACEXY PRELIMINARY;
031278;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2003 (TrEMBLrel. 24,
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Q9EXYS ECOLI PRELIMINARY;
Q9EXYS;
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GGYLWN 192
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                                                                                                                                                                        December 30, 2005, 13:11:26 ; Search time 54 Seconds (without alignments) 78.392 Million cell updates/sec
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                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2166443 seqs, 705528306 residues
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Q4KHY9 PSEFS
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LH18 EUGGR
Q4UPI7 XANCP
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Q4PIK9_USTMA
Q6EVV9_USTMA
Q9VA99_DROMB
Q8IMI9_DROMB
Q50R94_DROMB
Q522J8_MAGGR
MSMG_STRMU
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0016828; F:mannose-1-phosphate guanylyltransferase (GD. . .; IEA.
GO; GO:0016779; F:nucleoridyltransferase activity; IEA.
GO; GO:001679; F:nucleoridyltransferase activity; IEA.
GO; GO:0009058; P:injosynthesis; IEA.
GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
GO; GO:0005976; P:polysaccharide metabolism; IEA.
InterPro; IPR00113; Cupin. region.
InterPro; IPR006375; GMP PMI.
InterPro; IPR001538; ManoPP_isomerII.
InterPro; IPR001538; MannosPP_isomerII.
Pfam; PF01050; MannoseP_isomer; 1.
Pfam; PF01050; MannoseP_isomer; 1.
ProDom; PD002664; ManofP_isomerII; 1.
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Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI TaxID=283643;
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Wicke B.L., Fu J., Davis R.W.;

"Cryptococcus neoformans serotype D sequencing.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAEYOLO00015; EAL21837.1; -; Genomic_DNA.

Hypothetical protein.

SEQUENCE 560 AA; 62193 MW, 9BD25DC23AE3B652 CRC64;
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                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 2; Length 492; 100.0%; Pred. No. 65; ive 0; Mismatches 0; Indels
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Bukaryotic translation initiation factor 3 62 kDa subunit,
putative.
                                                                                                                                                                                                                                                           492 AA; 54684 MW; 3ACCC80CBEF4317C CRC64;
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Last annotation update)
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Cryptococcus neoformans var. neoformans JEC21
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13-SEP-2005 (TrEMBLrel. 31, 1
13-SEP-2005 (TrEMBLrel. 31, 1
Hypothetical protein.
ORFNames=CNBC5380;
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QSKKT9_10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
10-MAY-2005 (TrEMBLrel. 30,
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Best Local Similarity
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Q55VE7;
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                                                                                                                                                    MEDILINE=97457201; PubMed=9311139; DOI=10.1016/S0378-1097(97)00358-3;
A Griffin A.M., Poelwick E., Morris V.J., Gasson M.J.;
Cloning of the acef gene encoding the phosphomannose isomerase and
GDP-mannose pyrophosphorylase activities involved in acetan
T biosynthesis in Acetobacter xylinum.";
FRES Microbiol. Lett. 154:389-396(1997).
RES Microbiol. Lett. 154:389-396(1997).
RESS Microbiol. Lett. 154:389-396(1997).
RESS Microbiol. Per Commic DNA.
RO; GO:0008928; P:mannose-1-phosphate guanylyltransferase (GD. .; IEA.
RO; GO:000476; P:mannose-1-phosphate isomerase activity; IEA.
RO; GO:0009103; P:inpopolyaeacharide biosynthesis; IEA.
RO; GO:0009103; P:inpopolyaeacharide metabolism; IEA.
RO; GO:0005976; P:polyaecharide metabolism; IEA.
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Ishida T., Sugano Y., Nakai T., Shoda M.;
"Effects of acetan on production of bacterial cellulose by Acetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BPR2001;
MEDLINE=22145717; PubMed=12150936; DOI=10.1016/S0006-291X(02)00663-0;
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"Novel glycosyltransferase genes involved in the acetan biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
NCBI_TaxID=28448;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mannose-6-phosphate isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Acetobacter xylinum.";
Biochem. Biophys. Res. Commun. 295:230-235(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biosci. Biotechnol. Biochem. 66:1677-1681(2002).
EMBL: AB059427; BAB88842.1; -; Genomic_DNA.
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       Mannose-6-phosphate isomerase (EC 5.3.1.8)
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InterPro; IPR006375; GMP PMI.
InterPro; IPR001538; ManGP isomerII.
InterPro; IPR005835; NTP transferase.
Pfam; PP01050; MannoseP isomer; 1.
Pfam; PF00483; NTP transferase; 1.
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QBRR87;
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Collyn F., Billault A., Mullet C., Simonet M., Marceau M.;
"YAPI, a new Yersinia pseudotuberculosis pathogenicity island.";
Infect. Immun. 72:4784-4790(2004).
EMBL, AJG27388; CAF28494.1; -; Genomic_DNA.
InterPro; IPR007001; Shufflon.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.
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BITTON B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,

BITTON B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,

A At-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,

A Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,

BAUL T., Blitshateyn B., Bloom T., Blye J., Boquslavskiy L.,

BOTOWSKY M., Boukhgalter B., Brunache A., Butler J., Calixte N.,

Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,

Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,

A David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,

Barickson J., Farina A., Faro S., Ferreira P., Fischer H.,

Etickson J., Farina A., Faro S., Ferreira P., Fischer H.,

Etickson J., Farina A., Gage D., Galagan J., Gearin G., Gnerre S.,

Etizgerald M., Foley K., Gage D., Grandbois E., Gyaltsen K., Hafez N.,

Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
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Bukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
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EMBL; AE017343; AAW42248.1; -; Genomic DNA.

GO; GO:0003743; F:translation initiation factor activity; IEA.

GO; GO:000446; P:regulation of translational initiation; IEA.

InterPro; IPR007116; EIF3 gamma.

PF04189; Gcd10p; 1.
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Bukaryota, Fungi, Basidiomycota, Ustilaginomycetes;
Ustilaginomycetidae, Ustilaginales; Ustilaginaceae; Ustilago.
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                                                                                                                                                                        Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome; Initiation factor.
SEQUENCE 560 AA; 62193 MW; 9BD25DC23AE3B652 CRC64;
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Last annotation update)
                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryptococcus neoformans."
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Van Aken S., Fraser C.;
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ORFNames=UM00054.1;
                                                                                      NUCLEOTIDE SEQUENCE.
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                                           NCBI_TaxID=214684;
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RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,

Jaffe D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E.,

RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,

Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,

Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,

RA Lindblad-toh K., Liu X., Macdonald J., Maclean C., Malor J.,

RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,

Morarthy M., Mcdonough S., Mcghee T., Meldrim J., Nemeus L.,

RA Morarthy M., Mcdonough S., Mcghee T., Mikkelsen T., Mlenga V., Moru K.,

RA Moryen N., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,

RA Moryen N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,

Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,

Rottan M., Schupbach R., Seaman C., Setripali S., Sharper T.,

Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,

Rutman M., Schupbach R., Seaman C., Settipali S.,

Retta R., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,

Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,

Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,

Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,

Nonketaraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,

A Wang S., Yang X., Yasger S., Yee E., Young G., Zainoun J., Zembeck L.,

The genome sequence of Ustilago maydis.",

The genome sequence of Ustilago maydis.",

The genome sequence shown here is derived from an

EMBL/Genbank/DbbJ whole genome shotgun (WGS) entry which is

C. Stone C.,

ROWEL S., Wall M., Lander E.,

RUML/Genbank/ObbJ atabases.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 368 AA; 40022 MW; 2B992BBDCFA44362 CRC64;
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28, Last annotation update)
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DOI=10.1128/IAI.70.11.6196-6205.2002;
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Infect. Immun. 70:6196-6205(2002).
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Query Match
Best Local Similarity 83.33,
Best Local Similarity 83.33,
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
                                                                           Gaps
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                                                                                                                                                                                                                                                                                                            Name-CG31028; ORFNames-CG31028;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                             Length 425;
                                                                           Indels
Pfam; PF04917; Shufflon N; 1.
SEQUENCE 425 AA; 45880 MW; 74021D2C2807F57B CRC64;
                                                                                                                                                                                                                                                                                Last annotation update)
                                                                                                                                                                                                                                                                   Last sequence update)
                                           Query Match 92.5%; Score 37; DB 2;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches (
                                                                                                                                                                                                                    PRT; 1097 AA.
                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                01-MAY_2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
CG31028-PA, isoform A.
                                                                                                                                                                                                                Q9VA99_DROME_PRELIMINARY;
Q9VA99;
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                                                                                                                            148 GGYVWN 153
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id FlyBase;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003772; AAF57015.4; -; Genomic_DNA.
REMBL; AE003772; AAF57015.4; -; Genomic_DNA.
REMBL; CG31028; Drosophila melanogaster.
REMBL; POTSOS; 1SRD.
REMBL; CG31028; Drosophila melanogaster.
REMBL; POTSOS; 1SRD.
REMBL; CG31028; CG31028.
REMBLS; FROMOSIO30; CG31028.
REMBLS; FROMOSIO30; CG31028.
REMBLS; FROMOSIO30; CG31028.
REMBLS; FROMOSIO30; CG31028.
REMBLS; FROMOSIOS; Remetal ion binding; IEA.
RG; GG:0016491; Froxidoreductase activity; IEA.
DR GG; GG:0016491; Froxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Raminker J.S., Perise B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
The transposable elements of the Drosophila melanogaster euchromatin:
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith B.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whiffield E.J., Bayraktaroglu L., Berman B.E Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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Last annotation update)
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1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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Name=CG31028; ORFNames=CG31028;
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBIMI9 DROME PRELIMINARY;
QBIMI97
01-MAR-2003 (TrEMBLrel. 23, C1
01-MAR-2003 (TrEMBLrel. 23, L4
01-MAR-2004 (TrEMBLrel. 26, L4
CG31028-PB, isoform B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomics perspective."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         917 GGYVWN 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGYLWN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systematic
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RAW MUCLECTIDE SEQUENCE.

RA Adams M.D., Celniker S. B., Holt R.A., Evans C.A., Gocayne J.D.

RA Adams M.D., Celniker S. B., Holt R.A., Evans C.A., Gocayne J.D.

RA Adams M.D., Celniker S. B., Holt R.A., Evans C.A., Gocayne J.D.

RA Adams M.D., Celniker S. B., Holt R.A., Evans C.A., Gocayne J.D.

RA Adams M.D., Celniker S. B., Holt R.A., Evans C.A., Galle R.F.,

Gocaye R.A., Lewis S. B., Richards S., Ashburner M., Henderson S.N.,

RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Chang Q., Chen L.X.,

RA Barlow R.M., Basu A., Barellan B.D., Bayraktaroglu L., Beasley B.M.,

RA Ballew R.M., Basu A., Barellan B.D., Bhandari D., Bolahakov S.,

Ra Barkova D., Botchan M.R., Bouck J., Broketein D., Bolahakov S.,

RA Berkova D., Botchan M.R., Bouck J., Broketein D., Bolahakov S.,

RA Burtis K.C., Buaman D.A., Buller H., Cadieu E., Center A., Candra I.,

RA Berkova D., Botchan M.R., Bouck J., Broketein D., Bolahakov S.,

RA Burtis K.C., Buaman D.A., Bahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Ge Pablos B., Delcher A., Dening S., Gelbart W.M., Glasser K.,

RA Gooff F., Goorf F., Gorrell J.H., Gu Z., Kennica S., Dunkov B.C.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Hocken M.,

Randel B.E., Kodiar C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Rander P., Matter B., McInton K.A., Nusoker B., McBerson D.,

Rander S.M., Woodage T., Simpson M., Strong R., Waller R., Waller R., Walle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426065; PubMed=12537568; Celniker S.E., Mheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Celniker S.E., Maesler D.A., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleron M., Sutron G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Fribse E., Whoeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22426069; PubMed=12537572;
Migra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426070; PubMed=12537573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000).
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Gaps
                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
Celniker S.,
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BT011091, ARR2757.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl; GG31028; Drosophila melanogaster.
Flyasae; FBgn051028; GG31028.
GG; GG:0016209; F:antioxidant activity; IEA.
GG; GG:0004785; F:copper, zinc superoxide dismutase activity; IEA.
GG; GG:00164912; F:metal ion binding; IEA.
GG; GG:0016491; F:oxidoreductase activity; IEA.
GG; GG:0016491; F:superoxide metabolism; IEA.
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GO; GO:0020037; F:heme binding; IEA.
GO; GO:0066872; F:metal ion binding; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006801; P:superoxide metabolism; IEA.
InterPro; IPR012282; Cytochrome c.R.
InterPro; IPR01424; SOD_CU_ZN.
                                                               "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota, Metezoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 2; Length 1109;
Pred. No. 5.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subjitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AE003772; AAN14221.1; -; Genomic_DNA. HSSP; P07505; 1SRD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124552 MW; 5D020EF2910000A6 CRC64;
                                                                                                                                                                                                                                                                                                                   Yu C., Rubin G.;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                             Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QENP40 DROME PRELIMINARY;
QENP40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00080; Sod Cu; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 83.3
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RE50384p (Fragment).
Name=CG31028;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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929 GGYVWN 934
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                                                                                                                                                                                                                                                                                        Hoskins R., Sta
Yu C., Rubin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,

Ant-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,

Radoul T., Blitchistern B., Brunache A., Baidavin J., Barry A.,

Bayul T., Blitchistern B., Brunache A., Baidarsekiy L.,

Rocowsky, M., Boukhaglater B., Brunache A., Baidarsekiy L.,

Radovo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,

Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,

Radovo R., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,

Bayul T., Borris. L., Duffero N., Dudges A., Bikins T., Engels R.,

Britgerald M., Poley K., Gage D., Galagan J., Gearin G., Gnerre S.,

Radopian D., Hagos B., Hall J., Hatcher B., Halber A., Haigins H.,

Radopian D., Hagos B., Hall J., Hatcher B., Haller A., Haigins H.,

Radopian D., Landers B., Hall J., Marchen S., Lewis D., Lewis T.,

Lundhad-took K., Liu X., Lokytsang T., Lokytseng E., Labutti K.,

Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,

Morachty M., Mcdonough S., Mcdher T., Mikkelsen T., Minera V.,

Maning J., Marabella R., Maru K., Matchews C., Mauceli E.,

Morachty M., Mcdonough S., Mcdher T., Mikkelsen T., Minera V.,

Mores J., Minhatan L., Minkova T., Mikkelsen T., Minera V.,

Radove J., Minhatan L., Minkova T., Mikkelsen T., Minera T.,

Roce J., Minhatan L., Minkova T., Mikkelsen T., Rederson S.,

Roce J., Minhatan L., Minkova C., Settipalis S.,

Rochon N., O'donnell P., Okoawo O., O'leary S., Retta R., Richardson S., Rise C., Rodriguez J., Rogers V., Rogers S.,

Roce J., Minhatan L., Minkova T., Mikkelsen T., Reders T.,

Retta R., Richardson S., Rise C., Settipalis S.,

Retta R., Richardson S., Rise C., Rottipalis S.,

Retten R., Stalker J., Samaen C., Settipalis S.,

Retson K., Stone C., Stone S., Smith C., Sougnes S.,

Resoner B., Stalker J., Samer S., Yenger S.,

Retton K., Stone C., Stone S., Smith C., Wang S., Wang S., Yang S., Yang X., Yang S., Yang S., Yang X., Yang S., Yang S., Yang
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                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
                                                                                                                        92.5%; Score 37; DB 2; Length 1199; 83.3%; Pred. No. 5.7e+02;
                                                                                                                                                                                0; Indels
                                                             SEQUENCE 1199 AA; 134574 MW; 55E0A00A85DA0FCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence of Magnaporthe grisea.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=70-15;
Dean R., Mitchell T., Brown D., Pan H., Thon M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1279 AA.
                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0522J8 MAGGR PRELIMINARY;
0522J8;
Pfam; PF00080; Sod_Cu; 1.
                                                                                                                                                    Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Magnaporthe grisea 70-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
ORFNames=MG04852.4;
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962 GGYVWN 967
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                                                                                                                                                                                                                                              1 GGYLWN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=70-15;
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
0922J8 MAGGR
0922J8 MAGGR
DT 13-SEP-2
DT 13-
                                                                                                                        Query Match
                                  NON TER
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Proc. Natl., Acad. Sci. U.S.A. 99:14434-14439(2002).
-!- FUNCTION: Involved in a binding protein-dependent transport system
responsible for the uptake of melibiose, raffinose and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Russell R.R.B., Aduse-Opoku J., Sutcliffe I.C., Tao L., Ferretti J.J.; "A binding protein-dependent transport system in Streptococcus mutans responsible for multiple sugar metabolism."; J. Biol. Chem. 267:4631-4637(1992).
                                                                                                                               preliminary data.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the cation transport ATPase (P-type)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: Belongs to the binding-protein-dependent transport system permease family. MalFG subfamily. SIMILARITY: Contains 1 ABC transmembrane type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=UA159 / ATCC 700610 / Serotype c;
MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
MADLINE=2295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Adic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
Ferretti J.J.;
                                                                                                                                                                                                                                                                                                                                                            TIGRPAMs; TIGRO1652; ATPase-Plipid; 1.
TIGRPAMs; TIGRO1494; ATPase P- type; 2.
PROSITE; PS00114; ATPASE ELEZ; UNKNOWN 1.
ATP-binding; Hydrolase; Hypothetical protein; Nucleotide-binding;
                                        Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-07N-1994 (Rel. 29, Created)
01-07N-1994 (Rel. 29, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Multiple sugar-binding transport system permease protein msmG.
Name=msmG; OrderedLocusNames=SMU.880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.5%; Score 37; DB 2; Length 1279; 83.3%; Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1279 AA; 143438 MW; 1A3E021D4AA1E99C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                          EMBL; AACU01000757; EAA52160.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                             InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR005834; Dehal_like_hydro.
InterPro; IPR006539; Flippase.
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MEDLINE=92165821; PubMed=1537846;
                                                                                                                                                                                                                                                                                                               Pfam; PF00702; Hydrolase; 1
PRINTS; PR00119; CATATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane.
                     STRAIN=70-15
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NUCLEOTIDE
                                                                                                                                                                                                     family
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MSMG_STRMU
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Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
Butkgalter B., Butler J., Calvo S.B., Camarata J., Chang J.,
Buckgalter B., Butler J., Calvo S.B., Camarata J., Chang J.,
Choepel Y., Collymore A., Cooke P., Corum B., DeArellano K.,
Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
Erickson J., Farco S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
Andria S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
Andrie D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
Andrie C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
Andriva T., Machon C., Macdonald P., Major J., Manning J.,
Minhova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
Anielsen C.B., Norbu C., O'Connor T., O'Donnell B., O'Neil D.,
Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
Andre B.,
Andr
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=211594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.0%; Score 36; DB 2; Length 370; 83.3%; Pred. No. 2.6e+02;
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Submitted (APR-203) to the EMBL/GenBank/DDBJ databases.
EMBL; AY279078, AAQ84559.1; -; Genonic DNA.
GO; GO:0016853; F:isomerase activity; TEA.
                                                                                                                                     Gibberella zeae PH-1.
Rukaryota, Fugli, Ascomycota, Pezizomycotina, Sordariom, Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella (CEI_TaxID=229533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Fusarium graminearum genome sequence.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AACM01000045; EAA67712.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 370 AA; 41068 MW; 32B07413C046F7D4 CRC64;
                                              Last sequence update)
Last annotation update)
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                        Created)
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                                              (TrEMBLrel. (TrEMBLrel.
                        (TrEMBLrel.
                   13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
Hypothetical protein.
ORFNames-PG00935.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
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                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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269 GGFLWN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                   STRAIN=PH-1;
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                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the ENED outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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X PubMed=15980861; DOI=10.1038/nbt1110;

RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,

RA Mavrodi D., DeBOY R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,

RA Mavrodi D., DeBOY R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,

RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,

RA Khouri H.M., Pierson B., Pierson I. III, Thomashow I., Loper J.;

RY "Complete genome sequence of the plant commensal Pseudomonas

RT fluorescens Pf-5.";

RL Nat. Biotechnol. 23:873-878(2005).

DR EMBL; CP000076; AAY93862.1; -; Genomic DNA.

SROUENCE 281 AA; 30668 MW; B2EF2A84BAZE4D5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugar ABC transporter, permease protein.
ORFNames=PFL 4615;
Pseudomonas fluorescens (strain Pf-5).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                   Pfam; PF00528; BPD transp 1; 1.
PROSITE; PS50928; ABC_TM1; 1.
Complete proteome; Membrane; Sugar transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 277;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                            Potential.
Potential.
Potential.
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Potential.
ABC transmembrane type-1.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2;
Pred. No. 2e+02;
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                                                                                                                                                           EMBL; M77351; AAA26936.1; -; Genomic DNA.
EMBL; AE014929; AAN58595.1; -; Genomīc_DNA.
PIR; D42400; D42400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                InterPro; IPR000515; BPD_transp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         141
198
243
69
277 AA;
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Best Local Similarity
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RESULT 13

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Gaps

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0; Indels

RESULT 14

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Gaps
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                                                                           Query Match 90.0%; Score 36; DB 2; Length 430; Best Local Similarity 83.3%; Pred. No. 3.1e+02; Matches 5; Conservative 0; Mismatches 1; Indels
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189 GGYFWN 194
                                                                                            1 GGYLWN 6
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Search completed: December 30, 2005, 13:33:29 Job time : 57 secs

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LENGTH: 480
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Sequence 12462, A
Sequence 3, Appli
Sequence 3, Appli
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Sequence 12128, A
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Sequence 48720, A
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                             December 30, 2005, 13:14:26; Search time 13.4516 Seconds (without alignments) 36.877 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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1: /cgn2_6/ptodata/1/laa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/f_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          - protein search, using sw model
                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                             US-10-735-916A-8
40
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Match Length
                                                                                                                                    1 GGYLWN 6
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Perfect score:
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Sequence 12126, Application US/09489039A

Fatent No. 6610836

Fatent No. 6610836

Taria Orivina Cary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-2004601

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

FRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12128

LENGTH: 275

TYPE: PRT

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12128
                                                                                                                                                                                                                                                                                                            Sequence 19202, Application US/09252991A
Sequence 19202, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196,136
CURRENT FILING DATE: 1999-02-18
RIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
RIOR PAPLICATION NUMBER: US 60/094,190
RIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19202
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                                                                                                          46, Appl
48, Appl
46, Appl
48, Appl
4315, Ap
126, App
                                                                                                                                                                                      Sequence 5821, Ap
Sequence 7919, Ap
Sequence 199, App
                                   Sequence 1335,
Sequence 3067,
Sequence 2966,
Sequence 3549,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                 Sequence Sequence Sequence Sequence Sequence Sequence
                                                                                                                                              Sequence 4
Sequence 4
Sequence 1
             Sequence
                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
       Score 36; DB 2;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 GGFLWN 199
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US-09-252-991A-19202
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FOR DIAGN

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Sequence 17547, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                         Sequence 4262, Application US/09107433

Patent No. 6800744

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 290;
                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.5%; Score 35; DB 2; I ilarity 83.3%; Pred. No. 1.1e+02; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
APPLICATION NUMBER: 60/05153
APPLICATION NUMBER: 60/05153
APPLICATION NUMBER: 60/05153
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...290
; SEQUENCE DESCRIPTION: SEQ ID NO: 4262:
US-09-107-433-4262
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4262: SEQUENCE CHARACTERISTICS: LENGTH: 290 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
leg 5; Conserv
67 GGYYWN 72
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                                                         RESULT 5
US-09-107-433-4262
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Matches
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APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOU-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-12
PRIOR PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2944
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83.3%; Pred. No. 1.1e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35, DB 2; Length 278;
Pred. No. 1.16+02;
0; Mismatches 1; Indels
                   Score 35; DB 2; Length 275; Pred. No. 1.1e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-583-110-2944, Application US/09583110; Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Streptococcus pneumoniae US-09-769-787-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Streptococcus pneumoniae US-09-583-110-2944
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                     87.5%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
                     Query Match 87.5
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                       103 GGYTWN 108
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US-09-769-787-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ellingson, Jay L.E.
APPLICANT: Stabel, Judith R.
TITLE OF INVENTION: Species-Specific Genetic Identification
TITLE OF INVENTION: of Mycobacterium Paratuberculosis
UNDBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   DB 1; Length 144;
85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.0%; Score 34; DB 2; Length 144; 100.0%; Pred. No. 85; tive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC Compatible
OPERATIONS SYSTEM: PC-COMPATION
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/440,833
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/108,051
FILING DATE:
APPLICATION NUMBER: 09/108,051
FILING DATE:
APPLICATION NUMBER: 09/108,051
FILING DATE:
APPLICATION NUMBER: 27,976
REGISTRATION NUMBER: 27,976
REGISTRATION NUMBER: 27,976
TELEPHONE: 309/681-6513
TELEPHONE: 309/681-6513
                                                                                                                                                                                                                                                                                                                                     85.0%; Score 34; DB 100.0%; Pred. No. 85; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Curtis P. Ribando
STREBT: 1815 N. University Street
CITY: Peoria
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RIDANDO, CULTIS P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0229
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309/681-6513
FELEPAX: 309/681-658
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
1S-09-440-833-2
'Sequence 2, Application US/09440833
; Patent No. 6277580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 5; Conservative
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LENGTH: 144 amino act
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                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-108-051-2
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Patent No. 6573910

GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT PILING DATE: 2000-04-04
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APPLICANT: Ellingson, Jay L.E.
APPLICANT: Stabel, Judith R.
TITLE OF INVENTION: Species-Specific Genetic Identification
TITLE OF INVENTION: of Mycobacterium Paratuberculosis
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: Curtis P. Ribando
STREET: 1815 N. University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.5%; Score 35; DB 2; Length 739;
83.3%; Pred. No. 2.8e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                       Length 550;
                                                                                                                                                                                                                                     Score 35; DB 2; Length sur
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                               0; Mismatches
       CURRENT APPLICATION NUMBER: US/09/252,991A
                       CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09108051; Patent No. 5985576; GENERAL INFORMATION:
                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: M.catarrhalis
US-09-540-236-3594
                                                                                                                                                                                                                                                                                                                                                                         257 GGYYWN 262
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CITY: Peoria
STATE: IL
COUNTRY: US
                                                                                                                                                                                                                   US-09-252-991A-17547
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LENGTH: 739
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US-09-108-051-2
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Sequence 12893, Application US/09489039A
; Sequence 12893, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: GATY BRECON et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUMBER: POR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: NUMBER: 105/9/489, 039A
; CURRENT APPLICATION NUMBER: US 60/117,747
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR APPLICATION NUMBER: US 60/117,747
; SEQ ID NO 12893
; SEQ ID NO 12893
; TYPE: PRT
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12893
                                           APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9700
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Faquence No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILIG DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62217

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                    85.0%; Score 34; DB 2; Length 326; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9700
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Best Local Similarity 100.*
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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Patent No. 6610836
GENERAL INFORMATION:
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LENGTH: 349
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                                                                                                                                                                       Sequence 13, Application US/08913159

Fatent No. 6300109

Fatent No. 6300109

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
NUMBER OF SEQUENCES: 14

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATE:

RELING DATE:

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7439, Application US/09328352
Sequence 7439, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PAILICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7439
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; Sequence 9700, Application US/09489039A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Acinetobacter baumannii
US-09-328-352-7439
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amino acid
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Best Local Similarity
Matches 5; Conserv
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US-09-328-352-7439
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US-09-949-016-6846

i Sequence 6846, Application US/09949016

j Patent No. 6812339

j GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-00-01-14

PRIOR PELICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 6846

LENGTH: 609

TYPE: PRT

CORGANISM: Human
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Query Match 85.0%; Score 34; DB 2; Length 516; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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CCATION: (1)...(609)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-949-016-6846
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Search completed: December 30, 2005, 13:37:18 Job time : 14.4516 secs

2 GYLWN 6 ||||| 294 GYLWN 298

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3858, Ap 7378, Ap 257904, 32069, A 163133, 284834,

Sequence Sequence 5 Sequence

293, App 364926, 259100,

Sequence 3 Sequence 5 Sequence 5

4772, Ap 328910,

Sequence Sequence 270959, 141746, 152064,

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Sequence:

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Result

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Sequence 8, Application US/10735916A

Sequence 8, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GORYAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: EBCEK, Alain

APPLICANT: BECK, Alain

APPLICANT: BECK, Alain

APPLICANT: BECK, Alain

APPLICANT: DECK, Alain

STILE REFERENCE: 017753-183

TITLE OF INVERTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

TITLE OF INVERTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

TITLE OF INVERTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

TITLE OF INVERTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

TITLE OF INVERTION: NUMBER: PR 03/08 538

PRIOR APPLICATION NUMBER: PR 03/08 538

PRIOR PELING DATE: 2003-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PELING DATE: 2002-01-18
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            US-10-425-115-336772
US-10-106-698-4772
US-10-425-115-328910
US-10-424-599-270959
US-10-437-963-141746
US-10-437-963-152064
US-10-074-024-293
US-10-074-15-364926
US-10-424-599-259100
US-11-097-143-3858
US-10-97-143-3858
US-10-424-599-15313
US-10-424-599-163133
US-10-425-115-284834
US-10-425-115-3689
US-10-425-115-3689
US-10-425-115-368134
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US-10-767-701-51631
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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: Mus musculus
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Matches 6
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Sequence 75, Appl
Sequence 83, Appl
Sequence 82, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 82, Appl
Sequence 3242, Ap
Sequence 3009, Ap
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Sequence 414, App
Sequence 19203,
Sequence 137, App
Sequence 137, App
Sequence 137, App
Sequence 16, Appl
Sequence 16, Appl
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3940, Ap
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Sequence 201562,
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                                                                                                              December 30, 2005, 13:33:42; Search time 44.6129 Seconds (without alignments) 56.194 Million cell updates/sec
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cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-425-115-201562
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US-10-735-916A-83
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US-10-735-916A-81
US-10-735-917-37
US-10-453-698-137
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Sequence 79, Application US/10735916A

Sequence 79, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: EBCEK, Alain
APPLICANT: BECK, Alain
APPLICANT: BOONE ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
CURRENT FILING DATE: 2003-10-16
PRIOR PELING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR PELING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR APPLICATION NUMBER: PR 02/05 753
PRIOR PR 02/05 753
                                                                                    ## APPLICANT: Unito, Apain

## APPLICANT: BECK, Alain

## APPLICANT: BECK, Alain

## APPLICANT: HAEUW, Jean-Francois

## TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

## TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

## TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

## CURRENT APPLICATION WHERE: US/10/735,916A

## CURRENT FILING DATE: 2003-12-16

## PRIOR PILING DATE: 2003-01-20

## PRIOR PILING DATE: 2003-01-18

## PRIOR PILING DATE: 2002-01-18

## PRIOR APPLICATION NUMBER: FR 02/06 55

## PRIOR PILING DATE: 2002-01-18

## PRIOR PILING DATE: 2003-01-18

## PRIOR PILING DATE: 2003-01-
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                                                                               DUFLOS, Alain
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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US-10-735-916A-79
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                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: 18-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 87
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APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01773-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: R 02/08 538
PRIOR FILING DATE: 2003-01-11
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 4; Length 87; 100.0%; Pred. No. 18; o; Mismatches 0; Indels
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US-10-425-115-201562
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US-10-735-916A-69
; Sequence 69, Application US/10735916A
; Publication No. US20050084906A1
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APPLICANT: GOETSCH, Liliane APPLICANT: CORVAIA, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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US-10-735-916A-75
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 77
LENGTH: 135
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                    TYPE: PRT
ORGANISM: Mus musculus
US-10-735-916A-52
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ORGANISM: Homo sapiens
US-10-735-916A-77
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41 GGYLWN 46
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    SEQ ID NO 52
LENGTH: 127
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APPLICANT: GORIAGA, Liliane
APPLICANT: CORVALA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT PILING DATE: 2003-12-16
FRIOR PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
FRIOR PILING DATE: 2003-07-11
FRIOR PILING DATE: 2003-07-11
FRIOR PILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR PILING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 02/05 553
FRIOR PILING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 02/05 553
FRIOR FILING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 02/05 553
FRIOR FILING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 02/05 753
FRIOR FILING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 02/05 753
FRIOR FILING DATE: 2002-05-07
FRIOR FILING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 02/05 753
FRIOR FILING DATE: 2002-05-07
FRIOR APPLICATION NUMBER: FR 02/05 753
FRIOR FILING DATE: 2002-05-07
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Sequence 52, Application US/10735916A

Publication No. US20050084906A1

Sequence 52, Application US/10735916A

Publication No. US20050084906A1

GRNERAL INFORMATION:

APPLICANT: CORVAIA, Nathalie

APPLICANT: BGER, Olivier

APPLICANT: BGER, Alain

APPLICANT: BGER, Alain

APPLICANT: BEEK, Alain

APPLICANT: BEEK, Alain

APPLICANT: HAGUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

FRIOR APPLICATION NUMBER: PR 03/08 538

PRIOR PILING DATE: 2003-01-16

PRIOR FILING DATE: 2003-01-20

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR APPLICATION NUMBER: FR 02/05 753

PRIOR FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 02/05 753

PRIOR APPLICATION NUMBER: FR 02/05 753
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                                                                                                                                                                                               US-10-735-916A-83
Sequence 83, Application US/10735916A
Publication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
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31 GGYLWN 36
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871 GGYVWN 876
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ORGANISM: DROSOPHILA
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US-11-097-143-3009
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Best Local S
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Sequence 85, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GORYACHA, Nathalie
APPLICANT: USGER, Olivier
APPLICANT: UBGER, Olivier
APPLICANT: HEGER, Olivier
APPLICANT: HEGER, Olivier
APPLICANT: HEGER, Olivier
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 81
LENGTH: 135
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-735-916A-81
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US-10-320-797-3242
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Sequence 232932, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Roba Thomas J
APPLICANT: Exoral thomas J
APPLICANT: About thus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 232932
LENGTH: 75
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Publication No. US20030129601A1
GENERAL INFORMATION:
APPLICATION NO. US20030129601A1
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATHENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.018
FILE REFERENCE: 03495.0218
FULCRENT APPLICATION NUMBER: US/10/080,170
CURRENT PILING DATE: 2002-06-10
PRIOR PILING DATE: 2002-06-10
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 65-2
SOFTWARE: PATCHIN Ver. 2.1
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_52362C.1.pep
US-10-424-599-232932
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83.3%; Pred. No. 1.38+02;
ative 1; Mismatches 0
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Publication No. US20040121322A9
GENERAL INFORMATION:
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Best Local Similarity 83.3'
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Glycine max
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8 GGYLWS 13
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US-10-424-599-232932
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LENGTH: 83
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EXECUT. 1012-353-8

1 Sequence 8, Application US/11012353

2 Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GOCTORYLA, LILIANE
APPLICANT: GOCTORYLA, NATHALIB
APPLICANT: DUFLOS, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-OLISS THEREOF
FILE REFREENCE: 01733-198

CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2003-12-16
PRIOR PLILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PARCHAIN VET. 3.3
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1546, Ap
1607, Ap
34, Appl
2234, Ap
                                     3386, Ay
8, Appl
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                      US-10-467-677-338

US-10-892-379-8

US-10-892-379-8

US-11-054-515-1546

US-11-054-515-1607

US-10-512-184-71

US-10-67-657-234

US-10-67-657-624

US-10-67-657-624

US-10-67-657-624

US-10-67-697-318

US-10-67-697-318

US-10-67-697-318

US-10-97-98-64

US-10-97-98-64

US-11-082-386-64

US-11-075-185-5

US-11-075-185-5

US-11-075-087-950

US-11-075-087-950

US-11-075-087-950

US-11-075-087-950

US-11-075-087-950

US-11-075-087-950
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SEQ ID NO 8
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434, App
36, Appl
39, Appl
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55, Appl
1619, Ap
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                                                                                                                                                                                                                                   December 30, 2005, 13:35:07 ; Search time 2.22581 Seconds (without alignments) 20.187 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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8: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-012-353-69

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US-11-012-353-81

US-11-012-353-81

US-11-012-353-81

US-11-02-353-81

US-11-02-353-81

US-11-02-353-81

US-11-082-140-34

US-10-821-234-126

US-10-821-234-126

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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Result No.

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Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-11-012-353-75
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                LENGTH: 117
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Sequence 75, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GORTSCH, LILIANE

APPLICANT: GORTSCH, LILIANE

APPLICANT: OCNVAIA, NATHALIB

APPLICANT: DUFLOS, ALAIN

APPLICANT: HACUW, JEAN-FRANCOIS

APPLICANT: HACUW, JEAN-FRANCOIS

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGP-I HYBRID

TITLE OF INVENTION: NOVER ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NOVER ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NOVER ANTIBODIES AND USES THEREOF

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2002-01-20

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

SOFTWARE: PATCHIN VONSER: FR 0200654

PRIOR PILING DATE: 2002-01-18

SOFTWARE: PATCHIN VONS: 162

SOFTWARE: PATCHIN VONS: 162

SOFTWARE: PATCHIN VONS: 162
GENERAL INFORMATION:
APPLICANT: OOBTICAL
APPLICANT: OOBTICAL
APPLICANT: CORVAIA, INITIALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR PELING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR APPLICATION NUMBER: FR 0206573
PRIOR APPLICATION NUMBER: FR 0206573
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR APPLICATION NUMBER: PR 0200653
PRIOR APPLICATION NUMBER: PR 0200654
PRIOR APPLICATION NUMBER: PR 0200653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Mus musculus
US-11-012-353-69
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US-11-012-333-79

i Sequence 79, Application US/11012353

i Publication No. US20050249730A1

i Sequence 79, Application US/11012353

i Publication No. US20050249730A1

i GENERAL INFORMATION:

APPLICANT: GORVAIA, NATHALIE

APPLICANT: LEGER, OLIVIER

APPLICANT: LOWEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

ITILE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PLING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-01-20

PRIOR PLING DATE: 2003-01-20

PRIOR PLING DATE: 2003-01-20

PRIOR PLING DATE: 2002-01-18

SOFTWARE: PARCHET: VELING DATE: 2002-01-18

SEMPLIANT: LING DATE: 2002-01-18

SERVING PLING DATE: 2002
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US-11-012-353-83
US-11-012-353-83
Sequence 83, Application US/11012353
Sequence 83, Application No. US20050249730A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OGETSCH, LILIANE
APPLICANT: DUFLOS, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
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Best Local Similarity 100.0%; Pred. No. 0.67; Length 117;
Matches 6; Conservative 0; Mismatches 0; Indels
100.0%; Score 40; DB 7; Length 117; 100.0%; Pred. No. 0.67;
                                                                                                   0; Indels
                                                                                                   0; Mismatches
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GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: COCVAIA, NATHALIE
APPLICANT: COCVAIA, NATHALIE
APPLICANT: OFFICANT: DIFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANTION: RECEPTORS ANTI-INSULIN/IGF-I HYBRID
ITILE OF INVENTION: RECEPTORS ANTI-INSULIN/IGF-I HYBRID
ITILE OF INVENTION: RECEPTORS ANTI-INSULIN/IGF-I HYBRID
ITILE OF INVENTION: RECEPTORS ANTI-INSULIN/IGF-I HYBRID
FRICH TILING DATE: 2003-01-16
FRICH APPLICATION NUMBER: FR 020553
FRICH RILING DATE: 2003-07-11
FRICH APPLICATION NUMBER: FR 020553
FRICH RILING DATE: 2002-01-18
FRICH APPLICATION NUMBER: FR 0200554
FRICH RILING DATE: 2002-01-18
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Sequence 81, Application US/11012353

Publication No. US20050249730A1

Sequence 81, Application US/11012353

Publication No. US20050249730A1

APPLICANT: GORVALAN

APPLICANT: CORVALAN

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: HAEUW, JEAN-FRANCOIS

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 101753-196

FRIOR FILING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR APPLICATION NUMBER: PCT/FR03/00178

PRIOR APPLICATION NUMBER: PR 0205-73

PRIOR APPLICATION NUMBER: PR 0205-73

PRIOR APPLICATION NUMBER: PR 0205-73

PRIOR PLING DATE: 2003-07-07

PRIOR APPLICATION NUMBER: PR 0205-53
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100.0%; Score 40; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                      US-11-012-353-77; Sequence 77, Application US/11012353; Publication No. US20050249730A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-77
    41 GGYLWN 46
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| Sequence 52, Application US/11012353
| Publication No. US20050249730A1
| GENERAL INFORMATION:
| APPLICANT: GOETSCH, LILIANE
| APPLICANT: CORVAIA: NATHALIE
| APPLICANT: DUFLOS, ALAIN
| APPLICANT: LEGER, OLIVIER
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR APPLICATION NUMBER: US/11/012,353
| CURRENT FILING DATE: 2004-12-16
| PRIOR PILING DATE: 2003-12-16
| PRIOR PLING DATE: 2003-01-20
| PRIOR PLING DATE: 2003-01-20
| PRIOR PLING DATE: 2002-01-18
| PRIOR PLING DATE: 2003-01-18
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                 CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-12-16
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-12
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-01-18
SEQ ID NO 83
LENGTH: 117
CURRENT APPLICATION NUMBER: US/11/012,353
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Best Local Similarity 100.
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US-11-012-353-83
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; ORGANISM: Mus musculus
US-11-012-353-52
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US-11-092-140-34
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APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
ITILE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
ITILE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
ITILE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
ITILE OF INVENTION: APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR APPLICATION NUMBER: PR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2003-01-18
PRIOR APPLICATION NUMBER: FR 020653
PRIOR APPLICATION NUMBER: FR 020654
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2003-01-18
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                                                                                                                                                                                                                                                                                                                            100.0%; Score 40; DB 7; Length 135; 100.0%; Pred. No. 0.75; cive 0; Mismatches 0; Indels
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Publication No. US20050276814A1
GENERAL INPORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION WUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 81
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 85, Application US/11012353 Publication No. US20050249730A1
                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-11-012-353-81
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RESULT 11

US-11-092-140-34

US-11-092-140-34

Sequence 34, Application US/11092140

Publication No. US20050262590A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SUbramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y.

TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthe:

CURRENT APPLICATION NUMBER: US/11/092,140

CURRENT PILING DATE: 2005-03-29

PRIOR APPLICATION NUMBER: US/09/688,069

PRIOR PILING DATE: 2000-10-14

NUMBER OF SEQ ID NOS: 114

SEQ ID NO 34

LENGTH: 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1289, Application US/10821234
; Sequence 1289, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan,
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Andarmani, Susan
; TITLE OF INVENTION: Wethods for Diagnosis and Treatment of Preeclampsia
; TITLE OF INVENTION: WETHOR for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT FILING DATE: 2004-04-07
; PRIOR FILING DATE: 2004-04-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PLE SEQ genes Version 1.0
; SEQ ID NO 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 6; Length 278;
Pred. No. 10;
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TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/10/873,528
CURRENT FILING DATE: 2004-06-23
FRIOR APPLICATION NUMBER: US/09/769,787
PRIOR FILING DATE: 1001-01-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SEQ ID NO 19
LENGTHARE: PATENTIN Ver. 2.1
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Streptococcus pneumoniae
US-10-873-528-19
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Sequence 3278, Application US/10467657
; Sequence 3278, Application US/10467657
; Publication No. US200820260581A1
; GENERAL INFORMATION:
APPLICANT: CHIRON SpA
; APPLICANT: PIZZA MARIAGRAZIA
APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; APPLICANT: MONACI Elisabetta
; TILLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SCOTWARE: SeqWin99, version 1.04
; SEQ ID NO 3278
; LENGTH: 1032
; TWODE: PILING
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                         0; Indels
  Pred. No. 97;
1; Mismatches
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3278
  80.08;
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Best Local Similarity 80.0
Matches 4; Conservative
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| Publication No. US20502551441
| GENERAL INFORMATION NO. US200502551441
| GENERAL INFORMATION NO. US200502551441
| GENERAL INFORMATION NO. US200502551441
| APPLICANT: Stache-Crain, Birgit
| APPLICANT: Andarmani, Susan
| APPLICANT: Tang, Y. Tom
| TITLE OF INTENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INTENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INTENTION: Worthous No. 1004-04-07
| FILE REPERENCE: 821A
| CURRENT FILING DATE: 2003-04-07
| PRIOR APPLICATION NUMBER: US 60/462,047
| PRIOR PILING DATE: 2003-04-07
| NUMBER OF SEQ ID NOS: 1704
| SEQ ID NO 908-
| SEQ ID NO 908-
| LENGTH: 1029
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Pred. No. 34;
1; Mismatches 0; Indels
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Pred. No. 86;
1; Mismatches 0; Indels
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APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129W0
CURRENT APPLICATION WUMBER: US/09/769,787
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR STLING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
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Publication No. US20050276814A1
GENERAL INFORMATION:
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                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1289
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; ORGANISM: Homo sapiens
US-10-821-234-908
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US-10-821-234-908
LENGTH: 289
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or receptor (EGFR) and/or with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies that bind to human insulin-like useful for treatment, prevention and diagnosis
                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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AAR66826
AAX3848
AAX90100
AAX50634
AAX506372
AAB77005
AAB77005
ABP67968
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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WO2003059951-A2
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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Perfect :
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growth factor receptor, of cancers.

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hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
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                                                                                                                                                                                   100.0%; Score 40; DB 7; Length 6; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duflos A, Haeuw J,
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                                                                                                                                                                                                                                                                                                                                                                        ADZ67012 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-2003; 2003US-00735916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
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                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-321968/33.
N-PSDB; ADZ67011.
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CORVAIA N.
LEGER O.
                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       1 GGYLWN 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAEUW J.
                                                                                                                                                                                                                                                                          GGYLWN
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                                                                                                                                                       Sequence 6 AA;
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ADZ67012
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specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADD57006 and ADD57014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF IR and/or EGFR, and/or connected with an overexpression and/or an abnormal continuous secondary effects and/or EGFR, and/or connected with a administration of the transduction pathway of the signal mediated by the interaction of the transformation of normal cells into cells with tumoral receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral consideration of a medicament intended to inhibit the growth and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent cells, preferably IGF-dependent and/or IGF-dependent and/or IGF-dependent and/or EGF-dependent and/or EGF-dependent cells. (I) is useful in the preparation of a medicament intended for intended for prevention or for the treatment of cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, creatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention or for the prevention or for the creatment of psoriasis. (I) is useful in preparation of a medicament intended for the prevention or an underexpression of the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor is suspected, which involves contacting from a biological sample in which the abnormal present of IGF-IR and/or EGFR receptor is equenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MITK ) MITSUI TOATSU CHEM INC. (EDUC-) EDUCATIONAL FOUND FUJITA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR05974 standard; protein; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ichihara Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9006998-A.
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9 9 (first entry)

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Novel bispecific antibody substituting for function of cofactor that enhances enzyme reaction, and recognizing both enzyme and substrates of enzyme, useful for treating hemophilia A.
                                                                                                                                                                                                                                                                    bispecific antibody; blood coagulation factor VIII; bleeding; fibrinolysis; blood coagulation factor X; blood-coagulation factor IX; factor VIII deficiency; von Willebrands disease; hemostatic; immunostimulator; antibody engineering.
                                                                                                                                                                                                                                      Murine factor IX directed antibody CDR1 SEQ ID NO 110.
                                                                                                                                     ADZ45406 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-2004; 2004WO-JP014911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003; 2003WO-JP013062.
14-OCT-2003; 2003WO-JP013123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori K, Kojima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-315563/32.
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                 2 GYLWN
                                                   2 GYFWN
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                                                                                                                                                                       ADZ45406;
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DNA fragments related to human immunoglobulin genes - in which are markers for diagnosis of lymphoid tumours by detection of B- and T-type
                                                                                              DH immunoglogulin encoding sequences may be extracted as fragments and used in diagnosis of lymphoid tumours and leukaemias, detecting marker sequences from the VhDhJh gene cluster
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable region gene of high affinity monoclonal antibody of tumor necrosis factor and its preparation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              necrosis factor; TNF; monoclonal antibody; F6 mAb; chain variable region; heavy chain variable region; F6VH.
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ches l; Indels
                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                      Length 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNF resistant monoclonal antibody VH region, F6VH CDR1.
                                                                                                                                                                                                     Score 32; DB 2;
Pred. No. 2e+06;
                                                                                                                                                                                                                                      1; Mismatches
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                                                                  Disclosure; Page ?; -pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                          AEA40139 standard; peptide; 6 AA.
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80.0%;
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Best Local Similarity
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1 GYIWN 5
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                                                                                                                                                                   Sequence 6 AA;
                                 tumour cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             light
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Matches
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Ë Soeda

Miyazaki T,

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This invention describes a novel bispecific antibody which can act as a cofactor to enhance an enzyme reaction and can recognize the enzyme and the enzyme substrate. The antibody specifically binds to blood coagulation factor VIII. The invention a ki useful in preventing and/or treating bleeding associated with a disorder or from a disease caused by bleeding. The composition includes blood coagulation factor VIII. The antibody of the invention can be a blood-coagulation fibrinolysis related factor including blood-coagulation factor VIII, blood coagulation factor X, or blood-coagulation factor IX. The antibody comprises a complementary determining region (CDR) of anti-blood-coagulation is useful for preventing antibody. The novel antibody or composition is useful for preventing and/or treating a disease accompanying bleeding, or the disease resulting from bleeding develops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII. The disease the develops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII. The disease the develops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII and/or activation blood coagulation factor VIII, is hemophilia A. This sequence represents a tragment of the antibody described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but the wint of the brood or sequence of the blood coagulation the method of the invention. Note: The sequence for this patent did not form part of the printed specification, but the blood or the printed specification, but the blood or the printed specification, but the thin the method of the invention.
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Pred. No. 2e+06;
Disclosure; SEQ ID NO 110; 69pp; Japanese.
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80.0%;
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Best Local Similarity
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Gaps

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4; Conservative

Matches

Trp-containing cell adhesion recognition (CAR) sequence #8.

26-AUG-2004 (first entry)

ADP05843;

ADP05843 standard; peptide; 6 AA.

ADP05843

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody that immunospecifically binds a Toll-like receptor 4 (TLR4)/MD-2 complex, useful in preparing a composition for treating e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a new antibody that immunospecifically binds a Toll-like receptor 4 (TLR4)/MD-2 complex which inhibits 1 lippopolysaccharide (LPS)-induced LL-8 production in human TLR4/MD-2 transfected HEK293 cells. The antibody that immunospecifically binds a Toll-like receptor 4 (TLR4)/MD-2 complex is useful in preparing a composition for alleviating a symptom of a pathology associated with acherrant TLR4 signaling, such as sepsis, ventilator-induced lung injury, acute inflammation, chronic inflammation or autoimmune disorders induced by endogenous soluble stress factors, e.g., allergic condition, asthma, inflammatory bowel disorder, atherosclerosis, osteoarthritis or rheumatoid arthritis. The present sequence represents the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis. The present sequence represents the amino acid sequence of a Toll-like receptor 4 (TLR4)/MD-2 antibody 15C1 heavy chain
 Gaps
                                                                                                                                                                                                                                                                                                             antibody; Toll-like receptor 4; TLR4; MD-2; lipopolysaccharide-induced IL-8 production; sepsis; inflammation; autoimmune disease; allergy; asthma; inflammatory bowel disease; atherosclerosis; osteoarthritis; cardiovascular disease; metabolic disorder; gastrointestinal-gen.; gastrointestinal disease; respiratory disease; antiallergic; immunosuppressive; infection; immune disorder; antiarthritic; musculoskeletal disease; antiinflammatory; antibacterial; osteopathic; antiarteriosclerois; antiateathmatic; gene therapy; heavy chain variable region.
                                                                                                                                                                                                                                                                              Toll-like receptor 4 (TLR4)/MD-2 antibody 15C1 VH region CDR 1.
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2e+06;
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Pred. No. 2e+06
1; Mismatches
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; SEQ ID NO 23; 127pp; English.
                                                                                                                                                                     AEB70898 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2003; 2003US-0528811P.
10-DEC-2003; 2003US-0528812P.
10-DEC-2003; 2003US-0528962P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2004; 2004WO-IB004433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.5%;
66.7%;
                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 66.7
Matches 4; Conservative
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVI-) NOVIMMUNE SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-533459/54.
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                                      2 GYLWN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2005065015-A2.
                                                                       GYYWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                            22-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elson GCA;
                                                                                                                                                                                                       AEB70898;
   Matches
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The invention comprises a cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating agent comprises a Trp-containing cell adhesion recognition (CAR) sequence of a desmosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting cancer metastasis, inhibiting can angiogenesis in a mammal, ameliorating a demyelinating neurological disorder in a mammal, medilorating and emyelinating neurological cargiogenesis in a mammal, increasing vasopermeability in a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, preventing cargiorating synaptic stability in a mammal, simulating blood vessel captacing inhibiting stability in a mammal, enhancing blood flow to a tumour in a mammal, disrupting neovasculature in a mammal, inhibiting endometriosis in a mammal, consorved, and for ameliorating appinal cord injury in a mammal. The cougrowth, and for ameliorating a spinal cord injury in a mammal. The cougrowth, and for ameliorating a spinal cord injury in a mammal. The cell adhesion modulating agent of the invention is useful for treating disease conditions that are dependent on angiogenesis and neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell adhesion modulating agent that modulates desmosomal cadherin-
mediated cell adhesion, useful for inhibiting cancer metaetasis,
comprises Trp-containing cell adhesion recognition sequence of desmosomal
cadherin molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                     cell adhealon modulating agent; debemon; cacherin-mediated cell adhesion; cacherin-mediated cell adhesion recognition sequence; CAR sequence; Trp-containing cell adhesion recognition sequence; desmosomal cacherin molecule; cancer metastasis; angiogenesis; demyelinating neurological disorder; immune system modulation; perganacy prevention; vasopermeability; synaptic stability; blood vessel regression; neurite outgrowth; spinal cord injury; angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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60.0%; Pred. No. 2e+06;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 20; 507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-NOV-2002; 2002US-0426551P.
14-NOV-2002; 2002US-0426689P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2003; 2003WO-IB006208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michaud SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-450349/42.
                                                                                                                                                                                                                                                                                                                                                                                              WO2004048411-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUN-2004.
                                                                                                                                                                                                                                                                                                                dermatitis
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Gaps

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1; Indels

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1 GWMWN GYLWN

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The invention comprises a cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating agent comprises a Trp-containing cell adhesion recognition (CAR) sequence of a deemosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting a demyelinating neurological anadogenesis in a mammal, ameliorating a demyelinating neurological disorder in a mammal, modulating system of a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, preventing confibiliting system of a mammal, confidence in a mammal, confidence in a mammal, increasing blood flow to a tumour in a mammal, disrupting neovosculature in a mammal, inhibiting endometriosis in a mammal, containing inhearing adhesion of a contaroing inhelated compound delivery in a mammal, enhancing adhesion of a contaroing inhearing agent of the invention is useful for treating dlease conditions that are dependent or angiogenesis and neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis).

The present amino acid sequence represents a Trp-containing CAR sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell adhesion modulating agent that modulates desmosomal cadherin-
mediated cell adhesion, useful for inhibiting cancer metastasis,
comprises Trp-containing cell adhesion recognition sequence of desmosomal
                                                                                                                                                                      desmosomal cadherin-mediated cell adhesion;
Trp-containing cell adhesion recognition sequence; CAR sequence;
Trp-containing cell adhesion recognition sequence; CAR sequence;
desmosomal cadherin molecule; cancer metastrasis; andjodenesis;
demyelinating neurological disorder; immune system modulation;
pregnancy prevention; vasopermeability; synaptic stability,
angjogenesis; neovascularisation; psoriasis; diabetic retinopathy;
dermatitis.
                                                                                                                   Trp-containing cell adhesion recognition (CAR) sequence #215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 51; SEQ ID NO 1357; 507pp; English.
ADP07180 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                           adhesion modulating agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-2003; 2003WO-IB006208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-2002; 2002US-0426551P.
                                                                             26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michaud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-450349/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cadherin molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention
                                                                                                                                                                                                                                                                                                                                                                                                         WO2004048411-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                   Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blaschuk OW,
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                                   ADP07180;
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Cell adhesion modulating agent that modulates desmosomal cadherin-
mediated cell adhesion, useful for inhibiting cancer metastasis,
comprises Trp-containing cell adhesion recognition sequence of desmosomal
Gaps
                                                                                                                                                                                                         desmosomal cadherin molecule; cancer metastasis; angiogenesis; demyelinating neurological disorder; immune system modulation; perganary prevention; vasopermeability; synaptic stability; blood vessel regression; neurite outgrowth; spinal cord injury; anglogenesis; neovascularisation; psoriasis; diabetic retinopathy;
                                                                                                                                                                                                   Trp-containing cell adhesion recognition sequence; CAR sequence;
ö
                                                                                                                                                        Trp-containing cell adhesion recognition (CAR) sequence #4.
Indels
;
                                                                                                                                                                             cell adhesion modulating agent;
desmosomal cadherin-mediated cell adhesion;
Mismatches
                                                                                          ADP05839 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      (ADHE-) ADHEREX TECHNOLOGIES INC.
5
                                                                                                                                                                                                                                                                                                                                                  14-NOV-2003; 2003WO-IB006208;
                                                                                                                                                                                                                                                                                                                                                                       14-NOV-2002; 2002US-0426551P.
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Michaud SD;
3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cadherin molecule.
                    9
                                 1 GWMWN
                                                                                                                                                                                                                                                                                                         WO2004048411-A2
                    2 GYLWN
                                                                                                                                                                                                                                                                                                                                                                                                                            Blaschuk OW,
                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                   26-AUG-2004
                                                                                                                                                                                                                                                                                                                              10-JUN-2004.
                                                                                                                                                                                                                                                                dermatitis.
                                                                                                                ADP05839;
Matches
                                                                      RESULT 9
                                                                                 ADP05839
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The invention comprises a cell adhesion modulating agent that modulates Disclosure; SEQ ID NO 16; 507pp; English.

demonsorial cadherin-mediated cell adhesion. The cell adhesion modulating agent comprises a Trp-containing cell adhesion recognition (CAR) sequence of a desmosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting cancer metastasis, inhibiting cancer in a mammal, ameliorating a demyelinating neurological disorder in a mammal, modulating immune system of a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, preventing pregnancy in amammal, increasing vasopermeability in a mammal, corpression, increasing blood flow to a tumour in a mammal, createsion, increasing blood flow to a tumour in a mammal, createsion in a mammal, inhibiting endometriosis in a mammal, createsing neovasculature in a mammal, inhibiting endometriosis in a mammal, createsing disconting decine control of a foreign infaled compound delivery in a mammal, enhancing dhesion of a foreign modulating agent of the invention is useful for treating calesaes conditions that are dependent on angiogenesis and neovasculaties of sequence represents a Trp-containing CAR sequence

Length 6;

DB 8; 2e+06;

Score 27; Pred. No.

67.5%;

Query Match Best Local Similarity

Sequence 6 AA;

Gaps

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0; Indels Length 6;

Score 26; DB 8; Pred. No. 2e+06; ; Mismatches

65.0%;

Query Match Best Local Similarity

Sequence 6 AA;

S

3; Conservative

Matches

GYLWN 6

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GWVWN

ADP05872 standard; peptide; 6 AA.

RESULT 11 ADP0587 26-AUG-2004 (first entry)

ADP05872;

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The invention comprises a cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating agent comprises a Trp-containing cell adhesion recognition (CAR) sequence of a desmosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting cancer metastasis, inhibiting and an ammal, medulating admentance of a mammal, increasing wasopermeability in a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, corpression, increasing blood flow to a tumour in a mammal, corpression, increasing blood flow to a tumour in a mammal, corpression, increasing blood flow to a tumour in a mammal, corpression in a mammal, inhibiting endometriosis in a mammal, corpression in a mammal, corpression in a mammal, corpression, increasing delivery in a mammal, enhancing adhesion of a controwth, and for ameliorating a spinal cord injury in a mammal. The cell adhesion modulating agent of the invention is useful for treating disease conditions that are dependent on angiogenesis and neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis). The present amino acid sequence represents a Trp-containing CAR sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell adhesion modulating agent that modulates desmosomal cadherinmediated cell adhesion, useful for inhibiting cancer metastasis, comprises Trp-containing cell adhesion recognition sequence of desmosomal
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                         desmosomal cadherin-mediated cell adhesion;
Trp-containing cell adhesion recognition sequence; CAR sequence;
desmosomal cadherin molecule; cancer metastasis; angiogenesis;
demyelinating neurological disorder; immune system modulation;
pregnancy prevention; vasopermeability; synaptic stability;
blood vessel regression; neurite outgrowth; spinal cord injury;
angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;
                                            ö
                                                                                                                                                                                                                                                                                                                                   Trp-containing cell adhesion recognition (CAR) sequence #211.
                                            0; Indels
DB 8;
2e+06;
    Score 26; DB 8
Pred. No. 2e+06
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 51; SEQ ID NO 1353; 507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                  ADP07176 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                             adhesion modulating agent;
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14-NOV-2002; 2002US-0426689P.
        65.0%;
                                                                                                                                                                                                                                                                                                 (first entry)
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                                              3; Conservative
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        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cadherin molecule.
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                                                                                  2 GYLWN 6
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                                                                                                                      1 GWVWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                 26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatítis.
                                                                                                                                                                                                                                                          ADP07176;
                                              Matches
                                                                                                                                                                                  RESULT 10
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The invention comprises a cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating desmosomal cadherin-molecule. The cell adhesion modulating agent of a desmosomal cadherin molecule. The cell adhesion modulating agent of a desmosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting a demyelinating neurological angiogenesis in a mammal, mentiorating a demyelinating neurological clisorder in a mammal, medulating inamune system of a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, preventing controling increasing blood flow to a tumour in a mammal, disrupting neovasculature in a mammal, inhibiting endometriosis in a mammal, controling adhesion of a contacting inhaled compound delivery in a mammal, enhancing adhesion of a contactory and for ameliorating agent of the invention is useful for treating disease conditions that are dependent on angiogenesis and cervatitis).

The present amino acid sequence represents a Trp-containing CAR sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell adhesion modulating agent that modulates desmosomal cadherin-
mediated cell adhesion, useful for inhibiting cancer metastasis,
comprises Trp-containing cell adhesion recognition sequence of desmosomal
                                                                                                                                                                                                                      pregnancy prevention; vasopermeability; synaptic stability; blood vessel regression; neurite outgrowth; spinal cord injury; angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;
                                                                                                                                 desmosomal cadherin-mediated cell adhesion;
Trp-containing cell adhesion recognition sequence; CAR sequence desmosomal cadherin molecule; cancer metastasis; angiogenesis; demyelinating neurological disorder; immune system modulation;
                                                                           Trp-containing cell adhesion recognition (CAR) sequence #37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 49; 507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                    cell adhesion modulating agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-2002; 2002US-0426689P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-2003; 2003WO-IB006208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-2002; 2002US-0426551P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cadherin molecule.
                                                                                                                                                                                                                                                                                                                                                                         WO2004048411-A2.
                                                                                                                                                                                                                                                                                                                                  Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-2004.
                                                                                                                                                                                                                                                                                           dermatitis
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RESULT 12

à 셤 AAR24717

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Monoclonal antibodies which inhibit type II phospholipase A2 are useful in the treatment of myocardial infarction, cerebral infarction, acute findney failure, chronic rheumatism, carciac shock, pancreatitis, adult respiratory distress syndrome and colitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2 Sphen cells from the mice were fused with mouse myeloma byun companient (PaxGAAGS.U) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12HS, 1.4 and 10.1. These were cultured and the antibody isolated from the culture upernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CLAB. Because the antibody acts on the precipital testing. This peptide sequence corresponds to the first complementary determining region of the heavy chain of the monoclonal antibody isolated from the clone designated 1.4
                                                                                                                                                                Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis; cerebral infarction; acute kidney failure; colitis; chronic rheumatism; adult respiratory distress syndrome; cardiac shock; treatment; preclinical testing; disease; hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody inhibiting type II phospholipase A2 activity - for treatment of myocardial and cerebral infarction.
                                                                                                                              MAD 1.4 heavy chain CDR (MAb binds type II phospholipase A2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 2; Length 6;
Pred. No. 2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yasunaga T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminus of 6-SFT 49 kDa subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 42; 69pp; Japanese.
                   AAW01150 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR98564 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                   95WO-JP002714.
                                                                                                                                                                                                                                                                                                                                                                                                                       94JP-00340006.
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Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawauchi Y, Takasaki J,
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                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1994;
                                                                                                                                                                                                                                                                                                      WO9620959-A1
                                                                                                                                                                                                                                                                                                                                                                                   27-DEC-1995;
                                                                                                                                                                                                                                                                Aus musculus
                                                                                            10-FEB-1997
                                                                                                                                                                                                                                                                                                                                             11-JUL-1996.
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06-NOV-1996
                                                         AAW01150;
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AAW01150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              urokinase-recognising antibody heavy chain variable region conteg.at least town of the polypeptide chains G, H and I(AR24171,R24718,AR24719) and a human antibody heavy chain constant region. The chimeric Abs can be used both in vivo and in vitro and, since they have very low immunogenicity as compared with mouse Abs, they can be administered to humans for diagnostic and therapeutic purposes. They are also more stable and show a longer half-life in the blood as compared with the original mouse Abs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of an anti-urokinase antibody heavy chain variable region chain
                                                                                                              Gaps
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                                                                                                            0; Indels
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Pred. No. 2e+06;
0; Mismatches 1; Indels
                                                                           Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric monoclonal antibody, anti-urokinase antibody, antithrombotic agent; myocardial infarction therapy.
                                                                         Score 26; DB 8;
Pred. No. 2e+06;
2; Mismatches
                                                                                                                                                                                                                                                                                AAR24717 standard; protein; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 50; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tada H, Watanabe T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91JP-00294464.
                                                                         65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91EP-00121591
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Best Local Similarity 75.0%;
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                   Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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of the invention.
                                                                                                                                                                      GWVWN
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                                     Sequence 6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
28-DEC-1992
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Gaps ö

RESULT 13

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Search completed: December 30, 2005, 15:34:05
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Best Local Similarity 75.u
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                                                                                                                                                                                                                                                                                                                                                 Sucrose-fructan 6-fructosyl transferase, isolated from barley (Hordeum vulgare), is a key enzyme for the biosynthesis of franched fructans which are typical for grasses 6-SFT comprises 2 subunitafisoforms of 49 and 23 kDA resp. . The enzyme forms Kestose from sucrose and bifurcose from sucrose and isokestose. Transgenic plants contg. the cDNA can be used for the prodn. of oligosaccharides that have more desirable properties compared with the oligosaccharides prepared by known industrial processes. An advantage of the method is that the chain length distribution is narrower, with no or few free sugars occuring in the end product. This means lower cariogenicity and lower energy value. The present sequence is that of the N-terminal of the 6-SFT 49 kba subunit. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                           use as sugar
food prods. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable domain; lambda light chain; catalytic antibody; degradation; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Oligosaccharide production; sucrose-sucrose-fructosyl transferase; sucrose-fructan-6-frucotsyl transferase; SST; 6-SFT; barley; onion; Hordeum vulgare; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                       Prodn. of oligo:saccharide(s) by transgenic plants - for
substitutes, nutritional fibre and bifidogenic agents in
animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 23; DB 2; Length 6; 60.0%; Pred. No. 2e+06;
                                                                                                                                                                                                                        Ebskamp MJM, Geerts HAM, Weisbeek PJ;
                                                                                                                                                                                              (SCHE-) STICHTING SCHEIKUNDIG ONDERZOEK IN NEDER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heavy chain CDR1 of catalytic antibody 2A10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW39848 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                             Example 4; Fig 7; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US010965
                                                                                                                                                                      95NL-01000064.
                                                                                                                                95WO-NL000241
                                                                                                                                                       94NL-00001140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.5
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overdose; addiction.
                                                                                                                                                                                                                                                 WPI; 1996-097634/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||: |
2 GGFPW 6
                                                 Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6 AA;
                                                                                                                                                                                                                        Smeekens JCM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1997;
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                                                                            WO9601904-A1
                                                                                                                                07-JUL-1995;
                                                                                                                                                        08-JUL-1994;
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                                                                                                                                                                       05-APR-1995;
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                                                                                                      25-JAN-1996
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Gaps

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1; Indels Length 6;

Score 23; DB 2; Pred. No. 2e+06; 0; Mismatches

57.5%; 75.0%;

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AAM39848-50 represent the sequences of the heavy chain complementarity determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody SA10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
                                                                                                                                                                                                                                                                                                                                                                   New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; Page 89; 147pp; English.
                                                                                          (UYCO ) UNIV COLUMBIA NEW YORK
     96US-00672345.
                                                                                                                                                                                                                                                                              WPI; 1998-077166/07.
25-JUN-1996;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 30, 2005, 15:24:08; Search time 37 Seconds (without alignments) 15.603 Million cell updates/sec Run on:

US-10-735-916A-8 40 1 GGYLWN 6 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

110 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 6 Maximum DB seq length: 6

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	T-cell receptor be	dnaA protein - Pse	ameletin - rat	lipopeptide WS1279	T-cell receptor be		н	T-cell receptor be	_	_	_			alcohol dehydrogen	hypothetical prote	dihydrofolate redu	dihydrofolate redu	cerebellar degener	T-cell receptor be	T-cell receptor be			T-cell receptor be	pev-kinin 2 - pena	nin -	hypothetical TCL3	peptidyl-dipeptida	T-cell receptor ga	neuropeptide GNFFR
	ID	PT0519	B34835	A61411	JU0355	PT0514	PT0512	PT0720	PT0560	PT0723	PT0727	PT0730	F41946	PT0605	866195	B44510	A31263	B31263	B35640	PT0629	PT0532	PT0637	PT0641	PT0726	PD0028	A61068	179564	JN0861	A41946	A43129
	Length DB	6 2	9	9	9	9	9	6 2	9	9	9	9	9	9	9	9	9	9	9	6 2	9	9	9	6		9	6 4	9	6 2	9
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sarcosine dehydrog	collagen alpha 1(I	hydrogensulfite re	protamine P1 - gor	laminin B1 - weste	RNA-directed DNA p	halo-toxin - Pseud	phosphoglycerate t	hydrogensulfite re	mosquitocidal toxi	parasporal crystal	jacalin beta-ī1 ch	angiotensin-conver	variant surface gl	antineoplastic gly	H4 histone - Afric	
A61419	B56979	S11556	137027	149421	A35890	A61049	T11779	S11024	A44916	S14159	S29637	PQ0008	B61512	A60494	151434	
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: Pr0519
R;Peeney, A-J.
C;Accession: Pr0519
R;Peeney, A-J.
C;Accession: Pr0519
R;Peeney, A-J.
J; Exp. Med. 174, 115-124, 1991
A;Reference number: Pr0509; MUID:91277601; PMID:1711558
A;Accession: Pr0519
A;Accession: Pr0619
A;Accessi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LWN 6
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RESULT 2 B34835

Gaps ö Query Match
37.5%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels

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4 LW 5 5 LW 6 g ò

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T-cell receptor beta chain V-D-J region (126-1CB) - mouse (fragment)
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Best Local Similarity 100.
Matches 2; Conservative
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              C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C;Accession: A61411
R;Burzynski, S.R.
Anal. Biochem. 70, 359-365, 1976
A;Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the A;Reference number: A61411; MUID:76182447; PMID:1267130
A;Accession: A61411
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Streptomyces willmorei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: JU0355
R;Tsuda, Y; Okada, Y; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A;Title: Structure and synthesis of an immunoactive lipopeptide, WS1279, of microbial
A;Reference number: JU0355; MUD:91300586; PMID:2070441
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C;Species; Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0514
                                                                                                                                                                                                                                                                     A,Molecule type: procein
A,Residues: 1-6 <BUR>
A,Residues: 1-6 <BUR>
A,Cross-references: UNIPARC:UP1000017A501
C,Keywords: pyroglutamic acid
F;1/Modified site: pyrrollidone carboxylic acid (Gln) #status experimental
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C; Keywords: blocked amino end; lipoprotein
F;1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status exper:
F;1/Modified site: fatty acylated amino end (Cys) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.5%; Score 13; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor
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A;Residues: 1-6 <TSU>
A;Cross-references: UNIPARC:UPI000017AE43
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A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FES>
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Rifeeney, A.J...
7. Exp. Med. 114, 115-124, 1991
7. Exp. Med. 114, 115-124, 1991
A;Telle: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0519; MUID:91277601; PMID:1711558
A;Reference number: PT0512
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0548; PT0720
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0512
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A,Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1BB
A,Accession: Pr0720
A,Status: translation not shown
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A;Cross-references: UNIPARC:UPI000017C809
A;Experimental source: newborn thymus, strain BALB/c, clone 140-2J
C;Keywords: T-cell receptor
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Query Match
30.0%; Score 12; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
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A;Cross-references: UNIPARC;UPI000017C7BF
A;Experimental source: adult thymus, strain BALB/c
C;Ksywords: T-cell receptor
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T-cell receptor gamma chain (1a.27) - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Date: 03.Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C,Accession: F41946
R,Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A,Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma g
A,Reference number: A41946; MuID:92049316; PMID:1658619
                                                                                                                                                   T-cell receptor beta chain V-D-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0730; PT0594; PT0731
R:Feeney, A.J.
R:Feeney, A.J.
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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A; Residues: 1-6 <FE2>
A; Cross-references: UNIPARC:UPI000017C850
A; Experimental source: day 19 fetal thymus, strain BALB/c (clone 159-2F)
A; Accession: PT0731
A; Status: translation not shown
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A;Molecule type: DNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C850
A;Experimental source: newborn thymus, strain BALB/c (clone 163-2C)
A;Accession: PT0594
A;Status: translation not shown
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A,Zross-references: UNIPARC:UP1000017C850
A,Experimental source: newborn thymus, strain BALB/c (clone 165-3E)
C,Keywords: T-cell receptor
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Pred. No. 2.8e+05;
1; Mismatches 0;
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Best Local Similarity 100.
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                                                                                 J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional Sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0560
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J. Exp. Med. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0727
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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                                Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
Accession: PT0560
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0727
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30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C811
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
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A; Status: translation not shown
A; Residues: 1-6 <FEE>
A; Cross-references: UNIPARC: UDI000017C844
A; Experimental source: newborn thymus, strain BALB/c; Keywords: T-cell receptor
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision
C;Accession: PT0560
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Best Local Similarity 100.0
Matches 2; Conservative
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R;Renault, P.; Gaillardin, C.; Heelot, H.
B, Bacteriol. 171, 3108-3114, 1989
A;Title: Product of the Lactococcus lactis gene required for malolactic fermentation is A;Reference number: A44510; MUID:89255069; PMID:2498286
A;Accession: B44510
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A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases.
     C;Species: Mus musculus (house mouse)
C;Date: 17-011-1992 #sequence_revision 17-011-1992 #text_change 09-011-2004
C;Date: 17-011-1992 #sequence_revision 17-011-1992 #text_change 09-011-2004
C;Accession: PT0605
B;Feeney, A.J.
J; Exp. Med. 115-124, 1991
A;Feeney. Med. 115-124, 1991
A;Acference number: PT0609; MUD:91277601; PMID:1711558
A;Acference number: PT0605
A;Acferen
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A;Molecule type: protein
A;Residues: 1-6 <HJES.
A;Cross-references: UNIPARC:UP10000171EA5
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase
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C;Species: Lactococcus lactis
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
Species: Mus musculus (house mouse)
:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
;Accession: PT0605
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A,Molecule type: DNA
A,Residucus - 16 <RENJ
A,Cross references: UNIPARC:UPI000017AC46; EMBL:M90762
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Run on:

- protein search, using sw model

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December 30, 2005, 15:14:23 ; Search time 229 Seconds (without alignments) 18.485 Million cell updates/sec

US-10-735-916A-8 40

1 GGYLWN 6 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2166443 segs, 705528306 residues Searched:

19 Total number of hits satisfying chosen parameters:

seg length: 6 seg length: 6 四四四 Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	P82096 litoria rub	P41491 locusta miq	P41966 moniezia ex	P82655 lactobacill	P42985 leptinotars	P13736 mytilus edu	_	P83569 Bepia offic	P41495 sarcophaga	P81351 clostridium	P23210 human herpe	P83533 lactobacill	P25154 oryctolagus	P36414 pseudomonas	P82541 spinacia ol	P84005 penaeus mon	P84575 schistosoma	P82181 spinacia ol	P82182 spinacia ol
ID	BIO1 LITRU	LOK1_LOCMI	FARP MONEX	ASP2_LACSN	OVM LEPDE	CIPI MYTED	CIP2_MYTED	SAPP_SEPOF	TMOF SARBU	UN06_CLOPA	VP19 HHV1K	P8353 LACSN	ACPH_RABIT	TRPI PSEPU	P82541 SPIOL	PYF1 PENMO	MAF SCHMA	P82181 SPIOL	P82182 SPIOL
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# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                      Wallace J.C.;
Australian buzzing tree frog
skin peptides from Litoria
                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
101 TaxID=104895;
                                                                                                                                                                                                                                                                                                                                                              Amidation; Amphibian defense peptide; Direct protein sequencing.
MOD RES 6 Methionine amide.
SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
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0
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Pred. No. 2.2e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                   Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin glands.
                                                                                                                                      Wabnitz P.A., Bowie J.H., Tyler M.J., "Peptides from the skin glands of the Litori electrica. Comparison with the
              toria rubella (Desert tree frog)
                                                                                                                                                                                                                                                                                                                                                                                                                            32.5%;
50.0%;
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Bukaryota; Metazoa; Arhropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 6 AA. Locusta migratoria (Migratory locust). Locustakinin I LOCMI P41491;

PROTEIN SEQUENCE

"Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, primary structure and synthesis.";
Regul. 137:49-57(1992).
-!- FUNCTION: Myotropic peptide. May be important in the stimulation of ion transport and inhibition of diuretic activity in Malpighian TISSUB=Corpora cardiaca;
MEDLINE=92262851; PubMed=1585017; DOI=10.1016/0167-0115(92)90063-Z;
SCHOOGE L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.; 

-!- SUBCELLULAR LOCATION: Secreted.

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PIR; Ad1068, A61068.
Amidation; Direct protein sequencing; Neuropeptide.
MOD RES 6 Glycine amide.
CENTRNCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

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MEDLINE-93312289; PubMed-8323531;
MANLE 4.03.12289; PubMed-8323531;
MANLE 4.0.1, MAN C., Halton D.W., Thim L.;
"GNFFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CB1;
MEDLINE=1322712; PubMed=11429463;
MEDLINE=1322712; PubMed=11429463;
MEDAGELIS M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M.;
"The acid-etress response in Lactobacillus sanfranciscensis CB1.";
Microbiology 147:1863-1873(2001).
-i- INDUCTION: Overexpressed in acid environments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Blophys. Res. Commun. 193:1054-1060(1993).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the PARP (FWRFamide related peptide)
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16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Acid shock protein 2 (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco) .
Bacteria; Firmicutes; Lactobacillales; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
65-JUL-2004 (Rel. 44, Last annotation update)
FMRPamide-like neuropeptide GWPFRF-amide.
Moniezia expansa (Sheep tapeworm).
Eukaryota, Metazoa, Platyhelmithes; Cestoda; Cyclophyllidea; Anoplocephalidae; Moniezia.
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Amidation; Direct protein sequencing; Neuropeptide.
MOD RES
SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;
DB 1; Le
2.2e+06;
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27.5%; Score 11; DB 100.0%; Pred. No. 2.2
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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-!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 34, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation period.)
Leptinotarsa decemlineata (Colorado potato beetle).
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Roberta; Endopterygota; Coleoptera; Polyphaga; Chrysomeloidea; Chrysomelidae; Chrysomelidae; Chrysomelinae; Doryphorini;
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                                                                                                                                                                                                                                                                                                                                           DB 1; Length 6; 2.2e+06;
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                                                                                                                                                                                                                                                                               6 AA; 779 MW; 6AA45B5B132A8000 CRC64;
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(Rel. 13, Last sequence update)
(Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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P13736;
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MASS SPECTROMETRY: MW=596.6; METHOD=MALDI; RANGE=1-6; NOTE=Ref.1.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Sarcophagidae; Sarcophaga; Neobellieria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3; Zatylny C., Marvin L., Gagnon J., Henry J.; "Fertilization in Sepia officinalis: the first mollusk sperm-attracting peptide.";
                                                                                                                                                                                                                                                                   Sperm attracting peptide SapSAP.
Sepia officinalis (Common cuttlefish).
Bukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Decapodiformes, Sepioidea, Sepiidae, Sepia.
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MEDLINE=94211930; PubMed=8159807; DOI=10.1016/0167-0115(94)90192-9;
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
-!- FUNCTION: Attracts sperm increasing the chances of gamete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1096 (Rel. 44, Last annotation update)
Trypsin-modulating oostatic factor (TMOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
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MOD RES 6 6 Valine amide.

SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;
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100.0%; Pred. No. 2.2e+06;
tive 0; Mismatches 0;
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05-JUL-2004
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                                                                                                                                         TISSUE-Pedal ganglion;
MEDLINE-88340357; PubMed=3377776;
MEDLINE-88340357; PubMed=3377776;
Minter T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
"Structures and actions of Wytilus inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
-!- FUNCTION: Inhibitory action on contractions in several molluscan
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01-JAN-1990 (Rel. 13, Last sequence update)
01-FBE-2005 (Rel. 46, Last annocation update)
Contraction-inhibiting peptide II (MIP II).
Wytilus eduls (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilinae; Mytilus.
Contraction-inhibiting peptide I (MIP I).
Wytilus edulis (Blue mussel).
Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilinae; Mytilus.
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Amidatlon; Direct protein sequencing; Hormone.
MOD RES
SEQÜENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;
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6 AA; 637 MW; 72C9C68775B81000 CRC64;
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Amidation; Direct protein sequencing; Hormone.
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P83533 LAC
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                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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de Loof A.; 's sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
                                                                    (Sarcophaga) bullata.";
Regul. Pept. 50:61-72(1994).
-!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis in the midgut which indirectly reduces the vitellogenin concentration in the hemolymph resulting in inhibition of oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-i- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 5.0, its MW is: 75.9 kDa.
                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: Synthesized and released from follicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium pasteurianum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct protein sequencing; Hormone.
SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;
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ilarity 100.0%; Pred. No. 2.2e+06;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Unknown protein CP 6 from 2D-PAGE (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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; Pred. No.
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                                                                                                                                                                                                                                               epithelium after a blood meal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.0%; Best Local Similarity 100.0%; Matches 1; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct protein sequencing.
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tes 1; Conserv
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NCBI_TaxID=1501;
                                                                                                                                                                                                 development
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15-JUL-1998
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SEQUENCE
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Matches
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RESULT 11

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as lower as its contractions of the last and the second contractions of the last and the second contractions of the last and the second contractions of the last and the last and the last contractions of the last contractions of the last contractions of the last contraction of the last con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detween the SWISS Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on it use as long as its content is in no way modified and this statement is no removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                              Human herpesvirus 1 (strain KOS) (HHV-1) (Human herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of this unknown
                                                                                                                                                                                   Capsid assembly and DNA maturation protein (Virion protein UL38) (Capsid protein VP19C) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M57646; AAA45830.1; -; Genomic DNA.
Capsid protein; DNA packaging; DNA-bInding; Structural protein.
NON_TER 6 6
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"High pressure effects step-wise altered protein expression in
Lactobacillus sanfranciscensis.";
Proteomics 2:755-774 (2002).
-!- MISCELLANBOUS: On the 2D-gel the determined MW of this unkr
protein is 15 kba.
NON TER
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria, Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
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. 2.2e+06;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
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                                                                                                          (Rel. 20, Last sequence update) (Rel. 48, Last annotation update)
6 AA.
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100.0%; Pred. No. 2.2
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                            Alphaherpesvirinae; Simplexvirus NCBI_TaxID=10306;
                                                                         (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.0%;
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STANDARD;
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PubMed=12112860;
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SEQUENCE
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activator) (Fragment).
                                         Pseudomonas putida.
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Best Local Similarity
Matches 1; Conserv
                                                                                                   NCBI_TaxID=303;
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01-JUN-1994 (Rel. 29, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
HTH-type transcriptional regulator trpI (TrpBA operon transcriptional
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Lagomorpha, Leporidae,
                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Last sequence update)
1-FRB-2005 (Rel. 46, Last annotation update)
Acylamino-acid-releasing enzyme (RC 3.4.19.1) (AARB) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).
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                                       0; Indels
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   DB 2; Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the peptidase S9C family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetylation; Direct protein sequencing; Hydrolase. MOD RES
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                     2.2e+06;
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InterPro; IPR002471; Pept_S9_AS.
PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
15.0%; Score 6; DB 2
100.0%; Pred. No. 2.2
tive 0; Mismatches
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                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                   22, Created)
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                                       Conservative
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                 Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus.
NCBI_TaxID=9986;
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ID TRPI PSEPU
                                                                                                                                                                                                                                                                                                                                                 Name=APEH;
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 Query Match
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Matches
                                       Matches
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STRAIN=CV. ALWARO; TISSUE-Leaf;

MEDLINE=20435797; PubMed=10874039; DOI=10.1074/jbc.M004350200;

A Yamaquchi K., von Knoblauch K., Subramanian A.R.;

The plastid ribosomal proteins. Identification of all the proteins in the also subunit of an organelle ribosome (chloroplast).";

The jostid ribosomal proteins. Identification of all the proteins in the also subunit of an organelle ribosome (chloroplast).";

L. J. Biol. Chem. 275:28455-28465(2000).

-I. FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

-I. FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL CONTION: CHLOROPLAST.

-I. FUNCTION: WH=10477.0; METHOD=ELECTROSPRAY.

-I. MASS SPECTROMETRY: MW=10495; METHOD=ELECTROSPRAY.

-I. MASS SPECTROMETRY: MW=10495; METHOD=MALDI.

-I. MISCELLANBOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
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InterPro; IPR000847; HTH LyGR.
PROSITE; PSSO931; HTH LYGR; PARTIAL.
ACLIVATOr; Amino-acid biosynthesis; Aromatic amino acid biosynthesis; DNA-binding; Transcription; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                     MEDLINE=89335826; PubMed=2503057; DOI=10.1016/0300-9084(89)90183-1;
                                                                                                                                                                                                                                                                                                                                                                                                                  Biochimie 71:521-531(1989).

-!- FUNCTION: Activates the expression of the trpBA genes encoding two tryptophan synthase subunits. In the absence of the inducer (indoleglycerol phosphate), trpI binds upstream of the trpAB operon, overlapping its own promoter region.

-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                 Eberly L., Crawford I.P.;
"DNA sequence of the tryptophan synthase genes of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Chloroplast TrEMBLrel. 25, Last annotation update)
Spinacia 30s ribosomal protein S19 beta (Fragment).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
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                                                                                                                                                                  NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPIOL PRELIMINARY;
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us-10-735-916a-8.sizlim.rup

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0; Gaps
-1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.
-1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
GO; GO:0009843; F:rRNA binding; IEA.
GO; GO:0003735; F:rRNA binding; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
InterPro; IPR002222; Ribosomal S19.
FROSITE; PS00323; RIBOSOWAL S19; PARTIAL.
Chloroplast; Ribosomal protein; rRNA-binding.
Chloroplast; Ribosomal protein; rRNA-binding.
SEQÜENCE 6 AA; 732 MW; 63333735A411C000 CRC64;
                                                                                                                                                                                                                                               Query Match
10.0%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 8,678
REFERENCE DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBHONE: 212-278-0400
TELEBHONE: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                  US-08-672-345C-52

Sequence 52, Application US/08672345C

Patent No. 59486R2

Patent No. 59486R2

GENERAL INFORMATION:

APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSES: Cooper and Dunham LLP
US-09-620-091-471
US-07-822-924-9
US-07-805-727-7
US-07-718-577-5
US-07-718-577-5
US-07-98-370-71
US-08-351-058A-9
US-07-943-709-11
US-07-943-709-12
US-07-943-709-12
US-08-827-184A-4
                                                                                                                                                                                                                                                                        US-08-466-632-7
                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-22
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
**PMCTH: 6 amino acids
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Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 52, Appl Sequence 52, Appl Sequence 2, Appl Sequence 158, Appl Sequence 1588, Appl Sequence 1588, Appl Sequence 2, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 158, Appl Sequence 1688, Appl Sequence 165, Appl Sequence 165, Appl Sequence 155, Appl Sequence 158, Appl Sequence 155, Appl Sequence 94, Appl Sequence 94, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99, Appl
155, App
65, Appl
37, Appl
94, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                       December 30, 2005, 15:26:49; Search time 45 Seconds (without alignments) 11.023 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Ap
Sequence 11, A
Sequence 186,
Sequence 186,
Sequence 470,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-672-345C-52
US-09-214-095D-52
US-09-944-727B-52
US-09-127-574-14
US-09-135-348-1588
US-09-350-325-48
US-09-350-641C-1588
US-09-350-641C-1588
US-08-73-028-45
US-08-73-028-45
US-08-73-641-158
US-08-73-654-1658
US-08-354-616-45
US-08-354-616-45
US-09-35-9554-1658
US-09-35-9513-1658
US-09-31-715-155
US-09-31-715-155
US-09-578-063-65
US-08-08-253-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-620-091-470
                                                                                                                                                                                                                                                                                       572060 segs, 82675679 residues
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                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                       US-10-735-916A-8
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Match Length
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1 GGYLWN 6
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Maximum DB seq length: 6
                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                          Run on:
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Sequence 14, Application US/09127574

Releant No. 5985836

GENERAL INFORMATION:
APPLICANT: Bastek, Patrick
APPLICANT: Baumbach, George A.
APPLICANT: Carbonell, Ruben G.
TITLE OF INVENTION: Alpha-1 Proteinase Inhibitor Binding Peptides
FILE REFERENCE: MSP-1248
CURRENT PILING DATE: 1998-07-31

NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.0%; Score 22; DB 1; Length 6; 100.0%; Pred. No. 4.6e+05; tive 0; Mismatches 0; Indels
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                                              COUNTRY: UDARTE STATE ST
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
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US-09-315-304B-1588
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US-09-127-574-14
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TITLE OF INVENTION: Compounds Having the Antigenicity of TITLE OF INVENTION: hcG
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Utah Technology
ADDRESSEE: Transfer Office
STREET: 421 Wakara Way, Suite 170
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.5%; Score 23; DB 2; Length 6; 75.0%; Pred. No. 4.6e+05; Live 0; Mismatches 1; Indels
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US-09-214-095D-52;
Sequence 52, Application US/09214095D;
Patent No. 6290097;
GENERAL INFORMATION:
Patent NO. 6290097;
GENERAL INFORMATION:
PILLE OF INVENTION:
PILE REFERENCE: 51400-A-PCT-US;
CURRENT PILING DATE: 1999-07-19;
NUMBER OF SEQ ID NOS: 121;
SOFTWARE: Patentin version 3.0;
SEQ ID NO 52;
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 52, Application US/09940727B
; Sequence 52, Application US/09940727B
; Patent No. 6913917
; GENERAL INFORMATION:
   APPLICANT: Landry. Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
   TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; TITLE PEPERBRICE: 0575/51400-B
; CURRENT FILING DATE: 1090-004
; PRIOR PILING DATE: 1998-12-28
; PRIOR FILING DATE: 1999-10-25
; PRIOR PRILING DATE: 1998-10-28
; PRIOR PRILING DATE: 1997-06-25
; PRIOR PRILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 52
; LENGTH: 6

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Pred. No. 4.6e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%;
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Murinae gen. sp. US-09-214-095D-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YAWN 6
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US-09-940-727B-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-940-727B-52
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APPLICANT: ALMOST, M.
APPLICANT: ALMOST, M.
APPLICANT: Lamber, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES
FILE REFERENCE: 7872-067
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 1757
SOUTHARE: PASKSEQ for Windows Version 3.0
SEQ ID NO 1588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Herron, James N.
TITLE OF INVENTION: Compounds Having the Antigenicity of TITLE OF INVENTION: Compounds Having the Antigenicity of TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: University of Utah Technology ADDRESSEE: Transfer Office
STREET: 421 Wakara Way, Suite 170
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 2; Length 6; Pred. No. 4.6e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb floppy disk
COMPUTER: 1BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERRECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07605.
FILING DATE: 6 Jul 1993
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTATION NUMBER: 33,041
REGISTATION NUMBER: 3224
TELEPHONE: 801/531-9168
TELEPHONE: 801/531-9168
TELEPHONE: 801/531-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Core polypeptide US-09-350-641C-1588
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 389961 IPMO4UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
PCT-US94-07605-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGYLW 5
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Sequence 1588, Application US/09315304B
Patent No. 634856
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Barney, S.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT FILING DATE: 1999-05-20
FRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SEQ ID NOS: 1667
SEQ ID NO 1588
LENGTH: 6
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Fatent No. 65401020
GENERAL INFORMATION:
APPLICANT: Ding, S.
TYLLE OF INVENTION: HERAPEUTIC REAGENTS
TITLE OF INVENTION: HERAPEUTIC REAGENTS
TITLE OF INVENTION: THERAPEUTIC REAGENTS
TITLE OF INVENTION: 1999-07-09
CURRENT APPLICATION UNMER: US/09/350,325
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.0%; Score 22; DB 2; I Best Local Similarity 60.0%; Pred. No. 4.6e+05; Matches 3; Conservative 1; Mismatches 1.
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Patent No. 6656906
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Core polypeptide US-09-315-304B-1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: enhancer peptide US-09-350-325-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Gaps

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6300 Sears Tower, 233 South Wacker Drive
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              Chicago
: Illinois
RY: USA
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US-08-336-553A-32
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                                                       COUNTRY:
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Batent No. 5884070
GENERAL INFORMATION:
APPLICANT: Rose, Lynn M.
TITLE OF INVENTION: Alleviation of Symptoms Associated with TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                  55.0%; Score 22; DB 4; Length 6; 100.0%; Pred. No. 4.6e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.5%; Score 21; DB 1; Length 6; 100.0%; Pred. No. 4.6e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036
COMPUTER 10036
COMPUTER PLOEDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DAY
COMPATION: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,028
FILING DATE: 07-JUM-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Lautra A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 66141 PENNIE
INFORMATION POR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                     Sequence 45, Application US/08073028
Patent No. 5464933
  Query Match
Best Local Similarity 100.v
Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-073-028-45
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Best Local Similarity
Matches 3; Conserv
                                                                                                3 YLW 5
                                                                                                                                       4 YLW 6
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US-08-073-028-45
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Gaps
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| Sequence 32, Application US/08336553A |
| Patent No. 6054264 |
| GENERAL INFORMATION: |
| APPLICANT: CHIEN, DAVID Y. |
| APPLICANT: KUO, GEORGE |
| TITLE OF INVENTION: REAGENTS FOR USE THEREIN |
| NUMBER OF SEQUENCES: |
| ADDRESSEE: MORRISON & FOERSTER |
| STREET 755 Page Mill Road |
| CITY: Palo Alto |
| STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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CONDITE: USA

CONDITE: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/785,571

FILING DATE: 21-JAN-1997

CLASSIFICATION NUMBER: US/08/396,089

FILING DATE: WS/08/396,089

FILING DATE: US/08/396,089

FILING DATE: US/08/393

PRICK APPLICATION NUMBER: US/08/050,699

FILING DATE: US/08/336

FILING DATE: US/08/336
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Pacentaline Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 1; Ler
Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.5%; bcc.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Borun, Michael F. REGISTRAITON NUMBER: 25,447 REFERENCE/DOCKET NUMBER: 311 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (312)474-0448
TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (312) 474-6300
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Best Local Similarity 100
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
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Gaps
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                                                                                                                                                                                                                                                                                                        RESULT 14
US-08+439-157-32
iS-08-439-157-32
; Sequence 32, Application US/08439157
; Patent No. 6416944
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
COUNTRY: USA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,157
FILING DATE: 11-May-1995
CILASSIFCATION NUMBER: US/08/336,553A
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INPORMATION:
NAME: LEBINAARITON:
NAME: LEBINAARITON:
NAME: LEBINAARITON:
REGISTRATION NUMBER: 33,943
REPERENCE/DOCKET NUMBER: 33,943
                                                                           Length 6;
                                                                                                                           0; Indels
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                                                                        Score 21; DB 2; Le
Pred. No. 4.6e+05;
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illarity 75.0%; Pred. No. 4.6e+05;
Conservative 0; Mismatches 1;
                                                                                                                         Mismatches
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US-09-437-895-32
; Sequence 32, Application US/09437895
; Patent No. 6416946
                                                                        52.5%; Scillarity 100.0%; Py
Conservative 0;
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SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
; MOLECULE TYPE: peptide US-08-554-616-45
                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 3; Conserva
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US-08-554-616-45
; Sequence 45, Application US/08554616
; Parent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
; APPLICANT: Matthews, Thomas J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; STREET: USA
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 2; Length 6; Pred. No. 4.6e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Plopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,616
FILING DATE: 06-NOV-1995
CLASSIFICATION: 435
PTILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
PRILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZÍ, LBULEA N.
REGISTRATION NUMBER: 30,742
RELEFRANCE/DOCKET NUMBER: 782-2004-999
TELLEFRANCE (212) 790-9090
TELLEFRANCE (212) 790-9090
TELLEFRANCE (1212) 669-8864/9741
TELLER: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LEWITH.
        FILING DALES

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/060,400
FILING DATE: UO-MAY-1933
ATTORNEY/AGENT INFORMATION:
NAME: LEINHARDT, SUSAN K.
REGISTRATION NUMBER: 33,93
REFRENCE/POCKET NUMBER: 22300-20947.00
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELERA: 706141
INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acid
STAPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.5
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   ESS: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GYLW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GYPW 5
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US-08-336-553A-32
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GENERAL INFORMATION:

APPLICATION:

NUMBER OF INVENTION:

NUMBER OF SEQUENCES ASSAGNED FOR USE THEREIN

NUMBER OF SEQUENCES ASSAGNED FOR USE THEREIN

CORRESPONDENCE ADDRESS:

CORPUTER: Tallocation

APPLICATION NUMBER: 23300-20947.00

TELEBROWN

APPLICATION NUMBER: 23300-20947.00

TELEBROWN

TELEBROWN

CORPUTER: Tallocation

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Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence:

Run on:

Searched:

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Sequence 8, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: LEGER, Olivier
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGP-IR ANTIBODIES AND USES THEREOF
TILE REFERENCE: 01773-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 40; DB 5; L
100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
          US-10-714-564A-91
US-10-714-564A-219
US-10-714-564A-236
US-10-714-564A-236
US-10-714-564A-399
US-10-714-564A-552
US-10-714-564A-555
US-10-714-564A-555
US-10-714-564A-569
US-10-714-564A-569
US-10-714-564A-707
US-10-714-564A-714
US-10-714-564A-713
US-10-714-564A-713
US-10-714-564A-713
US-10-714-564A-713
US-10-714-564A-713
US-10-714-564A-713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: FR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR PELING DATE: 2003-07-11
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PAPLICATION NUMBER: FR 02/00 654
PRIOR PAPLICATION NUMBER: FR 02/05 654
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR STUING DATE: 2002-05-07
NUMBER OF SKO ID NOS: 156
NUMBER OF SKO ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 77, Application US/09791551; Publication No. US20030235584A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
GGYLWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGYLWN
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US-09-791-551-77
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 SEQ ID NO 8
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Sequence 17, Appl
Sequence 1357, Appl
Sequence 16, Appl
Sequence 1353, Appl
Sequence 1353, Appl
Sequence 684, Appl
Sequence 68, Appl
Sequence 1588, Appl
Sequence 11, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 64, Appli
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                                                                                                             December 30, 2005, 15:34:14 ; Search time 161 Seconds (without alignments) 15.571 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA Main:*

(cgn2_6/ptodata/1/pubpāa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*);

(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*);
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-735-916A-8
US-10-714-564A-1357
US-10-714-564A-1357
US-10-714-564A-1357
US-10-714-564A-1353
US-10-714-564A-1353
US-10-714-564A-1353
US-10-714-564A-1353
US-10-714-564A-1353
US-10-714-564A-1353
US-10-714-564A-1353
US-10-714-564A-1310-311-641-199-19
US-11-61-199-19
US-11-61-199-11
US-10-61-199-11
US-10-61-199-11
US-10-61-199-11
US-10-61-199-11
US-10-61-199-11
US-10-61-199-11
US-10-61-199-11
US-10-61-199-11
US-10-61-199-11
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                                                                                                                                                                                                                                                                                                             1867569 segs, 417829326 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Match Length
                                                                                                                                                                                                                     1 GGYLWN 6
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                                                                                                                                                                                                                                                         BLOSUM62
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                                                                                                                                                                                                                                                         Scoring table:
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Result

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Gaps

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) ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Trp-containing cell adhesion recognition sequence
US-10-714-564A-1357
                                                                                                             67.5%;
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ORGANISM: Artificial Sequence
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                                                                                            Query Match
Best Local Similarity 60.v.
3, Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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1 GWVWN 5
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1 GWMWN 5
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US-10-714-564A-49
                                                                                                                                                                                                                                                                                                                  US-10-714-564A-16
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| Sequence 20, Application US/10714564A
| Publication No. US20040175361A1
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. |
| APPLICANT: Michaud, Stephanie D. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING |
| TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS |
| TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS |
| CURRENT FILING DATE: 2003-11-14 |
| NUMBER OF SEQ ID NOS: 1402 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1357, Application US/10714564A

Publication No. US20040175361A1

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: EVNCTIONS OF NONCLASSICAL CADHERINS
FILE REPERENCE: 100086, 418
CURRENT FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1402
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1357
                                                                                                                                                                                                                                                                                                                    Score 29; DB 3; Length 6; Pred. No. 1.7e+06; 0; Mismatches 1; Indels
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                               CURRENT APPLICATION NUMBER: US/09/791,551
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/185,390
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin Ver. 2.1
LENGTH: 6
                                                                                                                                                                                                                                                                                                                      72.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                FILE REFERENCE: 037003/0277869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0°
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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Best Local Similarity
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1 GWMWN 5
                                                                                                                                                                                                                                                                                                                                                                                                        2 GYLWN 6
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                                                                                                                                                                                                                                                           , ORGANISM: Mus sp.
US-09-791-551-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-10-714-564A-1357
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LENGTH: 6
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                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49, Application US/10714564A

Publication No. US20040175361A1

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: 2003-11-14
CURRENT APPLICATION NUMBER: US/10/714,564A

CURRENT FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1402

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.0%; Score 26; DB 4; Length 6; Best Local Similarity 60.0%; Pred. No. 1.7e+06; Matches 3; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                            0; Indels
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Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Stephanie D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
FILE REFERENCE: 100086.418
CURRENT APPLICATION NUMBER: US/10/714,564A
NUMBER OF SEQ ID NOS: 1402
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
  Length
Score 27; DB 4; I
Pred. No. 1.7e+06;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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; Publication No. US20040175361A1
; GENERAL INFORMATION:
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| Sequence 68, Application US/10798380
| Publication No. US20040265960A1
| Publication No. US20040265960A1
| GENERAL INFORMATION:
| APPLICANT: YOUNG, DEBORAH A. | APPLICANT: WILLIAMS, MATTHEW J. | APPLICANT: WILLIAMS, MARY | APPLICANT: COLLINS, MARY | APPLICANT: WILLIAMS, ANDREW JAMES | APPLICANT: WILLIAMS, ANDREW JAT-00000 | TILLE REPREFENCE: 08702.0137-00000 | CURRENT PILING DATE: 2004-03-12 | PRIOR FILING DATE: 2004-03-12 | PRIOR FILING DATE: 2003-03-14 | SOFTWARE: PATENTIN Ver. 3.2 | SOFTWARE: VER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.7e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                         APPLICAT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 0575/511400-9
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR PILING DATE: 1998-12-28
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1995-06-25
NUMBER: OF SEQ ID NOS: 121
SEQ ID NO 52
                                                                                                                                  US-09-940-727B-52
; Sequence 52, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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; ORGANISM: Homo sapiens
US-10-798-380-68
   1 GGYIAN 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: mouse
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel B.H.
APPLICANT: Hubert, Rene S.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Tanaporter Protein Enclied 108P5H8 Useful in Treatment and
TITLE OF INVENTION: Detection of Cancer
TITLE OF INVENTION: WUMBER: 06/256,210
FRIOR APPLICATION NUMBER: 06/256,210
PRIOR APPLICATION NUMBER: 06/256,210
PRIOR PRILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2598
SOFTWARE: PASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Trp-containing cell adhesion recognition sequence US-10-714-564A-1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.0%; Score 26; DB 4; Length 6; 60.0%; Pred. No. 1.7e+06; vative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Blaschuk, Orest W.
APPLICANT: Michaud, Stephanie D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
FILE REFERENCE: 100086.418
CURRENT APPLICATION NUMBER: US/10/714,564A
CURRENT FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1402
SEQ ID NOS: 1402
SEQ ID NO 1353
LENGTH: 6
                                                                                                                                                                                                                          Sequence 1353, Application US/10714564A Publication No. US20040175361A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 844, Application US/10024652
Publication No. US20030219738A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 60.03
Matches 3; Conservative
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US-10-024-652-844
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2 GWVWN 6
2 GYLWN 6
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1 GWVWN 5
                                                                                                                                                                                             -10-714-564A-1353
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LENGTH: 6
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US-11-041-199-1
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| Sequence 1588, Application US/10351641
| GENERAL INPORMATION:
| GENERAL INPORMATION:
| APPLICANT: Buthrie, K. |
| APPLICANT: Metutka, G. |
| APPLICANT: Lambert, D. |
| TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC |
| TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC |
| TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC |
| TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC |
| TITLE OF INVENTION: HYBRES: US/10/351,641 |
| FILE REFERENCE: 7872-100 |
| CURRENT PEDILCATION NUMBER: 09/350,641 |
| PRIOR FILING DATE: 1999-07-09 |
| PRIOR FILING DATE: 1999-05-20 |
| PRIOR PLING DATE: 1999-05-20 |
| PRIOR PILING DATE: 1999-05-20 |
| PRIOR PILING DATE: 1999-05-20 |
| WUMBER OF SEQ ID NOS: 1757 |
| SOFTWARE: PRESEC FOR WINGOWS VERSION 3.0
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                                                                APPLICANT: Ding, S.
APPLICANT: Kang, M.
APPLICANT: Kang, M.
APPLICANT: Kang, M.
APPLICANT: Venetta, T.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF
TITLE OF INVENTION: THERAPEUTIC REAGENTS
FILE REPERENCE: 7372-104
CURRENT APPLICATION NUMBER: US/10/347,562
CURRENT FILING DATE: 2003-01-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 48
LENGTH: 6
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US-10-714-564A-413
; Sequence 413, Application US/10714564A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Core polypeptide US-10-351-641-1588
                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: enhancer peptide US-10-347-562-48
Sequence 48, Application US/10347562
Publication No. US20030165555A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 60.0°
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1 GGWNW 5
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APPLICANT: ILANUALS. CHILLICIA K.
APPLICANT: DENONEZ-GARCIA, COSME
APPLICANT: TAHERI, MAYAM
APPLICANT: SCREATON, Robert A.
APPLICANT: SCREATON, Robert A.
APPLICANT: FUKS, Abraham
APPLICANT: FUKS, Abraham
FILE REFERENCE: 14952
CURRENT APPLICATION NUMBER: 09/11/041,199
CURRENT FILING DATE: 2005-01-25
PRIOR APPLICATION NUMBER: C39/0119
PRIOR PLILING DATE: 2000-08-11
PRIOR PLILING DATE: 1999-02-11
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-12
SUMMER OF SEQ ID NOS: 30
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Publication No. US20040175361A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Michaud, Stephanie D.
TITLE OF INVENTION: FUNCTIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
FILE REFREENCE: 100086.418
CURRENT APPLICATION NUMBER: US/10/714,564A
CURRENT FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1402
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 413
LENGTH: 6
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Pred. No. 1.7e+06;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Exemplary cyclic peptide US-10-714-564A-413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/11041199; Publication No. US20050153375A1; GENERAL INFORMATION:
APPLICANT: STANNERS, Clifford P.; APPLICANT: ILANTZIS, Christian; APPLICANT: ORDONEZ-GARCIA, COSME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/11041199; Publication No. US20050153375A1 GENERAL INFORMATION: APPLICANT: STANNERS, Clifford P.
                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.0
Matches 2; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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2 GWMWD 6
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### PAPLICANT: ILANTZIS, Christian
### PAPLICANT: ORDOWER_CARCIA, Cosme
### APPLICANT: TAHERI, Maryam
### PAPLICANT: TAHERI, Maryam
### PAPLICANT: SCRENTOM, Robert A.
### PAPLICANT: SARAGOVI, H. Uri
### PAPLICANT: SARAGOVI, H. Uri
### PAPLICANT: SARAGOVI, H. Uri
### PAPLICANT: SARAGOVI, CRA/MCA-BASED DIFFERENTIATION CANCER THERAPY
### PAPLICANT: SARAGOVI, 14 Uri
### PAPLICANTON NUMBER: US/11/041,199
### PRIOR FILING DATE: 2005-01-25
### PRIOR FILING DATE: 1998-02-11
### PRIOR FILING DATE: 1998-02-11
### PRIOR PLICANTON NUMBER: CAS/224,129
### PRIOR PLICANTON N
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41, Apr e 2193, Ap 78, Appl

737, App 160, App 3, Appli 5, Appli

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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WS-11-012-353-8

Sequence 8, Application US/11012353

Publication No. US20050249730A1

SEQUENCE CORVAIN NO. US20050249730A1

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIN, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: DUFLOS, ALAIN

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REPERENCE: 0.1753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: FR 0306538

PRIOR APPLICATION NUMBER: FR 0306538

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-07-11

PRIOR PILING DATE: 2002-01-20

PRIOR PILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOUTHWARR: PARCHING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOUTHWARRE: PARCHING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162
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US-10-925-366A-88

US-10-485-788A-228

US-10-485-788A-448

US-11-057-058-3

US-11-055-168A-41

US-11-052-168A-41

US-11-13-224-78

US-11-13-224-78

US-11-097-912-737

US-11-097-912-737

US-11-097-912-737

US-11-097-912-737

US-11-12-882-43

US-11-12-449-7

US-11-192-449-7

US-11-192-449-7
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US-11-009-939-23
; Sequence 23, Application US/11009939
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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       SEQ ID NO 8
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Sequence 470, Appl
Sequence 470, Appl
Sequence 121, Appl
Sequence 122, Appl
Sequence 243, Appl
Sequence 243, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 64, Appl
Sequence 19, Appli
Sequence 19, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                          December 30, 2005, 15:34:55 ; Search time 12 Seconds (without alignments)
3.744 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7 NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIO NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO NEW_PUB.pep:*
                     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-009-939-23
US-10-929-988-470
US-10-929-988-471
US-11-054-515-3210
US-10-299-988-122
US-10-645-788A-243
US-11-090-497-18
US-11-090-497-18
US-11-119-098-9
US-11-048-781-15
US-10-494-781-15
US-10-494-781-15
US-11-13-224-58
US-11-13-224-58
US-11-13-224-58
US-11-13-224-58
US-11-13-224-58
US-11-13-224-58
US-11-108-185-64
US-11-108-185-64
US-11-108-185-64
US-11-108-185-64
US-11-108-185-197-1
US-11-105-197-1
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US-10-846-188C-7
US-10-522-398-2
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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APPLICANT: BALU, PALANI
APPLICANT: BALU, PALANI
APPLICANT: BALU, PALANI
APPLICANT: BIPLANI, SUNILA
APPLICANT: BIPLANI, SUNILA
APPLICANT: BIPLANI, SUNILA
APPLICANT: STENATION: STETEM JOSEPH
TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
TITLE OF INVENTION: USES
FILE REFERENCE: 0300-0014
CURRENT APPLICATION NUMBER: US/10/929,988
FILE REFERENCE: 2004-08-30
PRIOR APPLICATION NUMBER: US/99/620,091
PRIOR APPLICATION NUMBER: US/99/620,091
PRIOR APPLICATION POSS: 491
SOUTHARD PALENTE 2000-07-20
NUMBER OF SEQ ID NOS: 491
SEQ ID NO 470
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## Publication No. US20050265998A1
| GENERAL INFORMATION:
| APPLICANT: Blson, USEQUESTIVE Andrew |
| TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof FILE REFERENCE: 23135-402
| CURRENT APPLICATION NUMBER: US/11/009,939
| CURRENT APPLICATION NUMBER: US/11/009,939
| PRIOR PILING DATE: 2003-12-10
| PRIOR PLING DATE: 2003-12-10
| PRIOR FILING DATE: 2003-12-10
| PRIOR PLING DATE: 2003-12-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 4.4e+04;
2; Mismatches 0; Indels
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Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.5
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-23
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1 GGYSWH 6
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; Sequence 471, Application US/10929988 ; Publication No. US20050277588A1

US-10-929-988-471

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APPLICANT: CWIRLA, STEVEN E.
APPLICANT: CWIRLA, STEVEN E.
APPLICANT: BALU, PALANI
APPLICANT: BIPLANI, SUNILA
APPLICANT: PIPLANI, SUNILA
APPLICANT: PIPLANI, SUNILA
APPLICANT: PIPLANI, STREEN JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING APPLINITY FOR THE GRANULOCYTE-COLONY
TITLE OF INVENTION: STHOULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
CURRENT APPLICATION NUMBER: US/10/929,988
CURRENT APPLICATION NUMBER: US/09/620,091
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
SOUTWARE: PACENTIN Ver. 2.1
SEQ ID NO 471
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JATILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPREMENTS: PROSENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPREMENT: 2005-02-10
PRIOR PELING DATE: 2005-02-11
PRIOR PELING DATE: 2004-06-18
PRIOR PELING DATE: 2004-06-18
PRIOR PELING DATE: 2004-06-18
PRIOR PELING DATE: 2004-11-14
PRIOR PELING DATE: 2001-11-14
PRIOR PELING DATE: 2001-11-14
PRIOR PELING DATE: 2001-11-16
PRIOR PELING DATE: 2001-11-16
PRIOR PELING DATE: 2001-11-16
PRIOR PELING DATE: 2001-11-16
PRIOR PELING DATE: 2001-06-15
PRIOR PELING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-16
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SEQ ID NO 3210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-929-988-471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 4.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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Publication No. US20050255532A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0
Matches 2; Conservative
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CORGANISM: Homo sapiens
US-11-054-515-3210
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3 GWVW 6
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US-11-054-515-3210
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APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: FLEXIBLE VACCINE ASSEMBLY AND VACCINE DELIVERY PLATFORM
FILE REFERENCE: N8630
CURRENT APPLICATION NUMBER: US/11/090,497
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 60/386,921
PRIOR APPLICATION NUMBER: 60/386,921
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR PILING DATE: 2002-09-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
SEQ ID NO 18
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                                                                                  Length 6;
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Pred. No. 4.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 243, Application US/10485788A

Publication No. US2005022743A1

GENERAL INFORMATION:

APPLICANT: Lu, Peter S.

APPLICANT: Lu, Peter S.

APPLICANT: Schweizer, Joshua D.

APPLICANT: Schweizer, Joshua D.

APPLICANT: Carrick, Deanna Marie

APPLICANT: Arbor Vita Corporation

ITLLE OF INVENTION: Molecular Interactions in Cells

FILE REFERENCE: 20054-003320US

CURRENT FALING DATE: 2004-02-03

PRIOR PLING DATE: 2004-02-03

PRIOR APPLICATION NUMBER: US 60/309,841

PRIOR APPLICATION NUMBER: US 60/309,641

PRIOR PLING DATE: 2002-08-03

PRIOR FILING DATE: 2002-08-05

PRIOR PLING DATE: 2002-08-05

PRIOR PLING DATE: 2002-08-05

PRIOR PLING DATE: 2002-08-05

NUMBER OF SEQ ID NOS: 841

SOFTWARE: PatentIn version 3.1
                                                                          Score 15; DB 6; 1
Pred. No. 4.4e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                      RESULT 8
US-11-090-497-18
; Sequence 18, Application US/11090497
; Publication No. US20050282263A1
; GENERAL INFORMATION:
                                                                                37.5%;
                                                                          Query Match
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.5
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: human laminin
US-11-090-497-18
     ; ORGANISM: Homo sapiens
US-10-485-788A-288
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; ORGANISM: Homo sapiens
US-10-485-788A-243
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Best Local Similarity
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                                                                                                                                                                                                                                   2 GOYW 5
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APPLICANT: BALU, PALANI
APPLICANT: BLU, PALANI
APPLICANT: BIPLANI, STUNILA
APPLICANT: PIPLANI, STUNILA
APPLICANT: PIPLANI, STUNILA
APPLICANT: SCHATZ, PRETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
TITLE OF INVENTION: STIMULATING PACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
TITLE OF INVENTION: STIMULATING PACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
TITLE OF INVENTION: USES
FILE REFERENCE: 0300-0014
CURRENT APPLICATION NUMBER: US/10/929,988
CURRENT FILLING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: US/09/620,091
PRIOR APPLICATION NUMBER: US/09/620,091
PRIOR PILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 491
SEQ ID NO 122
LENGTH: 6
LENGTH: 6
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
US-10-929-988-122
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Score 18; DB 7; Length 6;
Pred. No. 4.4e+04;
1; Mismatches 0; Indels
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Sequence 288, Application US/10485788A

Publication No. US20050282743A1

GENERAL INFORMATION:

APPLICANT: Lu, Feter S.

APPLICANT: Schweizer, Joshua D.

APPLICANT: Schweizer, Joshua D.

APPLICANT: Carrick, Deanna Marie

CURRENT APPLICATION NUMBER: US 60/360,061

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 841

CONTRANT OF SECTION 10 11
                                                                                                                                                                                                                                                                           Sequence 122, Application US/10929988
Publication No. US20050277588A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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LENGTH: 6
TYPE: PRT
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GENERAL INFORMATION,
SCHEMEL INFORMATION,
APPLICANT: MacKinnon, Roderick
APPLICANT: MacKinnon, Rasays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
FILE REFERENCE: 01812-002901US
CURRENT APPLICATION NUMBER: US/09/275,252
PRIOR APPLICATION NUMBER: US/09/275,252
PRIOR PLIING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-24
PRIOR PLLING DATE: 1998-04-02
PRIOR PLLING DATE: 1998-04-02
PRIOR PLLING DATE: 1998-04-02
PRIOR PLLING DATE: 1998-04-02
PRIOR PLLING DATE: 1999-04-02
PRIOR PLLING DATE: 1999-04-05
PRIOR PLLING DATE: 1999-04-05
PRIOR PLLING DATE: 1999-04-05
PRIOR PLING DATE: 1999
                                  APPLICATION RINGS COllege London
TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
FILE REFERENCE: IT/KE/N13246
CURRENT APPLICATION NUMBER: US/10/494,781
CURRENT PELLING DATE: 2004-05-06
PRIOR FILING DATE: 2001-11-09
PRIOR PRICATION NUMBER: GB 0127000.8
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 6
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Pred. No. 4.4e+04;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (5)...(5)
CTHER INFORMATION: any amino acid
US-10-494-781-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE LOCATION: (3)...(3) OTHER INFORMATION: any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.5%;
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Publication No. US20050244895A1
GENERAL INFORMATION:
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Matches 2; Conservative
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ORGANISM: Bovine
FEATURE:
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2 FXW 4
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                                                                                                                                                                                                                                              Sequence 9, Application US/11119098
Publication No. US20050267030A1
Publication No. US20050267030A1
GENERAL INFORMATION:
APPLICANT: Teao, Philip S.
APPLICANT: Modelly-Rosen, Daria
APPLICANT: Beoon Paria
APPLICANT: Modelly-Rosen, Daria
TITLE OF INVENTION: Use of deliaPKC Peptides for Modulation of Reactive Oxygen Specie
FILE REFERENCE: 58600-8213.US00
CURRENT APPLICATION NUMBER: US/11/119,098
CURRENT PILING DATE: 2005-04-29
PRIOR FILING DATE: 2004-04-30
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 6
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US-10-494-781-13
i Sequence 13. Application US/10494781
i Sequence 13. Application US/10494781
i Publication No. US20050244895A1
i GENERAL INFORMATION:
i TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
i TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
i TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
i FILE REFERENCE: IT/RE/N13246
i CURRENT FILING DATE: 2004-05-06
i PRIOR PILING DATE: 2001-11-09
i PRIOR FILING DATE: 2001-11-09
i PRIOR FILING DATE: 2002-11-09
i PRIOR FILING DATE: 2002-02-04
i NUMBER OF SEQ ID NOS: 28
i SOFTWARE: PatentIn version 3.1
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Pred. No. 4.4e+04;
1; Mismatches 1; Indels
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         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: beta-PKC-selective activator peptide US-11-119-098-9
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         1; Mismatches
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; Sequence 15, Application US/10494781
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Similarity 33.3%;
1; Conservative
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            2; Conservative
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Best Local Similarity
Matches 1; Conserv
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ORGANISM: Bovine
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US-11-119-098-9
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; Publication No. US20050244899A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Young, David S.F.
APPLICANT: Warner, Andrea
APPLICANT: MCCOMPLY, Fortunata
APPLICANT: MCCOMPLY, Fortunata
APPLICANT: MCCOMPLY, CARTING DAVINGARY, POTTURE OF INVENTION: Laminin Receptor 1 Precursor Protein (37LRP) Epitope Delineated F
TITLE OF INVENTION: Heptocellular Carcinoma Specific Antibody
TITLE OF INVENTION: Heptocellular Carcinoma Specific Antibody
FILE REFERENCE: 2056.049
CURRENT APPLICATION NUMBER: US/11/079,969
CURRENT APPLICATION NUMBER: US 10/810,163
FRIOR FILING DATE: 2004-03-26
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 2000-11-29
FRIOR FILING DATE: 2000-11-29
FRIOR FILING DATE: 2000-11-29
FRIOR FILING DATE: 2000-11-3
FRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 6
SSOTHARE PATENTIN VERSION 3.1
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US-11-079-969-1
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                                                                                                US-10-485-788A-138

is Sequence 138, Application US/10485788A

is Sequence 138, Application US/10485788A

is Publication No. US20050282743A1

is GENERAL INFORMATION:

is APPLICANT: Lu, Peter S.

APPLICANT: Schweizer, Joshua D.

APPLICANT: Schweizer, Johannes

APPLICANT: Carrick, Deanna Marie

APPLICANT: Carrick, Deanna Marie

APPLICANT: Carrick, Deanna Marie

APPLICANT: Carrick, Deanna Marie

APPLICANT: APPLICATION: Molecular Interactions in Cells

FILE REFERENCE: 2005-0-03320US

FURRENTY FILING DATE: 2004-02-03

PRIOR APPLICATION NUMBER: US 60/369,841

FRIOR APPLICATION NUMBER: US 60/369,061

PRIOR APPLICATION NUMBER: US 60/360,061

PRIOR APPLICATION NUMBER: WO PCT/US02/24655

PRIOR PILING DATE: 2002-02-25

PRIOR FILING DATE: 2002-09-02

NUMBER OF SEQ ID NOS: 841

SOFTWARE: PatentIn version 3.1

LENGTH. 6
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US-10-485-788A-138
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2 IW 3
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32.5%; Score 13; DB 7; Length 6; 50.0%; Pred. No. 4.4e+04;
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Query Match
Best Local Similarity 50.0
Matches 1; Conservative
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                                                                                                                                      December 30, 2005, 13:02:01; Search time 142.194 Seconds (without alignments) 49.440 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Adz45405 Murine ta Aab73388 Anti-VHSV	_		_		<u>—</u>	_	Adz51254 Amino aci	_	Abb98908 Variable		Adj76904 Anti-IGF-	Mouse a	0	_	Adz51224 Amino aci	Adz42098 Mouse ant	Adz45309 Murine fa	Adz51222 Amino aci	Adz42096 Mouse ant	
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ADZ45405 AAB73388	ADZ45343	ADZ51256	ADZ42130	ABU56867	AEA40153	ADZ45341	ADZ51254	ADZ42128	ABB98908	ADR38665	ADJ76904	ADZ67074	ADZ45520	ADZ45311	ADZ51224	ADZ42098	ADZ45309	ADZ51222	ADZ42096	
o 4	6	σ	6	ø	σ	σ	σ	σ	9	œ	7	σ	0	Φ	σ	σ	σ	σ	σ	
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82.0	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	79.8	79.8	78.7	78.7	78.7	78.7	78.7	78.7	78.7	
73	7.2	72	72	72	72	72	72	72	72	72	71	71	70	70	70	70	70	70	70	
5 7	22	8	6	0	11	22	33	4	2	96	37	38	39	40	41	24	1 6	4	12	

13.

## ALIGNMENTS

cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR sequence for anti-IGF-1R antibody. (FABR ) FABRE MEDICAMENT SA PIERRE. ADJ76844 standard; peptide; 16 AA Leger 0; 18-JAN-2002; 2002FR-00000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178. (first entry) Corvaia N, WPI; 2003-569653/53 N-PSDB; ADJ76843 WO2003059951-A2. Mus musculus. 06-MAY-2004 24-JUL-2003 Goetsch L, ADJ76844;

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers. Claim 1; SEQ ID NO 10; 164pp; French

The invention relates to an isolated antibody (Ab), and its fragments, that bind to human insulin-like growth factor-1 ill and optionally: (1) inhibit natural binding of insulin-factors (IGF)-1 and/or -2; and/or (1) inhibit specifically kinase activity of IGF-1R. Ab and its fragments are used to treat diseases associated with overexpression and/or abnorm IGF-1R and/or epidermal growth factor receptor (EGFR) and/or

Aay94391 | Adz45407 |

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specifically inhibiting tyrosine kinase activity of the receptor,

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                          these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of ICRTR and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
   hyperactivity of signal transduction pathways mediated by interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 89; DB 7; Length 16; 100.0%; Pred. No. 6.1e-07;
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18-JAN-2002; 2002FR-0000654.

07-MAY-2002; 2002FR-00005753.

20-JAN-2003; 2003MO-FR001178.

11-JUL-2003; 2003FR-00008538.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                       Sequence 16 AA;
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(HAEU/)
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AD267014

AD27014

AD267014

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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of

Claim 1; SEQ ID NO 10; 125pp; English.

Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.

Beck A;

Leger O, Duflos A, Haeuw J,

Goetsch L, Corvaia N, WPI; 2005-321968/33.

BECK A.

BECK/)

N-PSDB; ADZ67013.

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Specializally initioning tyrosine kinase activity of the receptor, determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a an interaction of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 89; DB 9; Length 16; 100.0%; Pred. No. 6.1e-07;
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Best Local Similarity
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (1) inhibit natural binding of insulin-like growth and optionally: (1) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endomerrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; antipsoriatic; antibody; IGF-IR; tyrosine kinase activity; insulin-like growth factor-1 receptor; EGFR; signal transduction pathway; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                     antibodies that bind to human insulin-like growth factor receptor, iul for treatment, prevention and diagnosis of cancers.
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100.0%; Pred. No. 5e-06;
ive 0; Mismatches 0; Indels
                                                                                                                                                Disclosure; SEQ ID NO 69; 164pp; French
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                   Leger 0;
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18-JAN-2002; 2002FR-0000054.
07-MAY-2002; 2002FR-00005753.
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nes 16; Conservative
                   Corvaia N,
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                   Goetsch L,
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                                             The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or-2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. Jung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are a also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 83; 164pp; French
               Disclosure; SEQ ID NO 75; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; antipsoriatic; antibody;
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07-MAY-2002; 2002FR-00005753.
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treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
activity of IGF-1R. Ab and its fragments are used to prevent
                                                                                                                                                                                                                                                                                                                                                                            Sequence 117 AA;
88666666666688888
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Query Match

ö Score 89; DB 7; Length 117; Pred. No. 5e-06; ; Mismatches 0; Indels ch 1 Similarity 100.0%; Pi 16; Conservative 0; 1 YISYDGTNNYKPSLKD 16 Best Local Similarity Matches ð

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Gaps

99 51 YISYDGTNNYKPSLKD

ADJ76913 standard; protein; 117 AA. 

(first entry) 06-MAY-2004 ADJ76913;

cytostatic; antipsoriatic; antibody; Anti-IGF-1R related protein #24

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;

Homo sapiens

WO2003059951-A2

24-JUL-2003

20-JAN-2003; 2003WO-FR000178

18-JAN-2002; 2002FR-00000653. 2002FR-00005753 07-MAY-2002; (FABR ) FABRE MEDICAMENT SA PIERRE.

Goetsch L, Corvaia N,

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WPI; 2003-569653/53.

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Disclosure; SEQ ID NO 79; 164pp; French

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or recet diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells, so are useful against cancers of the

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prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriaais. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                  Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostet tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; colon tumor; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
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Pred. No. 5e-06;
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                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                              ADZ67083 standard; protein; 117 AA.
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                                                                                                          100.0%;
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; 2002FR-00005753.
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; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                          16; Conservative
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                                                                                                       Query Match
Best Local Similarity
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CORVAIA N
LEGER O.
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                                                                             Sequence 117 AA;
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11-JUL-2003;
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07-MAY-2002;
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(LEGE/)
(DUFL/)
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(BECK/)
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The preparation of a medicament intended for the prevention of Library activation of the IGP-IR and/or EGFR, and/or connected with a activation of the IGP-IR and/or EGFR, and/or connected with a activation of the transduction pathway of the signal mediated by the interactivation of the transduction pathway of the signal mediated by the interaction of IGPI or IGP2 with IGP-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGP-dependent, especially IGP1 and/or IGF2.

C dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or EGF-dependent.

C EBFZ/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of the IGF-IR and/or EGFR receptor overexpression or an underexpression of the IGF-IR and/or EGFR receptor is suspected, which involves contacting the sequence is used in the exemplification of the involves contacting the expense in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
preparation of a medicament intended for the prevention or treatment
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07-MAY-2002; 2002FR-00005733.
20-JAN-2003; 2003MO-FR000178.
11-JUL-2003; 2003FR-00008538.
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The invention relates to a novel isolated anti-insulin-like growth factor or receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting to human IGF-IR and, if necessary, capable of specifically inhibiting to human IGF-IR and, if necessary, capable of specifically inhibiting to one kind control of comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in a the preparation of a medicament intended for the prevention or treatment of an illness connected with and/or connected with an abnormal activation of the IGF-IR and/or EGFR, and/or connected with an abnormal activation of the IGF or IGF2 with IGF-IR and/or connected with an abnormal activation of the antibody is useful for preparation of the medicament does not induces accondary effects connected with inhibition of the insulan receptor. The antibody is useful for preparation of the connected with inhibition of the insulan receptor. The antibody is useful for preparation of a medicament intended connected with inhibition of the insulan condependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-depende
                                                                                                                                                                                             Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.
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                                                                                                                     Haeuw J,
                                                                                                                     Duflos A,
                                                                                                                                                                                                                                                                                                        Example 13; SEQ ID NO 83; 125pp; English.
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                                                                                                                       Goetsch L, Corvaia N,
                                                                                                                                                               WPI; 2005-321968/33
CORVAIA N.
LEGER O.
DUFLOS A.
                                                             HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 117 AA;
                                                                                   BECK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADZ67073;
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                                                             (HAEU/)
(BECK/)
                       (LEGE/)
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Matches
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(GOET/) GOETSCH

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Novel
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The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGP-IR) antibody (I) or its functional fragment, being
capable of binding to human IGP-IR and, if necessary, capable of
specifically inhibiting tyrosine kinase activity of the receptor,
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one complementary
comprising a light or heavy chain having at least one capable for the prevention of the IGF-IR and/or Edger, but of the prevention or treatment
cot an illness connected with an overexpression and/or an abnormal
cativation of the IGF-IR and/or Edger, and/or compected with a
hyperactivation of the IGF-IR and/or of Edger, with Edger, and/or of Edger, where
the administration of the medicament does not induce or only alightly
induces secondary effects connected with inhibition of the insulin
creceptor. The antibody is useful for preparation of a medicament intended
to inhibit the transformation of normal cells into cells with tumoral
character, preferably IGF-dependent, especially IGF1 and/or IGF2control or preparation of a medicament intended to inhibit the growth
and/or the proliferation of tumor cells, preferably IGF-dependent
control or IGF-dependent and/or EGF-dependent
control or IGF-dependent and/or EGF-dependent
control or IGF-dependent and/or EGF-dependent
control or IGF-dependent and/or IGF-dependent
control or IGF-dependent intended to inhibit the growth
control or IGF-dependent intended to inhibit the growth
control or IGF-dependent intended to inhibit the growth
control or IGF-dependent intended to inhibit the IGF-dependent
control or IGF-dependent intended to inhibit the IGF-dependent neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetries; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermacological disease; immune disorder; immune disorder; HERZ/neu-dependent cells. (1) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (1) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (1) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (1) is useful in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGFisolated anti-insulin-like growth factor I receptor (IGF-IR) ody or its functional fragment, being capable of binding human IGF-d specifically inhibiting tyrosine kinase activity of receptor, Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; Duflos A, Haeuw J, Example 13; SEQ ID NO 69; 125pp; English. Leger O, 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003MO-FR000178. 11-JUL-2003; 2003FR-00008538. 16-DEC-2003; 2003US-00735916. 2002FR-00000653 useful for treating cancer. Corvaia N, WPI; 2005-321968/33 GOETSCH L. CORVAIA N. LEGER O. DUFLOS A. US2005084906-A1 BECK A. Mus musculus. 8-JAN-2002; 21-APR-2005. antibody or Goetsch L, GOET/) DUFL/) HAEU/) BECK/) TEGE/) and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tryoshine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment
                                                                                                                                                                                                                                                                                                                                                                                       Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; andometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                            Gaps
IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                            Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beck A;
                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haeuw J,
                                                                                            Score 89; DB 9;
Pred. No. 5e-06;
; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; SEQ ID NO 75; 125pp; English.
                                                                                                                                                                                                                                                                  ADZ67079 standard; protein; 117 AA.
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2002FR-00005753.
2003WO-FR000178.
2003FR-00008538.
                                                                                              100.08;
                                                                                                              100.08;
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                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                         1 YISYDGTNNYKPSLKD
                                                                                                                                                                            51 YISYDGTNNYKPSLKD
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-321968/33.
                                                                                              Query Match
Best Local Similarity
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                   Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2002;
18-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-2002;
20-JAN-2003;
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                                                                                                                                                                                                                                                                                                                               30-JUN-2005
                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2005
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                                                                                                                                                                                                                                                                                                  ADZ67079;
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(BECK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LEGE/)
(DUFL/)
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                                                                                                                              Matches
                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                       ADZ6707
      ន្តដ្ឋប្រទទ
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of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cativation of the transduction pathway of the signal mediated by the interactivation of IGFI or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly conducted with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral constants, preferably IGF-dependent, especially IGF1 and/or IGF2.

C dependent and/or EGF-dependent and/or HER2/neu-dependent cells. [1] is useful for preparation of a medicament intended to inhibit the growth capecially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or EGF-dependent or IGF2-dependent and/or EGF-dependent or IGF2-dependent or IGF2-dependent and/or EGF-dependent or IGF2-dependent and/or EGF-dependent capecially IGF1-and/or IGF2-dependent and/or EGF-dependent or IGF2-dependent or IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 89; DB 9; Length 117; 100.0%; Pred. No. 5e-06; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; antipsoriatic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ76886 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-IGF-1R related protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2002; 2002FR-00000653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2002; 2002FR-0000654
07-MAY-2002; 2002FR-00005753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YISYDGTWNYKPSLKD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 YISYDGTNNYKPSLKD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-569653/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003059951-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ76886;
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                                                                            The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with these receptors with their ligands. Especially they inhibit transformation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the prostate. Iung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriaais. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endorentne disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipportatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.
New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    Length 127;
                                                                                                                                                                                                                                                                                                                     protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 89; DB 7; L
100.0%; Pred. No. 5.5e-06;
tive 0; Mismatches 0;
                                                  Disclosure; SEQ ID NO 52; 164pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .10
/note= "leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADZ67056 standard; protein; 127 AA.
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2002FR-00005753.
2003WO-FR000178.
2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41. .46
/note= "CDR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61. .76
/note= "CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YISYDGTNNYKPSLKD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YISYDGTWWYKPSLKD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .116
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                        Sequence 127 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2002;
18-JAN-2002;
07-MAY-2002;
20-JAN-2003;
11-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fus musculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;

cytostatic; antipsoriatic; antibody;

Anti-IGF-1R related protein #23.

06-MAY-2004 (first entry)

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The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
pecifically inhibiting tyrosine kinase activity of the receptor,
comprising a light or heavy chain having at least one complementary
determining region (CDR) consisting of one of two fully defined 16 anino
caids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
the preparation of a medicament intended for the prevention or treatment
of an illness connected with an overexpression and/or an abnormal
activation of the IGF-IR and/or EGFR, and/or connected with a
hyperactivation of the transduction pathway of the signal mediated by the
induces secondary effects connected with inhibition of the insulin
connectes of IGF-IR and/or EGFR, and/or of EGF with EGFR, where
the administration of the medicament does not induce or only slightly
induces secondary effects connected with inhibition of the insulin
creeptor. The antibody is useful for preparation of a medicament intended
to inhibit the transformation of normal cells with tumoral
character, preferably IGF-dependent, especially IGF and/or IGF2
dependent and/or IGF2-dependent and/or HER2/dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-adpendent or Colon cancer, optendent cells. (I) is useful in the preparation of a medicament intended for the specific targeting the IGF-IR and/or IMF2-adpendent or of IGF2-IMF2-IMF2-Adpendent and/or IMF2-adpendent and/or IMF2-IMF2-IMF2-IMF2-IMF2-IM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                   Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                    Beck A;
                                                                                                                                                                                                    Haeuw J,
                                                                                                                                                                                               Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; SEQ ID NO 52; 125pp; English.
                                                                                                                                                                                                 Leger 0,
                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating cancer.
                                                                                                                                                                                               Corvaia N,
                                                                                                                                                                                                                                                WPI; 2005-321968/33.
                       GOETSCH L.
CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                       N-PSDB; ADZ67055
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                                                                                                                                                   BECK A.
                                                                                                                                                                                                 Goetsch L,
                                                                                                  (DUFL/)
(HAEU/)
                            GOET/)
                                                                   (LEGE/)
                                                                                                                                                   BECK/)
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Gaps
                                  ö
      100.0%; Score 89; DB 9; Length 127; 100.0%; Pred. No. 5.5e-06;
                                 0; Indels
                                 Mismatches
                                  .
                                                           1 YISYDGTNNYKPSLKD 16
                                                                                    61 YISYDGTNNYKPSLKD 76
Query Match
Best Local Similarity 100.
                                                                                                                            RESULT 13
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ADJ76911 standard; protein; 135 AA.

ADJ7691:

ADJ76911;

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cytostatic, antipsoriatic, antibody, insulin-like growth factor-1 receptor; IGF-1R, tyrosine kinase activity, or epidermal growth factor receptor; EGFR; signal transduction pathway;
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                            Length 135;
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100.0%; Pred. No. 5.9e-06;
iive 0; Mismatches 0;
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This sequence represents a

protein sequence used to generate the Ab of the invention

abnormal expression of IGF-1R and/or EGFR.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-18) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-18. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-18 and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused also for treating psoriasis. Ab are also used to diagnose diseases caused

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

(FABR ) FABRE MEDICAMENT SA PIERRE

2002FR-00000654 2002FR-00005753

18-JAN-2002; 07-MAY-2002;

20-JAN-2003; 2003WO-FR000178. 18-JAN-2002; 2002FR-00000653.

WO2003059951-A2. Homo sapiens.

24-JUL-2003

Goetsch L, Corvaia N, Leger O;

WPI; 2003-569653/53.

Disclosure; SEQ ID NO 77; 164pp; French

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24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal calls, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; antipsoriatic; antibody; IGF-1R; tyrosine kinase activity; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.
ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                           New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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18-JAN-2002; 2002FR-0000654.
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                                         Homo sapiens
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100.0%; Pred. No. 5.9e-06;
tive 0; Mismatches 0;
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                                                                18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178
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Matches
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3 11:16:34 2006

Tue Jan

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein December 30, 2005, 13:11:41; Search time 22.7097 Seconds (without alignments) 67.789 Million cell updates/sec Run on:

1 YISYDGTWNYKPSLKD 16 US-10-735-916A-10 89 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description		ileavy cilatii v	heavy chain pr	heavy chain V	heavy	heavy chain V	heavy	chain V	heavy	heavy chain V	heavy chain V	heavy	heavy	heavy	heavy	g heavy chain pr	g heavy chain	g heavy	heavy chain	g lambda	g heavy	heavy chain pr	heavy cha	variable reg	heavy che	heavy chain V	heavy cha	heavy chain V	heavy cha	Ig heavy chain V r
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#### ALIGNMENTS

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Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Musculus (1995 #text_change 23-Jul-1999
R;Kavaler, J.
R;Kav

Gaps ö Query Match

84.3%; Score 75; DB 2; Length 104;
Best Local Similarity 81.2%; Pred. No. 5.2e-05;
Matches 13; Conservative 2; Mismatches 1; Indels

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YISYDGSNNYNPSLKN 57 1 YISYDGTWNYKPSLKD 16 셤 ઠ

### RESULT 2

.....gh heavy chain precursor V region (M115) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

C; Accession: JT0509

Rilevy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary ir A;Reference number: JT0501; MUID:89279149; PMID:2499654
A;Accession: JT0509
A;Status: translation not shown

A MOLECULE TYPE: MENA A; Residues: 1-116 < LEV> A; Cross-references: UNIPROT: P18531; UNIPARC: UPI00000278E0 A; Cross-references: Strain BALB/CJ C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;1-18/Domain: signal sequence #status predicted <SIG> F;19-116/Product: Ig heavy chain V region (M315) #status predicted <MAT> F;33-116/Domain: immunoglobulin homology <IMM>

Gaps .; 0 Length 116; Query Match

84.3%; Score 75; DB 1; Length 116

Best Local Similarity 81.2%; Pred. No. 5.8e-05;

Matches 13; Conservative 2; Mismatches 1; Indels

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Ajmolecule type: mRNA
AjRolecule type: mRNA
AjRosatuse: 1-116 <CIM>
AjCross-references: UNIPARC:UPI0000117542; EMBL:X76018; NID:g416102; PIDN:CAA53605.1; PII
G;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
A;Cross-references: UNIPARC:UP10000115E36; EMBL:X16740; NID:g52099; PIDN:CAA34714.1; PID:
A;Note: the authors translated the codon TAT for residue 112 as Ile, TAC for residue 113
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Ristischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F. submitted to the RMBL Data Library, August 1993
Ai; Pescription: Production and cloning of TMV-specific monoclonal antibodies.
Ai; Reference number: 837200
Ai; Status: preliminary
Ai; Status: preliminary
Ai; Status: Pusculus type: mRNA
Ai; Residues: 1-121 FFISs
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38718
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
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                         A,Note: the authors translated the codon TAT for residue 112 as C,Genetics:
A,Introns: 15.
A,Introns: 15.
A,Introns: 15.
C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-120 <OLL.>
A;Cross-recences: UNIPARC:UPI0000115D15; GB:X03374; NID:g51983; PIDN:CAA27071.1; PID:g
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
C;Accession: E25114
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A;Title: The idiotypic network and the internal image: possible regulation of a germ-lir
A;Reference number: A91028; MUID:86136012; PMID:3937730
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A25114

Igh heavy chain V region (HP22, HP27) - mouse
C;Species: Wus musculus (house mouse)
C;Species: Wus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
C;Accession: A25114
EMBO J. 4, 3681-368, 1985
A;Title: The idictypic network and the internal image: possible regulation of a germ-lint A;Reference number: A91028; MUID:86136012; PMID:3937730
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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S07637
S07637
Ig heavy chain V region (PTF.02) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C;Accession: S07637
R;Urakov, D.N.; Deev, S.M.; Polyanovsky, O.L.
Nucleic Acids Res. 17, 9481, 1989
A;Title: The structure of the expressible VH gene from a hybridoma producing monoclonal A;Reference number: S07637; MUID:90067954; PMID:2587273
A;Accession: S07637
A;Accession: S07637
A;Residues: 1-136 <URA>
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Pred. No. 0.00039;
3; Mismatches 1; Indels
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Pred. No. 0.00018;
3; Mismatches 1;
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Query Match
Best Local Similarity 75.0%;
Matches 12; Conservative

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RESULT

78.7%; 75.0%;

Best Local Similarity 75.0 Matches 12; Conservative

Query Match

A;Accession: E25114 A;Molecule type: mRNA A;Residues: 1-119 <OLL>

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C;Accession: D25114
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
Embo J. 4, 3681-3689, 1985
A;Title: The idiotypic network and the internal image: possible regulation of a germ-line A;Reference number: A91028; MUID:86136012; PMID:3937730
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-137 <RIN>
A;Cross-references: UNIPROT:P01822; UNIPARC:UPI000002727B; GB:M27638; NID:g602706; PIDN:
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A,Nolecule type: To',16-137 <RI2>
A,Regidues: L15,'G',16-137 <RI2>
A,Cross-references: UNIPARC:UPI000016CE1C; EMBL:X07880; NID:g51760; PIDN:CAA30727.1; PID
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Proc. Natl. Acad. Sci. U.S.A. 74, 5692-5696, 1977
A;Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin he
A;Reference number: A93814; MUID:78094475; PMID:414225
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24.Apr-1994 #sequence-revision 30-Jun-1992 #text change 09-Jul-2004
C;Accession: PL0102; S03262; A93814; A94462; A93787; S23599
R;Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.
A). Immunol. 26, 431-44, 1989
A;Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.
A;Reference number: PL0102; MUID:89238351; PMID:2497341
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A; Title: Structure and function of immunoglobulin genes and precursors. A; Reference number: A91462; MUID: 79148758; PMID: 428562
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (HP21) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
Gaps
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Pred. No. 0.011;
2; Mismatches
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R;Rinfret, A.; Dorrington, K.J.; Klein, M.
submitted to the EMBL Data Library, June 1988
A;Reference number: $03262
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A;Residues: 1,'X',3-11,'X',14-21 <SCH>
A;Cross-references: UNIPARC:UP1000017373F
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ilarity 68.8%;
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          11; Conservative
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Best Local Similarity
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A; Residues: 1-119 < OLL>
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                Matches
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Ig heavy chain V region (HP12) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: P25114
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
RMOJ, G. 4, 3681-3881, 1985
A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin A;Title: The image: WINDRAC:UPI000115D28; GB:X03379; NID:G52013; PIDN:CAA27101.1; PID:GC;Superially: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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19 heavy chain V region (anti-haloperidol antibody D) - mouse
19 heavy chain V region (anti-haloperidol antibody D) - mouse
19 heavy chain V region (anti-haloperidol antibody D) - mouse
19 heavy chain V region (anti-haloperidol)
19 heavy chain V region (anti-haloperidol)
19 heavy chain V region (anti-haloperidol)
19 heavy chain V region 30-Sep-1991 #text_change 23-Jul-1999
19 heavy chain V region N r.J.; Belger, M.B.
19 heavy chain V region W r.J.; Belger, M.B.
19 heavy chain V region W r.J.; PMID:3267217
19 heavy chain V region W region W region amino acid show the authors translated the codon AAC for residue 61 as Thr, and did not translated; Superfamily: immunoglobulin homology
19 heterotetramer; immunoglobulin homology clMM>
19 heterotetramer; immunoglobulin homology clMM>
19 heterotetramer; immunoglobulin homology clMM>
10 heavy chain immunoglobulin homology clMM>
10 heavy chain region with region region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region with region region with region region with region with region with region region with region with region with region region with region region with region with region with region region region with region region with region region region region region region region region region region region region region region region region region 
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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[19 heavy chain V region (HP20) - mouse
[10 heavy chain V region (HP20) - mouse
[10 heavy chain V region (HP20) - mouse
[11 heavy chain V region (12 house mouse)
[12 heavy chain V region (13 heavy 1987 # text_change 20 Jun-2000
[13 heavy chain V region (13 heavy V region V region (13 heavy V region V region V region (13 heavy V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V region V reg
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Pred. No. 0.011;
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Best Local Similarity 68.8
Matches 11; Conservative
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December 30, 2005, 13:34:56
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Job time : 23.7097 secs
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A; Note: the authors translated mRNA in vitro to obtain the precursor protein
R; Francis, S.H.; Leslie, R.G.Q.; Hood, L.; Eisen, H.N.
Proc. Natl. Acad. Sci. US.A. 71, 1123-1127, 1974
A; Title: Amino-acid sequence of the variable region of the heavy (alpha) chain of a mous
A; Reference number: A93787; MUD: 74170779; PMID: 4524622
A; Accession: A93787
A; Molecule type: protein
A; Residues: 19-52, K., 53-75, 'BYGB', 80-101, 'D', 103-106, 'ZB', 109-122, 124-137 < FRA>
A; Cross-references: UNIPARC: UPIO000173740
R; Hood, L.; Margolies, M.; Givol, D.; Zakut, R.
unpublished results, cited by Padlan, B.A., Davies, D.R., Pecht, I., Givol, D., and Wrig
A; Reference number: A94484
                                                                                                                                                                                                                                                                                                                                            A.Contents: annotation; revision to residue 53
R.Cheadle, C.; Hook, D.B.; Givol, D.; Ricca, G.A.
Mol. Immunol. 29, 21-30, 1992
A;Title: Cloning and expression of the variable regions of mouse myeloma protein MOPC315
A;Reference number: S23599; MUID:92114886; PMID:1731188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
15.95639
15.9649
16.596468: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Mar-1999
C;Accession: 859639
R;Bossart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S. J. Mol. Biol. 253, 559-575, 1995
J. Mol. Biol. 253, 559-575, 1995
A;Rieference number: 859639; MUID:96068846; PMID:7473734
A;Accession: 859639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
Kresidues: 19-137 cCHB>
A;Cross-references: UNIPARC:UPI0000113794; EMBL:X63972; NID:953532; PIDN:CAA45384.1; PID
C;Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitrophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C'Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-136/Product: Ig heavy chain V region (MOPC 315) #status experimental <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan_1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 8-91/Domain: immunoclobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61; DB 1; Length 137;
Pred. No. 0.013;
3; Mismatches 3; Indels
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Pred. No. 0.03;
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Best Local Similarity 62.5%;
Matches 10; Conservative
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A; Residues: 1-106 < BOS>
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submitted to the EMBL Data Library, April 1991

A;Reference number: $26459

A;Recession: $26464

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 < KAV>

A;Cross-references: UNIPARC:UPI0000115F68; EMBL:X59114; NID:g51926; PIDN:CAA41840.1; PID:C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology < IMM>
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Best Local Similarity 66.7
Matches 10; Conservative
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ses 10; Conservative
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SMR; P1853; 19-116.
Ensembl; ENSWUSGO0000057048; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00466; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
SIGNAL.
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                                                       December 30, 2005, 13:11:26 ; Search time 144 Seconds (without alignments) 78.392 Million cell updates/sec
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Q7z3y6
Q6mzx7
Q8wux4
Q9bul0
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Q53vr7
Q99m22
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Q6gmx1
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                   2166443 seqs, 705528306 residues
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053VQ9 WOUSE
HV46 WOUSE
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09U173_HUMAN
HV47_MOUSE
0569B6_RAT
HV61_MOUSE
06GWX_HUMAN
04JSK6_CORJK
0652I1_MOUSE
0652I1_MOUSE
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Q53VR7 MOUSE
Q99M22 MOUSE
Q53VQ4 MOUSE
Q53VQ5 MOUSE
Q61BQ5 MOUSE
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Q6MZX7 HUMAN
Q8WUX4 HUMAN
Q9BU10 HUMAN
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Maximum Match 100%
Listing first 45 summaries
                                     model
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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1 YISYDGTNNYKPSLKD 16

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Ig heavy chain V region M315.
Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.

13095 MW; 4562E03E53DC9E10 CRC64; By similarity.

116 AA;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                   MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P. active and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03375; CAA27078.1; -; mRNA.
EMBL; X03374; CAA27071.1; -; mRNA.
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Forgereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03375; CAA27077.1; -; mRNA.
EMBL; X03374; CAA27071.1; -; mRNA.
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120 AA; 13892 MW; 013452306EBAA3BE CRC64;
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Pred. No. 0.00077;
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
VH-D-JH region (Fragment).
69 YISYDGSNNYNPSLKN
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TISSUB=Mammary tumor. WAP-TGF alpha model. 7 months old;
TISSUB=Mammary tumor. WAP-TGF alpha model. 7 months old;
TISSUB=Mammary tumor. WAP-TGF alpha model. 7 months old;
TISSUB=Mammary tumor. WAP-TGF alpha model. 10.103/pnas.242603899;
A traubberg R.D., Feingold B.A., Grouse L.H., Derge d.G.,
A listenia R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A listenia R.P., Joxdan H., Moore T., Max S.I., Mang J., Haishe F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boosk S.A., McEwan P.J., McKernan K.J., Malek J.J., Hulyk S.W.,
A villaion D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
A Rachquez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Benerthon and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                             Gaps
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       Length 120;
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                                                                         1; Indels
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SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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80.9%; Score 72; DB 2; I
75.0%; Pred. No. 0.00097;
iive 3; Mismatches 1;
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PROSITE; PS00290; IG MHC; UNKNOWN_2.
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                                                                                                                                               1 YISYDGTNNYKPSLKD 16
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       Query Match
Best Local Similarity 75.0
Matches 12; Conservative
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Name=LOC238447;
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QSU413;
            Query Match
Best Local Similarity 75.0
Matches 12; Conservative
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Name=LOC544903;
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MEDIATRE=8613012; PubMed=3937730;
MEDIATRE=8613012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (ant1-idiotypic) antibodies in the GAT system.";
EMBO J. 4:3681-3688 (1985)
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MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Pred. No. 0.0016;
3; Mismatches 1; Indels
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27095.1; -; mRNA.
NON_TER 11 119 119
SEQÜENCE 119 AA; 13931 MW; 502E51A5213F056E CRC64;
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27096.1; -; mRNA.
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                                                                                                                                                                                                                                              13-SRP-2005 (TrEMBLrel. 31, Created)
13-SRP-2005 (TrEMBLrel. 31, Last sequence update)
13-SRP-2005 (TrEMBLrel. 31, Last annotation update)
VH region (Fragment).
Mus musculus (Mouse).
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YINYDGSNNYNPSLKN 84
1 YISYDGTNNYKPSLKD 16
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Q53VQS;
                                                                                                                                                                                                        Q53VQ4_MOUSE PRELIMINARY;
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nes 12; Conservative
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MEDLINE=90067954; PubMed=2587273;

MEDLINE=90067954; PubMed=2587273;

Urakov Din, Deev S.M., Polyanovsky O.L.;

Urakov Din, Deev S.M., Polyanovsky O.L.;

Urakov Din, Deev S.M., Polyanovsky O.L.;

The structure of the expressible VH gene from a hybridoma producing monoclonal antibodies against porcine transferrin.";

Nucleic, Acids Res. 17:9481-9481(1989).

R. RhSP; PRB532; IKCV.

R. RhSP; PRB532; IKCV.

R. RhSP; PRB532; IC.

R. InterPro; IPR007110; Ig-like.

R. InterPro; IPR007110; Ig-like.

R. RhART; SM00409; IG, 1.

R. SMART; SM00409; IG, 1.

R. SMART; SM00409; IG, 1.

R. SMART; SM00406; IGV; 1.

R. SMART; SM00406; IGV; 1.

R. SMART; SM00409; IG, 1.

R. SMART; SM00406; IGV; 1.

R. SMART; SM00409; IG, 1.

R. SMART; SM00406; IGV; 1.

R. SEQÜENCE 136 AA; 15307 MW; SB0F439CCFB15C3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Murinae; Mus.
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Bumanalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus
                                                           Gaps
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78.7%; Score 70; DB 2; Length 119; 75.0%; Pred. No. 0.002; 1; Mismatches 1; Indels
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
VH gene product (Fragment).
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                                                                                                                          1 YISYDGTWNYKPSLKD 16
                                                                                                                                                            51 YISYDGSHNYNPSLKN 66
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QGLBQ5 MOUSE
TD QGLBQ5_MOUSE PRELIMINARY;
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98
98 AA;
        NON TER
SEQUENCE
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B.Cherrion and initial analysis of more than 15,000 full-length human
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Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentla; Sciurognathi;
Muridae; Murinae; Mus.
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BMBL; BC083312; AAH85312.1; -; mRNA.

BMSembl; BRNMUSG0000054328; Mus musculus.

GO; GO:003823; P:antigen binding; IEA.

InterPro; IPR003599; Ig.

InterPro; IPR003110; Ig-11ke.

InterPro; IPR003006; Ig-NHC.

InterPro; IPR003006; Ig-NHC.

InterPro; IPR003596; Ig-V.

FRAM; SM00409; IG; 3.

SMART; SM00407; IGC1; 3.

SMART; SM00406; IGV; 1.

SMART; SM00409; IG 3.

SMART; SM00409; IG ILKE; 4.

PROSITE; PS50835; IG LIKE; 4.
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Pred. No. 0.021;
1; Mismatches 2; Indels
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; x03379; CAA27102.1; -; mRNA.
NON FER. 1
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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80.0%;
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STRAIN=FVB/N; TISSUE=Colon;
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Q53VQ0;
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nes 12; Conservative
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MEDILIFE=86136012; PubMed=3937730;
MEDILIFE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
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What musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Musmalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Murinae; Mus.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalai, Butheria, Buarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae, Musinae, Mus.
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                                                                                                             Score 65; DB 2; Length 98;
Pred. No. 0.011;
2; Mismatches 2; Indels
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98
11191 MW; B3585BEB6F080616 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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13-SEP-2005 (TrEMBLrel. 31, Last anno
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                                                                                             Query Match
Best Local Similarity 73.3%;
Watches 11; Conservative
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G537R2 MOUSE PRELIMINARY;
AC G534R2,
DT 13-SEP-2005 (TERMELRE) 31,
DT MURIAGE, MURIAGE, MUS.
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Q53VQ1 MOUSE PRELIMINARY;
Q53VQ1;
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Best Local Similarity 68.8
Matches 11; Conservative
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MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
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Bammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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68.8%; Pred. No. 0.05;
iive 2; Mismatches 3; Indels
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03377; CAA27089.1; -; mENA.
                                                                                                                                                                       Fougereau M.; Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases. EMBL; X03377; CAA27090.1; -; mRNA.
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119 AA; 13844 MW; 6B1BC8C7DC77E147 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
                                                                                                                                                                                                                              Score 65, DB 2; Length 115;
Pred. No. 0.013;
2; Mismatches 2; Indels
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EMBL; X03379; CAA27101.1; -; mRNA.
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115 AA; 13257 MW; D465A5854DF459A3 CRC64;
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VH-D-JH region (Fragment).
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                             [4]
PROTEIN SEQUENCE OF 19-136.
MEDLINE=4170779; Pubmed=4524622;
Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;
Of a mouse myeloma protein with anti-hapten activity.";
Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                 Rinfret A., Horne C., Dorrington K.J., Klein M.; "Choning, sequencing and expression of the rearranged MOPC 315 VH gene segment.";
              [1] -
NUCLEOTIDE SEQUENCE.
MEDLINE=89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8;
                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 1-21.
MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE REVISION TO 53.
MEDLINE=77244979; PubMed=268248;
MEDLINE=77244979; PubMed=268248;
Hood L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
                                                                                                                                                    Jilka R.L., Pestka S.; Annual S.; More and S.; More and S.; More and Sequence of the precursor region of MOPC-315 mouse immunoglobulin heavy chain., 74:5692-5696(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region MOPC 315.
Framework-1.
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Complementarity-determining-3.
Framework-4.
By similarity.
G -> GG (in Ref. 1; CAA30727).
G -> H (in Ref. 2).
G -> H (in Ref. 4).
N -> D (in Ref. 4).
Missing (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; PL0102; AVM335.
HSSP; P01820; 1G7J.
SMR; P01822; 20-137.
SMR; P01822; 20-137.
InterPro; IPR007110; IG-like.
InterPro; IPR001596; IG-v.
SMART; SM00406; IGV; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M27638; AAA61337.1; -; Genomic_DNA
EMBL; X07880; CAA30727.1; -; Genomic_DNA
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                                                                                                          [2]
PROTEIN SEQUENCE OF 1-31.
MEDLINE=78094475; PubMed=414225;
                                                                                                Mol. Immunol. 26:431-434(1989)
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NCBI_TaxID=10090;
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      Query Match
      68.5%; Score 61; DB 1; Length 137;

      Best Local Similarity 62.5%; Pred. No. 0.072;

      Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

      Qy 1 YISYDGTNNYKPSLKD 16

      :| | | | | | | | | |

      Db 69 FIXYDGSNGYNPSLKN 84

      Search completed: December 30, 2005, 13:33:30

      Job time: 145 secs
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Score 75; DB 2; Length 118;
Pred. No. 9.4e-05;
2; Mismatches 1; Indels
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Best Local Similarity 81.2%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide US-09-065-059-11
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Sequence 11, App]
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                                                                    December 30, 2005, 13:14:26; Search time 35.871 Seconds (without alignments) 36.877 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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                                                                                                                                                                                                                                                                                                         1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-065-059-11

US-08-913-555-11

US-08-902-486-13

US-08-902-486-13

US-08-902-486-13

US-09-109-207C-2

US-09-296-005-2

US-09-920-171-2

US-09-920-171-2

US-09-920-171-2

US-09-920-171-3

US-09-920-171-3

US-09-920-171-3

US-09-920-171-3

US-09-920-171-3

US-09-920-179-3

US-09-920-179-46

US-09-920-179-46

US-09-920-179-46
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-09-424-840B-110
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                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                              Listing first 45 summaries
                                                  - protein search, using sw model
                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                 1 YISYDGTNNYKPSLKD 16
                                                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                           US-10-735-916A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                      Scoring table:
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                                                   OM protein
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                                                                                                                                   Sequence:
                                                                                                                                                                                     Searched:
                                                                       Run on:
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Sequence 42, Assequence 53, Assequence 51, Assequence 41, Assequence 49, Assequence 43, Assequence 23, Assequence 23, Assequence 140, Sequence 13, Assequence 140, Sequence 140, Sequence 48, Assequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 142,
        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, Motomi
ITITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/09/065,059
US-08-851-362D-35
US-10-194-975-101
US-10-194-975-52
US-10-194-975-52
US-10-194-975-53
US-10-330-613A-49
US-10-330-613A-69
US-10-194-975-43
US-08-111-080-23
US-08-211-980-23
US-08-211-980-23
US-08-211-980-23
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US-08-211-980-23
US-08-211-980-23
US-08-211-980-23
US-08-211-080-23
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US-08-211-080-23
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US-08-545-809A-142
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BUCCA Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
TELEPHONE: 703-684-1124
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09065059
Patent No. 6068841
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ruseal, David R.
APPLICANT: Ruseal, David R.
APPLICANT: Ruseal, David R.
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
NUMBER OF SEQUENCES:
ADDRESSE: Ouarles & Brady
STREET: South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPTTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPTTER: BATENTIN DATA:
COMPTTER: PATENTIN DATA:
APPLICANTON NUMBER: US/08/902,486
FILING DATE:
CLASSIFCATION NUMBER: G70513.90261
FILING DATE:
NAME: Seay, Nicholas J.
RETERENCE/DOCKET NUMBER: 670513.90261
TELECHONE: 608-251-5000
TTELEPHONE: G08-251-5000
TTELEPHONE: G08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.7%; Score 62; DB 2; Length 241; 68.8%; Pred. No. 0.027; ive 2; Mismatches 3; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DEAD PC COMPATIBLE
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,486
FILING DATE:
CLASSIFICATION NUMBER: US/08/902,486
FILING DATE:
RACISTRATION NUMBER: 27386
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 27386
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
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Patent No. 6140075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 YIRYDGİSEYTPSLKN 195
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Best Local Similarity 68.8<sup>§</sup>
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                             Sequence 11, Application US/08913555

Patent No. 6946255

Patent No. 6946255

GENERAL INFORMATION:

APPLICANT: RAYGAXI, NO. 6946255uhiko

APPLICANT: NAKATA, Kideo

APPLICANT: NAKATA, Mocomi

TITLE OF INVENTION: MONOCIONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: MONOCIONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: MONOCIONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: RAZTING WITH FAS LICAND AND PRODUCTION PROCESS THEREOF

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS: 31

TORRESPENDENCE ADDRESS: 31

TORRESPENDENCE ADDRESS: 32

ADDRESSEE: MCDermott, Will & Emery

STREET: 99 Cannal Center Plaza, Suite 300

CITY: Alexandria

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: BALCATION DATA:

MEDIUM TYPE: 19-SEP-1997

CLASSIFICATION NUMBER: 10-SEP-1997

CLASSIFICATION NUMBER: 530

ATTORNEY/AGENT INPORMATION:

REGISTRATION NUMBER: 50356-150

TELECOMMUTICATION NUMBER: 42,368

TELECOMMUTICATION NUMBER: 50356-150

TELECOMMUTICATION NUMBER: 50356-150

TELECOMMUTICATION NUMBER: 50356-150
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US-08-902-486-13

US-08-902-486-13

Sequence 13, Application US/08902486

Patent No. 6140075

GENERAL INFORMATION:
APPLICANT: Russel, David R.
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.2%; Pred. No. 9.4e-05;
Matches 13; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Quaries & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-756-8699
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
          50 YISYDGSNNYNPSLKN 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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                                                                                                             RESULT 2
US-08-913-555-11
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GENERAL INCOMMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REPERBNE: P1123CIT
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 2
LENGTH: 121
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| Sequence 2. Application US/09920171
| Patent No. 6662735
| Patent No. 6662735
| Patent No. 6662735
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66.7%; Pred. No. 0.027;
iive 4; Mismatches 1; Indels
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66.7%; Pred. No. 0.027;
tive 4; Mismatches
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Patent No. 6290957
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52 ITYDGSSNYNPSLKN 66
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52 ITYDGSSNYNPSLKN 66
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52 ITYDGSSNYNPSLKN 66
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Best Local Similarity 66.74
Matches 10; Conservative
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Best Local Similarity 66.77
Matches 10; Conservative
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; TYPE: PRT --
; ORGANISM: Mus musculus
US-09-109-207C-2
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Best Local Similarity
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US-09-296-005-2
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Sequence 2, Application US/08887352B

Sequence 2, Application US/08887352B

Patent No. 5994511

GREERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: IDAM May

CITY: South San Francisco

STATE: California

COUNTRY: USA
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Pred. No. 0.027;
4; Mismatches 1; Indels
                                         Score 62; DB 2; Length 496;
Pred. No. 0.06;
                                                                                                                             3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                         Query Match 69.7%; Score 62; DB Best Local Similarity 68.8%; Pred. No. 0.06 Matches 11; Conservative 2; Mismatches
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NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMINICATION INFORMATION:
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
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52 ITYDGSSNYNPSLKN 66
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TYPE: Amino Acid
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Best Local Similarity 66.7.
The Conservative
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US-09-109-207C-2
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US-08-887-352B-2
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                                                                                                                                                                                                                                                                                   COMPUTER PARABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER; IBM PC compatible OPERATING SYSTEM: PC-DS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE: 06-Jun-1995
FILING DATE: 06-Jun-1995
FILING DATE: 15-MAR-1995
RICHARTION NUMBER: 08/466163
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 44-MG-1991
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 14-MG-1991
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 07/744768
FILING DATE: 14-MG-1991
ATTORNEY/AGENT INFORMATION: RESCOMMUTICATION INFORMATION: TELESCOMMUTICATION INFORMATION: TELESCOMMUTICATION INFORMATION: TELESCOMMUTICATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08466163B
Fatent No. 6329509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: PO718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR PILING DATE: 1995-01-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1994-01-26
PRIOR PILING DATE: 1994-01-26
PRIOR PLING DATE: 1992-05-07
PRIOR PLING DATE: 1992-05-07
PRIOR PLING DATE: 1992-05-07
TITLE OF INVENTION: Immunoglobulin Variants
                           NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                             STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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52 ITYDGSSNYNPSLKN 66
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TYPE: Amino Acid
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Matches 10; Conservative
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US-08-466-163B-3
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                                                    US-09-716-028-2

Sequence 2, Application US/09716028

Sequence 2, Application US/09716028

Sequence 2, Application US/09716028

Sequence 2, Application US/09716028

GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123R1

CURRENT APPLICATION NUMBER: US/09/716,028

CURRENT FILING DATE: 2000-11-17

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 2.

LENGTH: 121
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; Patent No. 6/61809;
; Patent No. 6/61809;
; APPLICANT: Lowman, Henry B.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Lowe, John
: APPLICANT: Lowe, John
: TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123/305
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR PILING DATE: 1999-04-21
; PRIOR PILING DATE: 2001-08-01
; PRIOR PILING DATE: 2001-08-01
; RIOR FILING DATE: 2001-08-01
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Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
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52 ITYDGSSNYNPSLKN 66
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ORGANISM: Mus musculus
US-09-716-028-2
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VERENCE 3, Application US/09925179

VERENCE 1. NPORMATION:

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Anti-1gE Antibodies (as amended)

FILE REFERENCE: P0718P2CIDIC10S

CURRENT APPLICATION NUMBER: US/09/925,179

CURRENT PILING DATE: 1995-06-06

PRIOR FILING DATE: 1995-06-06

PRIOR FILING DATE: 1995-06-06

PRIOR FILING DATE: 1995-03-15

PRIOR FILING DATE: 1995-03-15

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-05-07

PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 68

LENGTH: 134

TYPE: PRIOR THING DATE: 1991-08-14

TYPE: PRIOR FILING DATE: 1991-08-14
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; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 3
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-3
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52 ITYDGSSNYNPSLKN 66
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52 ITYDGSSNYNPSLKN 66
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APPLICANT: Jardieu, Paula M.
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended;
FILE REPRENCE: P0718P2C3US
CURRENT FILING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: DCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-07
PRIOR FILING DATE: 1992-05-07
PRIOR FILING DATE: 1991-08-14
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TILE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 1995-03-15
PRIOR PILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-05-07
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Pred. No. 0.03;
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Patent No. 6699472
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                PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 3
LENGTH: 134
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52 ITYDGSSNYNPSLKN 66
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ORGANISM: Mus musculus
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CORGANISM: Mus musculus
US-08-466-163B-3
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US-09-802-077-3
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US-09-802-096-3
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                                                                                                                                                                                           December 30, 2005, 13:33:42; Search time 118.968 Seconds (without alignments) 56.194 Million cell updates/sec
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GenCore version 5.1.6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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i Sequence 10, Application US/10735916A

publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, Liliane

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: DEGER, Olivier

APPLICANT: HAEUW, Jean-Francois

APPLICANT: HAEUW, Jean-Francois

APPLICANT: HAEUW, Jean-Francois

APPLICANT: HAEUW, Jean-Francois

APPLICANT: HAEUW, NOWEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REPERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT FLING DATE: 2003-12-16

PRIOR PILING DATE: 2003-01-10

PRIOR APPLICATION NUMBER: FR 03/08 538

PRIOR APPLICATION NUMBER: FR 02/00 653

PRIOR APPLICATION NUMBER: FR 02/00 653

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR PILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR APPLICATION NUMBER: FR 02/05 753

PRIOR APPLICATION NUMBER: FR 02/05 753

PRIOR APPLICATION NUMBER: FR 02/05 753

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                                                                            US-10-822-306A-23
US-10-822-306A-23
US-10-822-306A-9
US-10-822-306A-11
US-09-925-179-66
US-10-968-237-66
US-10-968-137-66
US-10-453-698-131
US-10-453-698-131
US-10-453-698-136
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US-10-735-916A-10
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Best Local Similarity
Matches 16; Conserv
        US-10-735-916A-69
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Sequence 79, Application US/10735916A Publication No. US20050084906A1
51 YISYDGTWNYKPSLKD 66
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ORGANISM: Homo sapiens
US-10-735-916A-79
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     APPLICANT: DUFLUS, ALGALIA
APPLICANT: BECK, ALGALIA
APPLICANT: BECK, ALGALIA
APPLICANT: BECK, ALGALIA
APPLICANT: BECK, ALGALIA
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REPERENCE: 01773-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
FRIOR FILING DATE: 2003-01-1
PRIOR FILING DATE: 2003-01-18
FRIOR APPLICATION NUMBER: PCT/PR 03/00 653
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR APPLICATION NUMBER: FR 02/00 654
FRIOR PILING DATE: 2002-01-18
FRIOR FILING DATE: 2003-01-18
FRIOR FILING
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US-10-735-916A-75
i Sequence 75, Application US/10735916A
publication No. US20050084906A1
i GENERAL INFORMATION:
APPLICAMT: GORTSCH, Liliane
APPLICAMT: LEGER, Olivier
APPLICAMT: LEGER, Olivier
APPLICAMT: DUFLOS, Alain
APPLICAMT: BECK, Alain
APPLICAMT: BECK, Alain
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APPLICAMT: BECK, Alain
APPLICAMT: BOWEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOVER: US/10/735,916A
CURRENT APPLICATION NUMBER: FR 03/00 538
PRIOR PILING DATE: 2003-07-11
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
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DUFLOS, Alain
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US-10-735-916A-69
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1 YISYDGTNNYKPSLKD 16

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Gaps
FUDILICANT: COCKNAIA, Machalie

APPLICANT: GORESCH, Liliane

APPLICANT: GORESCH, Liliane

APPLICANT: GORESCH, Liliane

APPLICANT: BEER, Malain

APPLICANT: BEER, Malain

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APPLICANT: BEER, Malain

APPLICANT: BEER, Malain

APPLICANT: BOOST 12-16

FILE OF INVENTION NUMBER: R 03/08 538

PRIOR PELING DATE: 2003-01-1

PRIOR APPLICATION NUMBER: PCT/FR 03/00 178

PRIOR APPLICATION NUMBER: F 02/00 653

PRIOR APPLICATION NUMBER: F 02/00 654

PRIOR PELING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002
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Sequence 83, Application US/10735916A

Publication No. US20050084906A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, Liliane

APPLICANT: GOETSCH, Liliane

APPLICANT: LEGER, Olivier

APPLICANT: LEGER, Olivier

APPLICANT: LEGER, Olivier

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01753-183

CURRENT APPLICATION NUMBER: US/10/735,916A

CURRENT APPLICATION NUMBER: FR 03/08 538

PRIOR PELING DATE: 2003-01-11

PRIOR PELING DATE: 2003-01-11

PRIOR PELING DATE: 2003-01-18

PRIOR PELING DATE: 2002-01-18

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US-10-735-916A-81

Sequence 81, Application US/10735916A

Publication No. US20050084906A1

Sequence 81, Application US/10735916A

Publication No. US20050084906A1

SERENAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: LEGER, Olivier
APPLICANT: BECK, Alain
APPLICANT: HEGER, Olivier
APPLICANT: HEGER, Olivier
APPLICANT: HEKW, Jean-Francois
APPLICANT: HEKW, Jean-Francois
APPLICANT: HEKW, Jean-Francois
APPLICANT: HEKW, Jean-Francois
APPLICANT: HEKW, Jean-Francois
APPLICANT: HEKW, Jean-Francois
APPLICANT: HEKW, Jean-Francois
APPLICANT: HOUSE 107753-183

CURRENT APPLICATION NUMBER: US/10/735, 916A

PRIOR FILING DATE: 2003-01-18

PRIOR FILING DATE: 2003-01-18

PRIOR APPLICATION NUMBER: FR 02/00 653

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR APPLICATION NUMBER: FR 02/00 654

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18
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100.0%; Score 89; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.7e-06;
iive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: FLIFE, VILLED PRIOR FILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: RR 02/00 654
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 77
LENGTH: 135
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Best Local Similarity 100.0
Matches 16; Conservative
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US-10-735-916A-77
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ORGANISM: Homo sapiens
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Sequence 52, Application US/10735916A

Publication No. US2050084906A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT APPLICATION NUMBER: PR 03/08 538
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE PATENTIN VET: 2.1
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| Publication No. US200084906A1
| Publication No. US200084906A1
| GENERAL INFORMATION:
| APPLICANT: GOSTSCH, Liliane
| APPLICANT: LEGER, Olivier
| APPLICANT: LEGER, Olivier
| APPLICANT: BECK, Alain
| APPLICANT: BECK, Alain
| APPLICANT: BECK, Alain
| APPLICANT: HEWUW, Jean-Francois
| APPLICANT: HEWUW, Jean-Francois
| APPLICANT: HEWUW, Jean-Francois
| APPLICANT: HEWUW, Jean-Francois
| APPLICANT: HEWUW, Jean-Francois
| APPLICANT: HEWUW, Jean-Francois
| TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
| FILE REFERENCE: 017753-183
| CURRENT APPLICATION NUMBER: US/10/735,916A
| CURRENT PILLION DATE: 2003-12-16
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Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0;
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CORGANISM: Mus musculus
US-10-735-916A-52
                     ; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83
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SEQ ID NO 52
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Gaps

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Sequence 67, Application US/10632706

Publication No. US20040173385A1

GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: MARKS, JAMES D.
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OF INVENTION: NEUROTOXINS
TITLE OF INVENTION: NUMBER: US/10/632,706
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR FILING DATE: 1998-08-01
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PAECHLIN VERSION 3.2
SEQ ID NO 67
LENTING TO A SEQ ID NOS: 278
SEQ ID NO 67
LENTING TO A SEQ ID NOS: 278
SEQ ID NO 67
LENTING TO A SEQ ID NOS: 278
SEQ ID NO 67
## APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Abellinum Neurotoxins
FILE REFERENCE: 2500.117050
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 198-08-31
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 70
LENGTH: 121
TYPE: RR
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
OTHER INFORMATION: 286 region VH epitope 3
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APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
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80.9%; Score 72; DB 4; Length 121;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 3; Mismatches 1; Indels
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75.0%; Pred. No. 0.0013;
tive 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YISYDGTWNYKPSLKD 16
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Best Local Similarity 75.04
Matches 12; Conservative
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Sequence 2, Application US/09858349

Patent No. US20020012909A1

GENERAL INFORMATION:

APPLICANT: PLAKSIN, Daniel

TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
FILE REFERENCE: 87534-2800

CURRENT FILING DATE: 2000-06-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

TYPE: PRT
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                APPLICANT: LEGER, Ollvier
APPLICANT: LEGER, Ollvier
APPLICANT: LEGER, Ollvier
APPLICANT: BUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Joan-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION UNMER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 03/00 178
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-01-18
PRIOR PELING DATE: 2002-05-07
SOFTWARE PATENTIN VOT: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mouse hybridoma specific for H-2D + RGPGRAFVTI peptide
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Pred. No. 0.00047;
2; Mismatches 1; Indels
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GENERAL INFORMATION: APPLICANT: MATKS, James D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.2%;
Matches 13; Conservative ;
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           CORVAIA, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (99)...(107)
COTHER INFORMATION: variable US-09-858-349-2
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Best Local Similarity 100.
Matches 16; Conservative
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| Sequence 17, Application US/10372481
| Publication No. US20030202975A1
| GENERAL INFORMATION:
| APPLICATION TENGER, Thomas F. | TILLS OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES |
| TILLS OF INVENTION NUMBER: US/10/372,481
| CURRENT FILING DATE: 2002-02-21
| PRIOR FILING DATE: 2003-02-21
| PRIOR FILING DATE: 2002-10-21
| PRIOR FILING DATE: 2002-02-21
| PRIOR PLING DATE: 2002-02-21
| PRIOR PLING DATE: 2002-02-21
| SOFTWARE: PRECTIN VERSION 3.2
| SOFTWARE: PRECTIN VERSION 3.2
| SOFTWARE: PRECTIN VERSION 3.2
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Pred. No. 0.0018;
2; Mismatches 2; Indels
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APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TEDDES,
THEDICANT: TEDDES, THOMAS
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-12-16
FRIOR APPLICATION NUMBER: FR 03/08 538
FRIOR FILING DATE: 2003-07-11
FRIOR FILING DATE: 2003-01-20
FRIOR FILING DATE: 2003-01-20
FRIOR FILING DATE: 2002-01-18
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Best Local Similarity 75.0%;
Matches 12; Conservative
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Best Local Similarity 75.0
Matches 12; Conservative
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ORGANISM: Mus musculus
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1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
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equence 13,	Sequence 18, Appl		Sequence 7, Appli	9, A	71,	Sequence 2002, Ap	Sequence 1339, Ap	Sequence 4, Appli		93			36,	•	Sequence 39, Appl	Sequence 50, Appl	œ	Sequence 1316, Ap	Sequence 1619, Ap
-10-923-3	US-10-923-327-18	US-10-923-327-15	US-10-923-327-7	US-10-923-327-9	US-11-012-353-71	US-11-054-515-2002	US-11-054-515-1339	US-11-185-615-4	US-11-054-515-1847	US-11-054-515-1993	US-11-054-669-35	US-11-084-554-49	US-11-054-669-36	US-11-054-669-38	US-11-054-669-39	US-11-084-554-50	US-11-054-515-1981	US-11-054-515-1316	US-11-054-515-1619
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## ALIGNMENTS

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APPLICANT: CORVAILOR

APPLICANT: CORVAILANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, ALAIN

APPLICANT: DUFLOS, ALAIN

APPLICANT: LEGER, OLIVIER

APPLICANT: LEGER, OLIVIER

APPLICANT: LEGER, OLIVIER

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR PLILOR DATE: 2003-07-11

PRIOR PELICATION NUMBER: FR 020553

PRIOR PELICATION NUMBER: FR 020553

PRIOR PELICATION NUMBER: FR 020654

PRIOR PELICATION NUMBER: FR 020654

PRIOR PELICATION NUMBER: FR 020654

PRIOR PELICATION NUMBER: FR 020655

PRIOR PELICATION NUMBER: FR 020654

PRIOR PELICATION NUMBER: FR 020654

PRIOR PELING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOFTWARE: PRECENT OF SEC ID NOS: 162

SEQ ID NO 10

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100.0%; Score 89; DB 7; I
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 16; Conservative 0; Mismatches 0;
                                        Sequence 10, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
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JS-11-012-353-10
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RESULT 2 US-11-012-353-69 ; Sequence 69, Application US/11012353

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1 YISYDGTNNYKPSLKD 16
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Best Local Similarity 100.
Matches 16; Conservative
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CORGANISM: Homo sapiens
US-11-012-353-79
                      ; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens US-11-012-353-75
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US-11-012-353-83
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US-11-012-353-75

US-11-012-353-75

Sequence 75. Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORTAIA, NATHALIE
APPLICANT: LEGER, JEAN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION WUMBER: U07135-916
RRIOR PILLING DATE: 2004-12-16
RRIOR PILLING DATE: 2003-12-16
PRIOR PILLING DATE: 2003-01-20
PRIOR PILLOATION WUMBER: FR 020553
PRIOR FILLING DATE: 2003-01-20
PRIOR FILLING DATE: 2002-05-07
PRIOR PILLING DATE: 2002-01-18
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GENERAL INFORMATION:
APPLICANT: GOGTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CONVAIA, NATHALIE
APPLICANT: CONVAIA, NATHALIE
APPLICANT: CONVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: LEGER, OLIVIER
TITLE OF INVERTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVERTION: NOVEL ANTI-IGF-IR AND USES THEREOF
TITLE OF INVERTION: NOVERER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
FILE REPERENCE: 017753-198
CURRENT PLING DATE: 2003-12-16
FRIOR FILING DATE: 2003-07-11
FRIOR APPLICATION NUMBER: FR 0308538
FRIOR APPLICATION NUMBER: FR 0200553
FRIOR APPLICATION NUMBER: FR 0200553
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FRIOR FILING DATE: 2002-01-18
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-012-353-69
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Sequence 79, Application US/11012353
| Sequence 79, Application US/11012353
| Publication No. US20050249730A1
| GENERAL INFORMATION:
| APPLICANT: GOETSCH, LILIANE
| APPLICANT: CORVAIA, NATHALIE
| APPLICANT: DUFLOS, ALAIN
| APPLICANT: LEGER, OLIVIER
| APPLICANT: LEGER, OLIVIER
| APPLICANT: LEGER, OLIVIER
| APPLICANT: LEGER, OLIVIER
| APPLICANT: LEGER, OLIVIER
| APPLICANT: LEGER, OLIVIER
| APPLICANT: LEGER, ALAIN
| TITLE OF INVENTION: NOVEER: 2001-10-16
| TITLE OF INVENTION: NOVEER: US/735,916
| PRIOR PRILING DATE: 2003-01-16
| PRIOR PLILATION NUMBER: PC7/FR03/00178
| PRIOR PLILATION NUMBER: PC7/FR03/00178
| PRIOR PLILATION NUMBER: PC7/FR03/00178
| PRIOR PLILATION NUMBER: PC7/FR03/00178
| PRIOR PLILATION NUMBER: PC8-07
| PRIOR PLILATION NUMBER: PC8-07
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Publication No. US20050249730A1
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: DUFLOS, AIAIN
APPLICANT: LEGER, OLLVIER
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REPERENCE: 017753-198
                                                                                                     Gaps
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100.0%; Score 89; DB 7; Length 117; 100.0%; Pred. No. 2e-08;
                                                                                                          0; Mismatches
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Sequence 77, Application US/11012353 Publication No. US20050249730A1 GENERAL INFORMATION:
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       61 YISYDGTNNYKPSLKD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-012-353-77
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US-11-012-353-52

Sequence 5.2. Application US/11012353

Publication No. UG2005249730A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVALA, NATHALIE

APPLICANT: DUFLOS, ALAIN

APPLICANT: BECK, ALAIN

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

TITLE OF INVENTION: NUMBER: US/11/012,353

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT PILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-0-11

PRIOR FILING DATE: 2003-0-11

PRIOR FILING DATE: 2003-0-11

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100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Score 89; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR PLICATION NUMBER: 10/735,916
PRIOR PLING DATE: 2003-12-16
PRIOR PLING DATE: 2003-12-16
PRIOR PLING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR PLING DATE: 2003-01-20
PRIOR PILING DATE: 2002-05-07
PRIOR PILING DATE: 2002-05-07
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 83
SEQ ID NO 83
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; ORGANISM: Homo sapiens
US-11-012-353-83
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1 YISYDGTNNYKPSLKD 16

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Sequence 81, Application US/11012353

Sequence 81, Application US/11012353

Publication No. US2000249730A1

GENERAL INFORMATION:
APPLICANT: CORVIA, NATHALIE
APPLICANT: DUFLOS, ANATHALIE
APPLICANT: DUFLOS, ANATHALIE
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: RECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 011753-198

CURRENT FILING DATE: 2004-12-16
APPLICANT: GOETSCH, LILIANE
APPLICANT: GOETSCH, MATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: RECEPTORS ANTIEDDIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIEDDIES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
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                                                                                                                                                                                                                                                                                                                     CURRENT FILING NOTES.

CURRENT FILING NOTES.

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR PILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOPTWARE: PARLENTIN VET: 3.3

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PRIOR APPLICATION NUMBER: 10/735,916
PRIOR PLILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-05-05
PRIOR FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: FR 020653
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; Sequence 71, Application US/10512184
  HAEUW, JEAN-FRANCOIS
LEGER, OLIVIER
BECK, ALAIN
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Best Local Similarity 75.0
Matches 12; Conservative
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US-10-512-184-71
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APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: DEGEK, OLIVIER
APPLICANT: LEGEK, OLIVIER
APPLICANT: LEGEK, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR PILLING DATE: 2003-12-16
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2003-01-10
PRIOR PLILING DATE: 2003-01-10
PRIOR PLILING DATE: 2003-01-20
PRIOR PLILING DATE: 2003-01-20
PRIOR PLILING DATE: 2003-01-18
PRIOR PLILING DATE: 2003-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARR: PATENTING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
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                                                                                                                                                                                                                                                    100.0%; Score 89; DB 7; Length 135; 100.0%; Pred. No. 2.4e-08; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-11-012-353-70
US-11-012-353-70
Sequence 70, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GORTSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION WUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 81
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-11-012-353-85
; Sequence 85, Application US/11012353
; Publication No. US2050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative 0;
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Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 135
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Sequence 34, Application US/10512184
; Sequence 34, Application US/10512184
; Sequence 34, Application No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: 101801
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 259
; TYPE: PRT

CRABILISM: Artificial Sequence
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APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-196
CURRENT PELLING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: U0/115,916
PRIOR APPLICATION NUMBER: PR 0108538
PRIOR PILING DATE: 2003-01-12
PRIOR PLING DATE: 2003-01-12
PRIOR PLING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: PR 0200553
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
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PRIOR FILING DATE: PRIOR PLICATION NUMBER: PR 0200654
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PRIOR FILING DATE: 2002-01-18
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OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
OTHER INFORMATION: specificity against Phoma lingam; originates from
OTHER INFORMATION: Mus musculus.
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Search completed: December 30, 2005, 14:15:22 Job time : 6.93548 secs
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Best Local Similarity 66.7%;
Matches 10; Conservative
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US-11-144-248-36
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Sequence 49, Application US/10512184

Publication No. US20050244901A1

Full CANT. Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.

TITLE OF INVENTION: Antibodies recombinant antibodies, recombinant antibody fragments and fusions mediated plant disease;

TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease;

TITLE OF INVENTION: resistance against fungi

TITLE OF INVENTION: VUMBER: US/10/512,184

CURRENT APPLICATION NUMBER: US/10-22

NUMBER OF SEQ ID NOS: 72

SOFTWARE PATENTION OF 2.1

SEQ ID NO 49

LENGTH: 626
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
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                                                                          TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.010501
CURRENT PELLING NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 71
LENGTH: 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: fusion protein; OTHER INFORMATION: comprising the leader peptide - chitinase- linker; OTHER INFORMATION: - SCEV PL2 - cmyc/His6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising ACE - linker - OTHER INFORMATION: scFv PL2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 YISYDGTNNNNPSLKN 409
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US-11-144-248-36
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APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PP2
CURRENT PAPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-01-00
PRIOR PILING DATE: 2002-01-04
PRIOR FILING DATE: 2002-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Pred. No. 0.0055;
1; Mismatches 4; Indels
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US-11-054-669-42

Sequence 42, Application US/11054669

Publication No. US20050261480A1

GENERAL INFORMATION:
TITLE FOOTE, Jefferson

TITLE FOOTE 10219/US/3

CURRENT APPLICATION NUMBER: US/11/054,669

CURRENT FILING DATE: 2005-02-08

PRIOR FILING DATE: 2005-07-12

PRIOR FILING DATE: 2001-07-12

PRIOR FILING DATE: 2001-07-12

PRIOR FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 124

SEQ ID NO 42

LENGTH: 97
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December 30, 2005, 13:37:27 ; Search time 132.5 Seconds (without alignments) 53.057 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                   protein search,
                                                                                                                                                                                Title:
Perfect score:
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                                                                     protein
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length: 16 length: 16

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Minimum I Maximum I

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adj76844 CDR seque Ads67014 Murine in Aca461011 TNF resis Adz45407 Murine fa Adz21256 Amino aci Adz42130 Mouse ant Adz42130 Murine fa Adz45311 Murine fa Adz4508 Mouse ant Adz4708 Mouse ant Adz4708 Mouse ant Adz4708 Murine fa Aaz4718 Sequence Aaz4718 Sequence Human ant Human ant Murine de Human ant M-ČSF spe Human trk S9 cell d VH CDR2 f CDR2 regi Heavy cha Ado58086 Ado58086 Adz66143 Adw90327 Adw90297 Adw90297 Adw90297 Adw90297 Ade19315 Ade19315 SUMMARIES ADZ45343 ADZ51256 ADZ42130 ADZ45520 ADZ51224 ADZ42098 ADZ45479 AAU81236 ADO58086 ADZ66143 AAW90327 AAO17789 ADS19315 AAR24718 AAB73650 AEC20782 AEA40141 ADZ45407 ADZ45311 AAW90297 ADJ76844 B Length Query Match 1 80.9 80.9 78.7 78.7 78.7 76.4 669.7 65.2 65.2 Result

MAb	_	Aaw44174 Monoclona	Aeb00995 Human IP1	Aae10502 Humanised	Aae10499 Humanised	Aae10527 Humanised	Aae10500 Humanised	Aau81239 Human trk	Abp66457 Human RSV	Abp66395 Human RSV	Abp66379 Human RSV	Abp66391 Human RSV	Aae28034 Human mod	Aae28046 Human mod	Aae28050 Human mod	Abu69320 Respirato	Abu69242 Respirato	Abu69254 Respirato	Abu69258 Respirato	Ade35749 SYNAGIS a
2 AAW01151	2 AAW24541	2 AAW44174	9 AEB00995	4 AAE10502	4 AAE10499	4 AAE10527	4 AAE10500	5 AAU81239	5 ABP66457	5 ABP66395	5 ABP66379	5 ABP66391	5 AAE28034	5 AAE28046	5 AAE28050	6 ABU69320	6 ABU69242	6 ABU69254	6 ABU69258	7 ADE35749
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RESULT 1 ADJ76844

CDR sequence for anti-IGF-1R antibody. ADJ76844 standard; peptide; 16 AA (first entry) 06-MAY-2004 ADJ76844; 

insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.

18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753. 20-JAN-2003; 2003WO-FR000178 2002FR-00000653 WO2003059951-A2. Mus musculus. 18-JAN-2002; 24-JUL-2003

(FABR ) FABRE MEDICAMENT SA PIERRE. Leger 0; Corvaia N, Goetsch L,

WPI; 2003-569653/53. N-PSDB; ADJ76843.

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Claim 1; SEQ ID NO 10; 164pp; French

οĘ The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with

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hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and prostate, lung psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF+IR and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beck A;
                                                                                                                                                                      100.0%; Score 89; DB 7; Length 16; 100.0%; Pred. No. 6.1e-07; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 10; 125pp; English.
                                                                                                                                                                                                                                                                                                                                              ADZ67014 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2002; 2002FR-00000653.
18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                     1 YISYDGTNNYKPSLKD 16
                                                                                                                                                                                                                                                         1 YISYDGTNNYKPSLKD 16
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                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2005 (first entry)
                                                                                                                                                                                                        16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-321968/33.
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CORVAIA N.
LEGER O.
                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                           Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                               ADZ67014;
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(HAEU/)
(BECK/)
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(LEGE/)
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                                                                                                                                                                                                      Matches
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of

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comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined is amino decrafining region (CDR) consisting of one of two fully defined is amino caids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illiness connected with an overexpression and/or an abnormal activation of the IGR-IM and/or EGRP, and/or connected with a decivation of the IGR-IM and/or EGRP, with IGR-IM and/or connected with a historic indication of the transduction pathway of the signal mediated by the induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGR-dependent, especially IGR1 and/or IGR2.

CC dependent and/or EGR-dependent and/or HERZ/neu-dependent cells. (1) is useful for preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGR-dependent and/or EGR-dependent and/or EGR-dependent and/or EGR-dependent and/or EGR-dependent and/or IGR-dependent and/or IGR-dependent and/or IGR-dependent cells. (1) is useful in the preparation of a medicament intended for the treatment of proriation of the invention or for the cancer, endometrial cancer or colon cancer. (1) is useful in the prevention or for the preparation of a medicament intended for the prevention or for the prevention or for the treatment of psoriasis. (1) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to treatment of psoriasis. (1) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to searching from a biological sample in which the abnormal present of IRR and/or EGR receptor is suspected, which invented or the preparation of the invented in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INF resistant monoclonal antibody VH region, F6VH CDR2.
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Best Local Similarity
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N-PSDB; AEA40140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 AA;
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This invention describes a novel bispecific antibody which can act as a cofactor to enhance an enzyme reaction and can recognize the enzyme and the enzyme substrate. The antibody specifically binds to blood coagulation factor VIII. The invention also describes a composition comprising the antibody and a carrier, a kit useful in preventing and/or treating bleeding associated with a disorder or from a disease caused by Murine factor IX directed antibody CDR2 SEQ ID NO 111. Disclosure, SEQ ID NO 111; 69pp; Japanese. Miyazaki T, ADZ45407 standard; peptide; 16 08-OCT-2004; 2004WO-JP014911. 10-OCT-2003; 2003WO-JP013062. 14-OCT-2003; 2003WO-JP013123. 1 YISYDGTNNYKPSLKD 16 1 YISYDGSNNYNPSLKN 16 (first entry) (CHUS ) CHUGAI SEIYAKU KK Conservative Hattori K, Kojima T, WPI; 2005-315563/32. 1 Similarity 13; Conserv WO2005035756-A1. Sequence 16 AA; Mus musculus 30-JUN-2005 21-APR-2005. ADZ45407; Query Match Local Matches ADZ45407

ID ADZ45407

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Variable region gene of high affinity monoclonal antibody of tumor necrosis factor and its preparation.
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81.2%; Pred. No. 0.0001;
ive 2; Mismatches 1; Indels
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                                                                                                                                                 Claim 1; Page 3; 20pp; Chinese
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bleeding. The composition includes blood coagulation factor VIII. The antibody of the invention can be a blood-coagulation fibrinolysis related factor including blood-coagulation factor VIII. blood coagulation factor X, or blood-coagulation factor IX. The antibody comprises a complementary determining region (CDR) of anti-blood-coagulation factor IX/IXa factor antibody. The novel antibody or composition is useful for preventing and/or treating a disease accompanying bleeding, or the disease resulting crown bleeding where the disease accompanying bleeding or the disease the cresulting from bleeding develops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII. The disease the captelops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII. The disease the coagulation factor VIII and/or activation blood coagulation factor VIII. The mophilia A or von Willebrand disease, where the hemophilia is an acquired hemophilia A. This sequence represents a fragment of the antibody described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but the well print by the print by the print directly from WIPO at the print but by the print directly from WIPO at

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Sequence 16 AA;

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This invention describes a novel bispecific antibody which can act as a cofactor to enhance an enzyme reaction and can recognize the enzyme and the enzyme substrate. The antibody specifically binds to blood coaquilation factor VIII. The invention also describes a composition comprising the antibody and a carrier, a kit useful in preventing and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel bispecific antibody substituting for function of cofactor that enhances enzyme reaction, and recognizing both enzyme and substrates of enzyme, useful for treating hemophilia A.
                                                                                                                                                                                                                                                                                                                                                                       bispecific antibody; blood coagulation factor VIII; bleeding; fibrinolysis; blood coagulation factor X; blood-coagulation factor IX; factor VIII deficiency; von Willebrands disease; hemostatic; immunostimulator; antibody engineering.
82.0%; Score 73; DB 9; Length 16;
81.2%; Pred. No. 0.00021;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                   Murine factor IX directed antibody CDR2 SEQ ID NO 47.
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                                                                                                                                                                                                                      ADZ45343 standard; peptide; 16 AA.
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14-OCT-2003; 2003WO-JP013123
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                    Best_Local Similarity 81.2
Matches 13; Conservative
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        Query Match
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                                                                                                                                                                                                                                                                                                                                                         bispecific antibody; blood coagulation factor VIII; bleeding; fibrinolysis; blood coagulation factor X; blood-coagulation factor IX; factor VIII deficiency; von Willebrands disease; hemostatic; immunostimulator; antibody engineering.
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bleeding. The composition can be a blood coagulation factor VIII. The antibody of the invention can be a blood-coagulation factor VIII. The antibody of the invention can be a blood-coagulation factor vIII. The factor including blood-coagulation factor including blood-coagulation factor IX. The antibody comprises a complementary determining region (CDR) of anti-blood-coagulation factor IX/IXa factor cantibody. The novel antibody or composition is useful for preventing and/or treating a disease accompanying bleeding, or the disease resulting cand/or treating a disease accompanying bleeding or the disease resulting crom bleeding develops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII. The disease the capulation factor VIII and/or activation blood coagulation factor VIII. is hemophilia A or von Willebrand (seese, where the hemophilia is an acquired hemophilia A. This sequence represents a fragment of the antibody described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the was obtained in electronic format directly from WIPO at the was obtained when the method published_pot_esquences. treating bleeding associated with a disorder or from a disease caused by 0555555555555555555555555888

Sequence 16 AA;

80.9%; Score 72; DB 9; Length 16; 75.0%; Pred. No. 0.0003; ive 3; Mismatches 1; Indels 1 YISYDGTNNYKPSLKD 16 1 YINYDGSNNYNPSLKN 16 Best Local Similarity 75.0 Matches 12; Conservative Query Match ð 쉱

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ADZ51256 RESULT

ADZ51256 standard; peptide; 16 AA. (first entry) 30-JUN-2005 ADZ51256;

Amino acid sequence of a variable heavy chain region CDR.

bispecific antibody, AR1 chain, AR2 chain, hemostatic; bleeding, antibody therapy; blood coagulation factor VIII; factor VIII deficiency, von willebrands disease; heavy chain; complementarity determining region;

Mus musculus.

WO2005035753-A1.

21-APR-2005.

10-OCT-2003; 2003WO-JP013062

10-OCT-2003; 2003WO-JP013062

(CHUS ) CHUGAI SEIYAKU KK.

Natori O; Senoo C, Soeda T, Miyazaki T, Kojima T, Ishii S; Hattori K, | Kasutani K,

WPI; 2005-315560/32.

Novel bispecific antibody substituting for functional protein or substituting for ligand for receptor comprising two types of molecules, useful as pharmaceutical for treating or preventing diseases e.g. bleeding

Claim 18; SEQ ID NO 73; 143pp; Japanese.

The specification describes a bispecific antibody substituting for functional protein or substituting for a ligand for a receptor comprising two types of molecules. The antibody comprises AR1 and AR2 chains. 

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The invention relates to a bispecific antibody (I) substituting for: a functional protein and having ligand functional alternative activity with respect to receptor containing herecomolecule; or a functional cofactor which enhances an enzyme reaction and recognizes both substrates of enzyme. Also claimed are a composition (II) containing (I). (I) and (II) care useful for preventing and/or treating viral disease, neoplasm, or immunological disease, or bleeding or disease resulting from bleeding. The viral disease is a hepatitis C virus or hepatitis B virus infection. The viral disease is a hepatitis C virus or hepatitic carcinoma. The neoplasms are chronic myeloid leukemia, malignant melanoma, multiple myeloma, renal carcinoma, glioblastoma, medilloblastoma, astrocycoma, hairy cell leukemia, AlDS-related Kaposi's sarcoma, skin T cell lymphoma. The immunological disease is multiple clonenties. The bleeding disease is the disease is multiple clorents. The bleeding disease is the disease resulting from the active reduction or a defect of blood coagulation factor VIII such as hemophilia
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Bispecific antibodies of the invention are useful for preventing and treating bleeding, diseases accompanying bleeding or diseases resulting from bleeding. These diseases develop or progress by active reduction of blood coagulation factor VIII/activated blood coagulation factor VIII/activated blood manual actor VIII, present sequence represents a complementarity determining region (CDR) from a variable heavy chain region, which was used to construct bispecific antibodies of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel bispecific antibody substituting for functional protein and having ligand functional alternative activity to receptor containing heteromolecule, useful for preventing/treating viral disease, immunological disease or bleeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral infection; neoplasm; immune disorder; bleeding; infection; cardiovascular disease; Virucide; Hepatotropic; Antinflammatory; Neuroprotective; Hemostatic; Cytostatic; Immunotherapy; antibody.
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                                                                                                                                                                                                                                       80.9%; Score 72; DB 9; Length 16; 75.0%; Pred. No. 0.0003; ive 3; Mismatches 1; Indels
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Kasutani K, Ishii S;
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Matches
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This invention describes a novel bispecific antibody which can act as a cofactor to enhance an enzyme reaction and can recognize the enzyme aubstrate. The antibody specifically binds to blood coagulation factor VIII. The invention and describes a composition comprising the antibody and a carrier, a kit useful in preventing and/or treating bleeding associated with a disorder or from a disease caused by bleeding. The composition includes blood coagulation factor VIII. The antibody of the invention can be a blood-coagulation factor including blood-coagulation factor IX. The antibody comprises a complementary determining region (CDR) of anti-blood-coagulation factor IX. The antibody. The novel antibody or composition is useful for preventing and/or treating a disease accompanying bleeding or the disease realling from bleeding where the disease accompanying bleeding or the disease realling from bleeding develops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII. The disease the develops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII in the hemophilia is
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or von Willebrand disease. (II) is useful for manufacturing (I). (I) has high stability and low antigenicity in blood. The present sequence represents a mouse anti-s AR antibody CDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bispecific antibody, blood coagulation factor VIII; bleeding; fibrinolysis; blood coagulation factor X; blood-coagulation factor IX; factor VIII deficiency; von Willebrands disease; hemostatic; immunostimulator; antibody engineering; ds; gene.
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                                                                                                                                                                                                        80.9%; Score 72; DB 9; Length 16; 75.0%; Pred. No. 0.0003; 1; Indels ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine factor IX directed antibody CDR2 SEQ ID NO 224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADZ45520 standard; peptide; 16 AA
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14-OCT-2003; 2003WO-JP013123.
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Matches 12; Conservative
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                                                                                                                                                  Sequence 16 AA;
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CC This invention describes a novel bispecific antibody which can act as a cofactor to enhance an enzyme reaction and can recognize the enzyme and the enzyme substrate. The antibody specifically binds to blood coagulation factor VIII. The invention also describes a composition coagulation factor VIII. The invention also describes a composition of the antibody and a carrier, a kit useful in preventing and/or comprising the antibody and a carrier, a kit useful in preventing and/or treating bleeding associated with a disorder or from a disease caused by bleeding. The composition includes blood coagulation factor VIII. The antibody of the invention cator in Earth actor including blood-coagulation factor VIII, bomod coagulation factor of factor including blood-coagulation factor in the coagulation factor in the coagulation factor in the coagulation factor in the disease a complementary determining region (CDR) of anti-blood-coagulation factor in useful for preventing candior treating a disease accompanying bleeding or the disease resulting from bleeding develops and/or progresses by an active reduction or deletion of the blood coagulation factor VIII. The disease the coagulation factor VIII. The disease the blood coagulation factor VIII. The disease the blood coagulation factor VIII. The disease the blood coagulation factor VIII. The disease the blood coagulation factor viii blood coagulation factor viii blood coagulation factor viii blood coagulation factor viii blood coagulation factor viii blood coagulation factor viii blood coagulation factor viii blood coagulation factor viii blood coagulation factor viii blood coagulation factor viii and/or active reduction of the
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an acquired hemophilia A. This sequence encodes a fragment of the antibody described in the method of the invention. Note: The sequence adata for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bispecific antibody; blood coagulation factor VIII; bleeding; fibrinolysis; blood coagulation factor X; blood-coagulation factor IX; factor VIII deficiency; von Willebrands disease; hemostatic; immunostimulator; antibody engineering.
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                                                                                                                                                                                      78.7%; Score 70; DB 9; Length 16; 75.0%; Pred. No. 0.00061; ive 3; Mismatches 1; Indels
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14-OCT-2003; 2003WO-JP013123.
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                                                                                                                                                                                                                                         Conservative
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Les 12; Conserv
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                                                                                                                                               Sequence 16 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               bispecific antibody; AR1 chain; AR2 chain; hemostatic; bleeding; antibody therapy; blood coagulation factor VIII; factor VIII deficiency; von willebrands disease; heavy chain; complementarity determining region; CDR.
              an acquired hemophilia A. This sequence represents a fragment of the anthody described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 where the hemophilia is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel bispecific antibody substituting for functional protein or substituting for ligand for receptor comprising two types of molecules, useful as pharmaceutical for treating or preventing diseases e.g.
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                                                                                                                                                   78.7%; Score 70; DB 9; Length 16; 75.0%; Pred. No. 0.00061; ive 3; Mismatches 1; Indels
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 hemophilia A or von Willebrand disease,
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                                                                                                                                                                                                                                                                                                                                        ADZ51224 standard; peptide; 16 AA.
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                                                                                                                                                                                    12; Conservative
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Kasutani K, Ishii S;
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                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                     Sequence 16 AA;
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viii, is
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Score 70; DB 9; Length 16; Pred. No. 0.00061;

78.7%; 75.0%;

Query Match Best Local Similarity

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The invention relates to a bispecific antibody (I) substituting for: a functional protein and having ligand functional alternative activity with respect to receptor containing heteromolecule; or a functional cofactor which enhances an enzyme reaction and recognizes both substrates of enzyme. Also claimed are a composition (II) containing (I). (I) and (II) care useful for preventing and/or treating viral disease, neoplasm, or immunological disease, or bleeding or disease resulting from bleeding. The viral disease is a hepatitis C virus or hepatitis B virus infection who viral disease is a hepatitis C virus or hepatitic carcinoma. The neoplasms are chronic myeloid leukemia, medulloblastoma, multiple myeloma, real leukemia, AlDS-related Kaposi's sarcoma, skin T cell lymphoma or non-Hodgkin's lymphoma. The immunological disease is multiple sclosus. The bleeding disease is the disease resulting from the active reduction or a defect of blood coaqulation factor VIII such as hemophilia or von Willebrand disease. (II) is useful for manufacturing (I). (I) has chigh stability and low antigenicity in blood. The present sequence
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                                                                                                                                                                                                                                                                                    viral infection; neoplasm; immune disorder; bleeding; infection; cardiovascular disease; Virucide; Hepatotropic; Antiinflammatory; Neuroprotective; Hemostatic; Cytostatic; Immunotherapy; antibody.
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   IndelB
                                                                                                                                                                                                                                                      Mouse anti-s AR antibody heavy chain CDR 2 SEQ ID NO 41.
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunological disease or bleeding
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Best Local Similarity 75.0
Matches 12; Conservative
 12; Conservative
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Ishii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-315561/32.
                                                                                                                                                                                                                                                                                                                                                                                          WO2005035754-A1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 AA;
                                                                                                                                                                                                                        30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori K,
Kasutani K,
                                                                                                                                                                                       ADZ42098;
   Matches
                                                                                                                    RESULT 11
                                                                                                                                     ADZ42098
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cofactor to enhance an enzyme reaction and can recognize the enzyme and cofactor to enhance an enzyme reaction and can recognize the enzyme and coffice the enzyme substrate. The antibody specifically binds to blood coagulation factor VIII. The invention also describes a composition comprising the antibody and a carrier, a kit useful in preventing and/or comprising the antibody and a carrier, a kit useful in preventing and/or comprising the antibody and a carrier, a kit useful in preventing and/or composition includes blood coagulation factor VIII. The antibody of the invention can be a blood-coagulation fibrinolysis related cartor including blood-coagulation factor VIII, blood coagulation factor X, or blood-coagulation factor IX/IX factor antibody. The novel antibody or composition is useful for preventing cantibody. The novel antibody or composition is useful for preventing cantibody. The novel antibody or composition is useful for preventing from bleeding develops and/or progresses by an active reduction or deletion of the develops and/or progresses by an active reduction or deletion of the correct or the blood coagulation factor VIII. The disease the develops and/or progresses by an active reduction or deletion of the correct or deletion of the correct or von Willebrand disease, where the hemophilia is an acquired hemophilia A. This sequence represents a fragment of the antibody described in the method of the invention. Note: The sequence correct or this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel bispecific antibody substituting for function of cofactor that enhances enzyme reaction, and recognizing both enzyme and substrates of enzyme, useful for treating hemophilia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        bispecific antibody; blood coagulation factor VIII; bleeding; fibrinolysis; blood coagulation factor X; blood-coagulation factor IX; factor VIII deficiency; von Willebrands disease; hemostatic;
                                                                                                                                                                                                                                                                                                                                                       Murine factor IX directed antibody CDR2 SEQ ID NO 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soeda T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 183; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunostimulator; antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori K, Kojima T, Miyazaki T,
                                                                                 ADZ45479 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-2004; 2004WO-JP014911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003; 2003WO-JP013062
14-OCT-2003; 2003WO-JP013123
                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-315563/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2005035756-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                 30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2005
                                                                                                                                                                       ADZ45479;
RESULT 12
                                          ADZ45479
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The invention relates to a chimeric antibody, or an Fv-type single-chain fragment, derived from the murine monoclonal antibody IOR C5 expressed by hybridoma ECCS 97061101. It contains the CDRs (complementarity determining regions) of IOR C5 and human constant regions, in both heavy and light chains. The IOR C5 antibody specifically binds to the IOR C2 antigen which is expressed on malignant and normal colorectal cells. The invention also encompasses a cell line which expresses the humanised IOR C5 antibody, host cells which express the Fv fragment; a pharmaceutical composition for treatment, location or in vivo identification of malignant tumours of colon and rectum, including their metastases and recurrences, containing the humanised antibody or the Fv fragment thereof, plus an excipient; and a method for the in vivo diagnosis of thereof, plus an excipient; and a method for the in vivo diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumours comprising the administration of a 99m-technetium-labelled humanised IOR C5 antibody or Fv fragment, and monitoring biodistribution by radiography. The humanised IOR C5 antibody and/or its Fv fragment are used to treat malignant tumours of the colon or rectum, including their metastases or recurrences, and for in vivo diagnosis (imaging) of tumours, particularly when radiolabelled. Sequences AAB73649-AAB73651 represent, respectively, CDRs 1-3 of the heavy chain variable region (VH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mateo De Acosta Del Rio CM, Roque Navarro LT, Morales Morales A;
Perez Rodriguez R, Ayala Avila M, Gavilondo Cowley JV, Duenas Porto M;
Bell Garcia H, Rengifo Calzado E, Iznaga Escobar N, Ramos Zuzarte M;
                                                                                                                                                                                                                                                                    Monoclonal antibody IOR C5; hybridoma ECCC 97061101; mouse; humanised; IOR C2 antigen; colorectal cancer; tumour; metastasis; therapy; drug targetting; imaging; diagnosis; cytostatic; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant antibody, or single-chain fragment, derived from mur
monoclonal IOR C5, useful for treatment and diagnosis of colo-rectal
                                                                                                                                                                                                                                  Murine monoclonal antibody IOR C5 heavy chain variable region CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
                                                                                                        AAB73650 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 24; 30pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-NOV-2000; 2000WO-CU000004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99CU-00000196.
1 YISYDGNNRYNPSLKN 16
                                                                                                                                                                                              11-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of antibody IOR C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200136485-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                     AAB73650;
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                                                                   RESULT 13
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Gaps

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DB 4; Length 16; 2; Indels

69.7%; Score 62; DB 4; 73.3%; Pred. No. 0.011; iive 2; Mismatches

11; Conservative

Matches

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Gaps ô

76.4%; Score 68; DB 9; Length 16; 75.0%; Pred. No. 0.0013; ive 1; Mismatches 3; Indels

Local Similarity

Query Match

Sequence 16 AA;

1 YISYDGTWNYKPSLKD 16

Best Local Similarity 75.0 Matches 12; Conservative

Query Match

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cardiovascular-gen.; degeneration; eating-disorders-gen.;
                                                                                                                                                                                                         Liu C,
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                                                                                                                                                                                                                                                                                                                                                                            The inventors claim a chimeric monoclonal antibody which contains a urokinase-recognising antibody heavy chain variable region contg.at least one of the polypeptide chains G, H and I (ARM24717, R24718, ARM24719) and a human antibody heavy chain content region. The chimeric Abs can be used both in vivo and in vitro and, since they have very low immunogenicity as compared with mouse Abs, they can be administered to humans for diagnostic and therapeutic purposes. They are also more stable and show a longer half-life in the blood as compared with the original mouse Abs. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                      Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction.
                                                                                                   Sequence of an anti-urokinase antibody heavy chain variable region chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 2; Length 16;
Pred. No. 0.048;
2; Mismatches 3; Indels
                                                                                                                              Chimeric monoclonal antibody; anti-urokinase antibody; antithrombotic agent; myocardial infarction therapy.
                                  AAR24718 standard; protein; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEC20782 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 50; 87pp; English
                                                                                                                                                                                                                                                                                  Iwasa S, Tada H, Watanabe T,
                                                                                                                                                                                                                                     90JP-00413829.
91JP-00294464.
                                                                                                                                                                                                                  91EP-00121591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.2%;
                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YISYDGTNNYKPSLK 15
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                                                                                  (first entry)
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                                                                        (revised)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 AA;
                                                                                                            designated 'K'
                                                                                                                                                                                                                  17-DEC-1991;
                                                                                                                                                                                                                                     18-DEC-1990;
                                                                                                                                                                                                                                               11-NOV-1991;
                                                                                                                                                           Mus musculus
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                                                                       25-MAR-2003
28-DEC-1992
                                                                                                                                                                              EP491351-A2
                                                                                                                                                                                                24-JUN-1992
                                                     AAR24718;
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                  RESULT 14
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The invention describes a non-murine antibody (1) that competes with monoclonal antibody RX1 for binding to macrophage colony stimulating cator (M-CSP) by more than 75%, where the monoclonal antibody RX1 has the heavy chain and light chain mino acids sequences having a fully defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4) sequences given in the specification, respecitively. (1) is useful for preventing a subject afflicted with a disease that causes or contributes to osteolysis, where the antibody effectively reduces the severity of the lone loss associated with the disease. The disease is chosen from metabolic bone diseases associated with relatively increased osteoclast activity, including endocrinopathies, hypercalcemia, deficiency states, corronic diseases, and hereditary diseases, cancer, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteoporosis, osteolysis, metastatic cancer to bone and cancer. (1) is useful for preventing or reducing or reducing or manufacturing a medicament for preventing or reducing bone loss, osteolysis, metastatic cancer to bone and cancer. (1) is useful for manufacturing a medicament for preventing or contributes to osteolysis, and metastatic cancer to bone in a patient sifering a patient affilicted with a disease that causes or contributes to sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
endocrine disease; endocrine-gen.; endocrine-gen.; gastrointestinal-gen.; genetic disorder; heavy chain; hepatotropic; hypercalcemia; limmune disorder; immunotherapy; inflammation; monoclonal antibody; moth disease; musculoskeletal disease; neoplasm; nephrotropic; osteopethic; osteopetrosis; osteopersis; pagets disease; periodontal disease; pharmaceutical; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metastatic cancer, for manufacturing a medicament for treating a patient having cancer. (1) in synergistic combination, is useful for preparing a medicament for treating a patient exhibiting osteolysis. This is the amino acid sequence of macrophage colony stimulating factor (M-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel non-murine antibody that competes with monoclonal antibody RX1 binding to macrophage colony stimulating factor, useful for treating hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harrowe GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horwitz AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2004; 2004US-0535181P. 02-JUN-2004; 2004US-0576417P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP. (XOMA ) XOMA TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YISYDGTNNYKPSLK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zimmerman DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-597707/61
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005068503-A2.
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Search completed: December 30, 2005, 14:20:02

endocrine-gen.; antiarthritic; antibacterial; antiinflammatory; antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;

M-CSF specific murine antibody consensus heavy chain CDR2.

Job time : 134.5 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                Copyright
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sw model using - protein search, OM protein Run on:

December 30, 2005, 14:07:14; Search time 22.5 Seconds (without alignments) 68.421 Million cell updates/sec

US-10-735-916A-10 89 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 16 1 YISYDGTNNYKPSLKD Scoring table:

283416 seqs, 96216763 residues Searched: 250 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 16 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Jain V-D-J	-cell	T-cell receptor be	tail fiber protein	pyruvate dehydroge	chai	protein P8 - curle	casein kinase II (	rRNA N-glycosidase	glutathione, transf	T cell receptor al	T-cell receptor be	~	protein kinase, 80		heat shock protein	tical p	T-cell surface gly	Ig H chain V-D-J r	dihydrolipoamide S	calmodulin, vasoac	T-cell receptor be	receptor	-cell receptor	l receptor	-cell receptor	н	photosystem II 6.1	protein QA100047 -
	ΙD	PH1589	PH0749	A49255	A42291	A31963	PH1351	E28027	C45133	801669	S28213	PH1778	F49039	B60278	PL0137	\$23184	C44896	851610	B45895	PH1622	S00123	A44101	G49039	PH1474	PH1472	PH1477	PH1473	PH1480	A41170	PA0048
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Query	atch	3	31.5	30.3	25.8	25.8	24.7	24.7	22.5	22.5	22.5	22.5	22.5	22.5	21.3	21.3	21.3	20.2	20.2	20.2	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1
o	Score M	30		7		e								20								17	17	17	17	17	17	17	17	17
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calcium-dependent protein kinase C i	alpha-conotoxin Au	alpha-conotoxin Au	casein kinase II (	Ig heavy chain DJ	T-cell receptor al	major outer membra	cob protein - comm	taurocyamine kinas	transcription fact	melanotropin beta	hypothetical prote	T-cell receptor be	Ig H chain V-D-J r	T-cell receptor de
E45066 S10807	C59045	A59045	A45133	PH1346	PH0777	S28433	822040	A11488	B23692	MTDFBS	A39109	H49039	PH1634	B36300
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16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
19.1	18.0	18.0	18.0	18.0	18.0	18.0	18.0	18.0	18.0	17.4	16.9	16.9	16.9	16.9
17	16	16	16	16	16	16	16	16	16	15.5	15	12	15	15

## ALIGNMENTS

PHIS89

IG H chain V-D-J region (wild-type clone 140) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PHISS9
R;Levinson, D.A; Campos-Torres, J.; Leder, P.
J; Exp. Med. 178, ; Campos-Torres, J.; Leder, P.
J; Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PHISS0; MUID:93301609; PMID:8315387
A;Accession: PHISS9
A;Accession: PHISS9
A;Residues: 1-16 < LEW>
A;Residues: 1-16 < LEW>
A;Residues: 1-16 < LEW>
Cross-references: UNIPARC:UPI000017C6B0
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Gaps ö Score 30; DB 2; Length 10; Pred. No. 1.5e+02; 2; Mismatches 33.7%; illarity 62.5%; Conservative Query Match Best Local Similarity Matches 5; Conserv

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3 SYDGTNNY 10 Š

5 SYDGSPHY 12 g

RESULT 2

T-cell receptor beta chain (B83) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accesslan : Ph0749
B;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J; Exp. Med. 174, 1371-1383, 1991
A;Pitle: T cell receptor genes in a series of class I major histocompatibility complex-rallelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0749.

A;MOlecule type: mRNA A;Residues: 1-16 <CAS> A;Cross-references: UNIPARC:UPI0000115FA8; EMBL:X60840; NID:950116; PIDN:CAA43233.1; PID A;Experimental source: T lymphocyte C;Keywords: T-cell receptor

Gaps ö Length 16; Query Match
31.5%; Score 28; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels

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6 GTNNYKP 12 7 GTNNQAP 13 ઠે ద

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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1351
R;Wasserman, R.; Gallii, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphc
A;Reference number: PH1302; MUID:93094761; PMID:1460419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein P8 - curled-leaved tobacco (fragment)
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Species: Nava-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: E28027
R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-this A;Reference number: A94167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Casein kinase II (EC 2.7.1.-) alpha chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Accession: C45133
R;Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.
J. Biol. (Chem. 267, 23799-23796, 1992
A;Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the assoc
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                                                                                                                                                                                              Ig heavy chain DJ region (clone C100-109B) - human (fragment)
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A; Residues: 1-16 <OUI>
A; Cross-references: UNIPROT: O9TRK9; UNIPARC: UPI000008890
A; Experimental source: endoplasmic reticulum, pancreas
A; Experimental sequence extracted from NCBI backbone (NCBIP:118799)
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A;Note: 10-Lys was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: DNA
A;Residues: 1-16 < WAS>
A;Cross-ferences: UNIPARC:UPI000017C21F
C;Keywords: heterotetramer; immunoglobulin
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7 MSDPGTSSYR 16
2 ISYDGTNNYK 11
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Best Local Similarity
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Matches 3; Conserv
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A, Status: preliminary
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Latal fiber protein I - phage P2 (fragment)

C;Species: phage P2

C;Date: 10-Uul-1992 #sequence_revision 10-Uul-1992 #text_change 09-Jul-2004

C;Accession: A42291

R;Haggard-Ljungquist, E; Halling, C; Calendar, R.

J. Bacteriol. 174, 1462-1477, 1992

A;Title: DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizon

A;Reference number: A42291; MUID:92165720; PMID:1531648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A31963

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (frag C;Species: Ascaris suum (pig roundworm)

C;Species: Ascaris suum (pig roundworm)

C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004

C;Accession: A31963

R;Thissen, J: Komuniecki, R.

B;Thissen, J: Komuniecki, R.

A;Title: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerob A;Reference number: A31963; MUID:89066711; PMID:3198613

A;Accession: A31963

A;Status: preliminary
                                                                          C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: A49555
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using A;Reference number: A49039; MUID:92164737; PMID:1311263
                                                  receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)
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A;Residues: 1-16 <HAG>
A;Cross-references: UNIPROT:P26701; UNIPARC:UP1000017A829; GB:M64677
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Pred. No. 2e+03;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.3%; Score 27; DB 2; Length 16; Best Local Similarity 71.4%; Pred. No. 4.5e+02; Matches 5; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP100011C3B9
A;Note: sequence extracted from NCBI backbone (NCBIP:90722)
C;Keywords: T-cell receptor
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C;Keywords: mitochondrion; oxidoreductase; phosphoprotein
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25.8%; Score 23; DB 2;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 4; Mismatches
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Best Local Similarity 60.00,
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A; Status: preliminary
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4 VAYDG 8
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Gaps

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Length 16;

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A; Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood (
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R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using A;Reference number: A49039; MUID:92164737; PMID:1311263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24K antigen - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Species: Mycobacterium bovis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: B60278
R;Fifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A;Title: Purification and characterization of major antigens from a Mycobacterium bovis
A;Reference number: A60278; MUID:91147217; PMID:1900061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -cell receptor beta chain V-D-J-C region (V beta 2, J beta 1.5) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Romo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: F49039
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-16 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.5%; Score 20; DB 2; Length 16; 57.1%; Pred. No. 6.1e+03; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UP1000017C3B3
A;Note: sequence extracted from NCBI backbone (NCBIP:90718)
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references: UNIPROT: Q7M199; UNIPARC: UPI000017AD42
                                                              A; Reference number: PH1754; MUID: 93301585; PMID: 8391057
                                                                                                                                                                                                                                                             Query Match 22.5%; Score 20; DB 2; Le
Best Local Similarity 66.7%; Pred. No. 6.1e+03;
Matches 4; Conservative 1; Mismatches 1;
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Pred. No. 6.1e+03;
0; Mismatches 2;
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Best Local Similarity 57.1'
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4 Conservative
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A;Molecule type: protein
A;Residues: 1-16 <FIF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NDYKLS 15
                                                                                         A,Accession: PH1778
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-16 < POR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                             RESULT 9
$01669
rRNA N-glycosidase (EC 3.2.2.22) trichokirin - Mongolian snake-gourd (fragment)
N;Alternate names: ribosome-incativating protein trichokirin
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S01669
R;Casellas, P.; Dussossoy, D.; Falasca, A.I.; Barbieri, L.; Guillemot, J.C.; Ferrara, P. Bur: J. Biochem. 176, 581-588, 1988
A;Title: Trichokirin, a ribosome-inactivating protein from the seeds of Trichosanthes ki
A;Accession: S01669; MUID:89005108; PMID:3262509
A;Accession: S01669; MUID:89005108; PMID:3262509
A;Reference number: S01669; MUID:89005108; PMID:3262509
A;References: UNIPROT:P16093; UNIPARC:UP1000002BE47
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Superfamily: rRNA N-glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glutathione transferase (EC 2.5.1.18) - European toad (fragments)
C;Species: Bufo bufo (European toad)
C;Species: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S2813
C;Accession: S28213
A;Title: Purification and characterization of the major glutathione transferase from adv A;Reference number: S28213; MUID:93143709; PMID:8424786
A;Accession: S28213
A;Molecule type: protein
A;Residues: 1-16 <ACE>
A;Coss-references: UNIPARC:UP10000178FA9
A;Coss-references: UNIPARC:UP10000178FA9
A;Experimental source: liver
C;Keywords: transferase
           C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; heterotetramer; phosphotransferase; serine/threonine-specific protein
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PH1778
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (frag C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1778
S;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
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Pred. No. 6.1e+03;
3; Mismatches 7; Indels
                                                                                            Query Match 22.5%; Score 20; DB 2; Length 16; Best Local Similarity 42.9%; Pred. No. 6.1e+03; Matches 3; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 40.0%; Pred. No. 6.1e+03; Length 16; 4; Conservative 3; Mismatches 3; Indels
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28.6%;
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Best Local 4; Conservative
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9 FHGHDNY 15
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Length 16;

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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
C;Datesion: PLO137
C;Accession: Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.
J. Neurochert, U.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.
J. Neurochert, U.; Weber, J. 1989
J. Neurochert, U.; Weber, J. 1989
J. Neurochert, U.; Weber-Schaeuffelen, M.; Wollny, E.
J. Neurochert, J.; Weber-Schaeuffelen, M.; Wollny, E.
J. Neurochert, PLO137
J. Neurochert, M.; Weber-Schaeuffelen, M.; Wollon, E.
J. Nesidues: PLO137
J. Neurochert, M.; Weber-Schaeuffelen, M.; Wollon, E.
J. Nesidues: 1-16 cbEC-
J. Neurochert, M.; Weber-Schaeuffelen, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Weber-Schaeuffelen, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neurochert, M.; Wollon, J. Neuroch
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: 823184
R;Huq, I.; Haukanes, B.I.; Helland, D.E.
Eur. J. Biochem. 206, 833-839, 1992
A;Title: Purification to homogeneity and characterization of a redoxyendonuclease from A;Reference number: 823184; MUID:92299012; PMID:1376689
A;Accession: 823184
A;Molecule type: protein
A;References: UNIPARC:UPI000017C559
A;Cross-references: UNIPARC:UPI000017C559
A;Cross-references: thymus
C;Function:
A;Pergerimental source: thymus
C;Function:
A;Pergerimental source: thymus
C;Function: A;Pergerimental source: thymus
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21.3%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels
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4 VDVDGT 9
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 30, 2005, 14:06:48; Search time 141.5 Seconds (without alignments) 79.777 Million cell updates/sec Run on:

US-10-735-916A-10 89 Title: Perfect score: Sequence:

1 YISYDGTNNYKPSLKD 16

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched: 1144 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 16 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Oguc75 homo sapien	drosc		Q7rjel plasmodium		_			_		_												Q9prv4 gallus gall	homo		Q9ucr2 homo sapien			2 tritic	9 pinus r	Osyes4 prolis gunn
SUMMARIES	a	O9UC75 HUMAN	OSOL92 DROBP	Q9KJI0_STAHA	Q7RJE1_PLAYO	Q9F1R9_STRSU	Q9F1S1_STRSU	Q9QVL2_9MURI	Q9YQ11_9CORO	Q7M1V7_NICPL	Q9PRR9_9AVES	Q35214_OENBE	Q9GIA6_9PHAE	ARCD_PSEPU	RIPK_TRIKI	Q9TRK9_CANFA	021922_9CAUD	Q7Y0M3_MAIZE	Q79AT0_AGRRH	Q7M199_MYCBO	Q9R4J4_PSEFR	Q506K8_9CALI	Q4X7B4_PLACH	Q9PRV4_CHICK	Q96KQ2_HUMAN	Q9T2V8_HUMAN	Q9UCR2_HUMAN	Q50L70_9DIPT	Q50L82_9DIPT	Q6RY72_TRIMO	QBLLT9_PINRA	Q5YE54_PHOGU
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	* Query Match Length	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
	% Query Match	32.6	29.5	27.0	25.8	25.8	25.8	25.8	25.8	24.7	24.7	23.6	23.6	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	21.3	21.3	20.2	20.3	20.5	0	20.2	20.5	20.2	20.2
	Score	29	26	24	23	23	23	23	23	22	22	21	21	20	20	20	50	20	20	20	20	20	19	19	18	18	18	18	18	18	18	18
	Result No.		(7)	m	4	'n	9	7	Φ	σ	10	11	12	13	14	15	16	17		19	20	21	22	23	24	25	26	27	28	29	30	31

	P81438 myrmecia gu	P81437 myrmecia gu	P80410 palomena pr	P80411 palomena pr	P11179 bos taurus		Q9tnn9 homo sapien		Q9tr19 bos taurus	Q7mlw7 arabidopsis		Q988g3 oryza sativ			
Q9F9S4 HELPY	FORM1 MYRGU	FORM2 WYRGU	MK2B PALPR	MK3 PALPR	ODOZ BOVIN	SSIT_STRMB	Q9TNN9 HUMAN	Q9UCG5 HUMAN	Q9TRL9 BOVIN	Q7M1W7_ARATH	Q9S8C0_LUPAL	O9S8G3 ORYSA	Q9SBN2_TOBAC	l	
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17.5	17	17	17	17	17	17	17	17	17	17	17	17	17		
32	33	3.4	35	36	37	38	39	40	41	42	43	4	45		

# ALIGNMENTS

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Gaps

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Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                    Score 23; DB 2; Length 16;
Pred. No. 1.2e+04;
0; Mismatches 2; Indels
                                                                                         preliminary data.
EMBL; AABLO100941; BAA22886.1; -; Genomic_DNA.
Hyporhetical protein.
SEQUENCE 16 AA; 1824 MW; AEBS951B681C02A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Q9F1R9;
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Q9F1S1;
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Matches 4, Conservative
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                                                                                                                                                                                   Gaps
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Pallgren C., Utt M., Ljungh A.;

"Isolation and characterisation of a 17-kDa staphylococcal heparin-
binding protein with broad specificity.";
J. Med. Microbiol. 50:547-557(2001).

EMBL; AP169242; AAF89664.1; -; Genomic_DNA.
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                     Score 26; DB 2; Length 16; Pred. No. 3.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
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                                                             BFCAB1719C58B7D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Pred. No. 8e+03;
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      EMBL; AB194429; BAD98205.1; -; Genomic DNA
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66.7%;
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                                                             SEQUENCE 16 AA; 1933 MW;
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hes 4; Conservative
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phosphoribosyl carboxyamide aminoimidazole transformylase (EC 6.3.2.6)
                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phosphoribosyl carboxyamide aminoimidazole transformylase (EC 6.3.2.6)
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16 AA; 1980 MW; A73BD79FAE3C0946 CRC64;
16 AA.
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MEDLINE=95159435; PubMed=7856095
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10095;
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MEDLINE=88078100; PubMed=2825819; DOI=10.1016/0300-9084(87)90178-7;
Rasschaert D., Gelfi J., Laude H.;
"Enteric coronavirus TGEV: partial sequence of the genomic RNA, its
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Q9YQ11;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical fusion protein.
Transmissible gastroenteritis virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus; Group 1 species.
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Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.; "Byidence for horizontal transfer of the SsuDATII restriction-modification genes to the Streptococcus suis genome."; J. Bacteriol. 183:500-511(2001).
BENBL, AB045614; BAB208421; -; Genomic DNA.
GO: GO:0016874; Fligase activity; IEA.
GO: GO:0016874; F:phosphoribosylaminoimidazolesuccinocarboxam.
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Pred. No. 1.2e+04;
3; Mismatches 1; Indels
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Last annotation update)
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Pred. No. 1.2e+04;
3; Mismatches 4;
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01-MAR-2003 (TrEMBLrel. 23, Last annot
MEPRIN=METALLOENDOPEPTIDASE (Fragment)
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16 AA; 1998 MW;
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QQQVL2;
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Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids;
                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDILINE-99099045; PubMed-9882359;
Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
Enjuanes L.,
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Elecuet J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.; "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1 of transmissible gastroenteritis virus."; Virology 206:817-822(1995).
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Archosauria; Aves; Neognathae; Anseriformes; Anatidae.
NCBI_TaxID=8835;
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                                                                                                                                                                                                                                 "Replication and packaging of transmissible gastroenteritis coronavirus-derived synthetic minigenomes.";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
NA/K adenosine triphosphatase alpha subunit (Fragment).
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                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 16 AA; 2015 MW; B37776CE7AF3B62D CRC64;
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Protein P8 (Fragment)
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Pred. No. 1.7e+04;
3; Mismatches 3;
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EMBL; AJ011482; CAA09624.1; -; Genomic_RNA.
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NCBI_TaxID=4092;
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Q9PRR9;
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NUCLEOTIDE SEQUENCE.
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01-FEB-1995
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                                                   Boldyrev A.A., Lopina O.D., Kenney M., Johnson P.;
"Characterization of the subunit isoforms of duck salt gland Na/K adnosine triphosphatase."
Biochem. Biophys. Res. Commun. 216:1048-1053(1995).
SEQUENCE 16 AA; 1784 MW; 1A338DZECEF6B920 CRC64;
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NUCLEOTIDE N.E., Smith C.M., Morden C.W.;
"Testing systematic concepts of Sargassum (Fucales, Phaeophyceae)
using portions of the rbcLS operon.";
Phycol. Res. 53:1-10(2005).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
                                                                                                                                                                                                                             24.7%; Score 22; DB 2; Length 16; 37.5%; Pred. No. 1.7e+04; tive 3; Mismatches 2; Indels
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Pred. No. 2.5e+04;
1; Mismatches 2; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ATPase alpha subunit (16 aa) (Fragment).
Oenothera bertiana (Bertero's evening primrose).
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                              MEDLINE=96074588; PubMed=7488178;
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57.1%;
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Q35214;
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Q9GIA6;
                                                                                                                                                                                                     Query Match
Best Local Similarity 37.5
Local 3; Conservative
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1 GRDKYEPT 8
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9 NAKPYIK 15
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PROTEIN SEQUENCE.
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                                            (Fucales, Phaeophyceae).";
Thesis (1998), University of Hawaii.
EMBL; AF244339; AAF98104.2; -; Genomic_DNA.
GO; GO:0009507; C:chloroplast; IEA.
GO; GO:000573; C:ribulose bisphosphate carboxylase complex (. . .; IEA.
GO; GO:0016984; R:ribulose-bisphosphate carboxylase activity; IEA.
InterPro; IPR000894; RusiscO_small.
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Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Catalyzes an electroneutral exchange between arginine and ornithine to allow high-efficiency energy conversion in the
Phillips N.E.; "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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Pseudomonadaceae; Pseudomonas.
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Pred. No. 3.6e+04;
0; Mismatches 2; Indels
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Amino-acid transport; Antiport; Inner membrane; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                    16 AA; 1830 MW; B2096FF5A23D1210 CRC64;
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(Rel. 31, Last sequence update)
(Rel. 47, Last annotation update)
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ProDom; PD000290; RuBisCO small; 1.
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GCFSFLPDLSD 16
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MEDLINE=93054738; PubWed=1331100;
Ou W J., Thomas D.Y., Bell A.W., Bergeron J.J.;
"Casein kinase II phosphorylation of signal sequence receptor alpha and the associated membrane chaperone calnexin.";

    -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
    Type 1 RIP subfamily.

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Casein kinase II=24 kDa polypeptide (Fragment).
Canis familiaris (Dog).
Bukaryota; Metazoa; Choga, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S01669; S01669.
InterPro; IPR001574; RIP.
PROSITE; PS00275; SHIGA_RICIN; PARTIAL.
Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                   Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ribosome-inactivating protein trichokirin (BC 3.2.2.22) (rRNA N-
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40.0%; Pred. No. 3.6e+04;
ive 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                             Trichosanthes kirilowii (Mongolian snake-gourd)
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Q9TRK9 CANFA PRELIMINARY;
Q9TRK9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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Maximum DB E
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Sequence 19, Appl Sequence 45, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 15, Appl Sequence 17, Appl Sequence 7, Appli Sequence 2, Appli Sequence 91, Appl Sequence 91, Appl Sequence 11, Appl Sequence 111, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 2, Appli Sequence 91, Appl Sequence 91, Appl Sequence 91, Appl	INHIBITING CD14 MEDIATED CELL ACTIVA	Indels 0; Gaps 0;	ODIES
16 2 US-09-996-265-19 16 2 US-09-996-265-45 16 1 US-08-483-636-24 16 1 US-08-483-632-24 16 1 US-08-483-632-24 16 2 US-09-759-112A-15 16 2 US-09-996-288-2 16 2 US-09-996-288-9 16 2 US-09-996-288-9 16 2 US-09-996-288-10 16 2 US-09-996-288-10 16 2 US-09-996-288-11 16 2 US-09-996-288-11 16 2 US-09-996-288-11 16 2 US-09-996-288-11 16 2 US-09-996-265-2 16 2 US-09-996-265-9 16 2 US-09-996-265-9 16 2 US-09-996-265-9	ONS FOR	No. 0.0089;	ENERAL INFORMATION:  ENERAL INFORMATION:  APPLICANT: Berchtold, Peter  APPLICANT: Berchtold, Peter  TILE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  FILE REFERENCE: 100564-09049  CURRENT PAPLICATION NUMBER: US/09/424,840B  CURRENT FILING DATE: 1999-12-03  PRIOR FILING DATE: 1999-12-03  PRIOR FILING DATE: 1998-05-08  PRIOR FILING DATE: 1997-12-12  PRIOR FILING DATE: 1997-12-12  PRIOR FILING DATE: 1997-12-12  PRIOR FILING DATE: 1997-12-12  PRIOR FILING DATE: 1997-12-12
28 41 46.1 33 41 46.1 32 33 34 46.1 34 46.1 34 46.1 35 33 37 41.6 36 35 39.3 37 39.3 38 39.3 41 35 39.3 42 35 39.3 44 35 39.3 45 39.3	RESULT 1 US-09-170-769A-14 US-09-170-769A-14 Sequence 14, Application US/09170769A Patent No. 644420E GENERAL INFORMATION: APPLICANT: LETURCO, Didier APPLICANT: LETURCO, Didier APPLICANT: LETURCO, Didier APPLICANT: ULEVITCH, Richard APPLICANT: ULEVITCH, Richard APPLICANT: TOBIAS, Peter TITLE OF INVENTION: METHODS AND COMPOSITION FILE OF INVENTION: METHODS AND COMPOSITION CURRENT PILING DATE: 1998-10-13 CURRENT PILING DATE: 1998-10-13 FRIOR PILING DATE: 1998-10-13 SOFTWARE: PALING DATE: 1998-10-13 SOFTWARE: PALING DATE: 1998-10-13 SOFTWARE: PALING DATE: 1998-10-13 TYPE: PRI CORGANISM: Murine US-09-170-769A-14	Duery Matches 10; Conservative 2; Miss Autches 10; Conservative 2; Miss Qy 1 YISYDGTNNYKPELK 15  Db 1 YISYGGTSYNPSLK 15  RESULT 2  US-09-424-840B-110  ; Sequence 110, Application US/09424840B  ; Patent NO. 6790338	4 0

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APPLICANT: TSCHCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BALDANHA, JOSE
TITLE OF INVENTION: RESEAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSE: Poley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READBEIS FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.7%; Score 54; DB 1; Length 16; 66.7%; Pred. No. 0.027;
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                     COMPOURNEY IN PRODUCTION OF THE PROPER PROPER PROPER PROPER PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPER
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CLASSIFICATION: 536
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
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APPLICATION NUMBER: US/08/436,71
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Patent No. 5817790
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INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity
Matches 10; Conserva
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US-08-436-717-126
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Fatent No. 6790338
GENERAL INFORMATION:
FAPPLICANT: Berchtcld, Peter
FITE BERCHENCE: 100564-09049
CURRENT FILING DATE: 1999-12-03
FILE REFERENCE: 100564-09049
CURRENT FILING DATE: 1999-12-03
FRIOR PELICATION NUMBER: US/09/424,840B
FRIOR PELICATION NUMBER: US 1995-12-03
FRIOR FILING DATE: 1999-12-03
FRIOR FILING DATE: 1999-12-12
FRIOR FILING DATE: 1997-12-12
FRIOR FILING DATE: 1997-12-12
FRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Ratentin Version 3.1
FRIOR FILING DATE: 1997-06-06
FRIOR FILING DATE: 1997-06-06
FRIOR FILING DATE: 1997-06-06
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US-08-137-117D-126
; Sequence 126, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K °--
CITY.
                                                                                                                                                                                                                                                                                                                        Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 16;
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                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                    Query Match 62.9%; Score 56; DB 2; Best Local Similarity 66.7%; Pred. No. 0.013; Matches 10; Conservative 1; Mismatches
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Pred. No. 0.019
0; Mismatches
                                 SOFTWARE: Patentin version 3.1
SEQ ID NO 110
LENGTH: 16
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Best Local Similarity 66.7%;
Matches 10; Conservative
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ZIF: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
NUMBER OF SEQ ID NOS: 128
                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-424-840B-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGANISM: Homo sapiens US-09-424-840B-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-424-840B-112
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Gaps

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COUNTRY: ANG.
COMUTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPAGNEDOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UNM-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPRENCE JOHN P.
REPRENCE JOHN P.
REPRENCE JOHN P.
REPRENCE JOHN INFORMATION:
TELLEPAK: 212-278-0400
TELLEFAK: 212-391-0525
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
'PMCTH: 16 amino acids
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.1%; Score 49; DB 1 60.0%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                       STREET: 1185 Avenue of the Americas CITY: New York COTATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-940-727B-53
; Sequence 53, Application US/09940727B
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60.0%;
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Best Local Similarity 60.03
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-672-345C-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-214-095D-53
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APPLICANT: Berchcold, Peter
APPLICANT: Berchcold, Peter
TITLE OF INVENTION: ANTI-GPIDE/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 10054-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-0364
FRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR PILING DATE: 1999-05-08
FRIOR PRILING DATE: 1999-05-08
FRIOR PILING DATE: 1999-05-08
FRIOR PILING DATE: 1997-06-06
FRIOR PILING DATE: 1997-06-06
SPRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PARENTIN VERSION 3.1
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 2; Length 16;
Pred. No. 0.084;
2; Mismatches 3; Indels
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      APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REGISTRATION INFORMATION:
TELEFOWNINICATION INFORMATION:
TELEFOWNINICATION INFORMATION:
TELEFRONS: (202) 672-5399
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Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/09424840B
Patent No. 6790938
                                                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 64.3
Matches 9; Conservative
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ORGANISM: Homo sapiens
US-09-424-840B-35
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Length 16; 6; Indels

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Secretary Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICAMY: LANGENATION:
APPLICAMY: LANGEN, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
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Pred. No. 0.18;
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Sequence 41, Application US/0996288

Sequence 41, Application US/0996288

Patent No. 6818211

GENERAL INFORMATION:

APPLICANT: Young, James

APPLICANT: Leslie, Johnson

TITLE OF INVENTION: and Treatment

TITLE OF INVENTION: and Treatment

TITLE OF INVENTION: and Treatment

TITLE OF INVENTION: APPLICATION NUMBER: 1021-047-999

CURRENT APPLICATION NUMBER: 2001-11-28

NUMBER OF SEQ ID NOS: 259

SOFTWARE: PatentIn version 3.1

SEQ ID NO 41

LENGTH: 16
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Patent No. 6818216

GENERAL INFORMATION

APPLICANT: Young, James

APPLICANT: Scott, Koenig

APPLICANT: Leslie, Johnson

TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxie;

TITLE OF INVENTION: and Treatment

FILE REFERENCE: 10271-047-999
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                                                                                                                                                                       53.9%; Score 48; DB 2; Length 16; 60.0%; Pred. No. 0.26; ive 2; Mismatches 4; Indels
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Pred. No. 0.26;
2; Mismatches
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CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 103
LENGTH: 16
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NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
LENGTH: 16
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Best Local Similarity 60.09
Matches 9; Conservative
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Best Local Similarity 60.03
Matches 9; Conservative
                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-09-996-288-37
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CORGANISM: Homo sapiens
US-09-996-288-41
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-996-288-103
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APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Scott, Koenig
APPLICANT: Boott, Koenig
APPLICANT: Boott, Koenig
APPLICANT: Boott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT PAPLICATION NUMBER: US/09/996,288
CURRENT PILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 16
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Sequence 37, Application US/0996288

GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Blick, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
FILE REFERENCE: 1027-1047-999
CURRENT PELING DATE: 2001-11-28
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                               GENERAL ANTOGRAPH DORAID W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERBENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT PILING DATE: 2002-09-04
PRIOR PELING DATE: 1998-12-28
PRIOR PELING DATE: 1999-12-8
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR PILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR PILING DATE: 1996-06-25
SRIOR APPLICATION NUMBER: 08/672,345
PRIOR PILING DATE: 1996-06-15
SQCTWARE: PATENTIN UMBER: 09/6-15
SQCTWARE: PATENTIN UMBER: 09/6-15
SQCTWARE: PATENTIN UMBER: 05/6-16-15
SQCTWARE: PATENTIN UMBER: 05/6-16-15
SQCTWARE: PATENTIN UMBER: 05/6-16-15
SQCTWARE: PATENTIN UMBER: 05/6-16-15
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Pred. No. 0.18;
0; Mismatches
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Pred. No. 0.26;
2; Mismatches
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60.0%;
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60.0%;
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Best Local Similarity 60.0.
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Best Local Similarity 60.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: mouse
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US-09-996-288-25
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US-09-996-288-37
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2 IWWDGKKDYNPSLKD 16

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squence 25, Application US/0996265
; Bacent No. 685543;
; Cardence 25, Application US/0996265
; Patent No. 685543;
; Cardent INFORMATION:
; APPLICANT: Young James
; APPLICANT: Scott, Koenig
; APPLICANT: Scott, Koenig
; APPLICANT: Leslic, Johnson
; TITLE OF INVENTION: And Treatment
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US-09-96-265-37
US-09-96-265-37
Sequence 37, Application US/09996265
Patent No. 6855493
GENERAL INFORMATION:
APPLICANT: Voung, James
APPLICANT: Scott, Koenig
APPLICANT: Leelie, Johnson
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-048-999
CURRENT APPLICATION WUMBER: US/09/996,265
CURRENT APPLICATION WUMBER: US/09/996,265
CURRENT PILLNG DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
LENGTH: 16
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2 IWWDGKKHYNPSLKD 16
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Best Local Similarity 60.0
Matches 9; Conservative
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		ULT 1 10-735-9 iequence imblicati whblicati APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPL	che E		SULT 2 -10-822-3 Sequence Publicati GENERAL 3
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APPLICANT: Abbott Laboratories APPLICANT: Reilly, Edward B. APPLICANT: Lacy, Susan E.

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Publication No. US2004017513A1

GENERAL INFORMATION:

APPLICANT: Generatech, Inc.

APPLICANT: Hongo, Jo-Anne S.

APPLICANT: Presta, Leonard G.

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Sequence 110, Application US/10844424

Publication No. US20040202659A1

GENERAL INFORMATION:
APPLICANT: Berchtold, Peter

APPLICANT: Berchtold, Peter

TILE OF INVENTION: ANTI-GFIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049

CURRENT APPLICATION NUMBER: US/10/844,424

CURRENT APPLICATION NUMBER: US/09/424,840

PRIOR APPLICATION NUMBER: US/09/424,840

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-05-08

PRIOR PLING DATE: 1999-05-08

PRIOR PLING DATE: 1999-05-08
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Pred. No. 0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.2%; Score 58; DB 5; Length 16; 66.7%; Pred. No. 0.025; ive 2; Mismatches 3; Indels
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TITLE OF INVENTION: Antibodies TO Erythropoietin Receptor TITLE OF INVENTION: And Uses Thereof FILE REFERENCE: 7340WSP1 FILE REFERENCE: 7340WSP1 CURRENT APPLICATION NUMBER: US/10/822,306A PRIOR APPLICATION NUMBER: 10/821,497 PRIOR PPLING DATE: 2004-04-09 NUMBER OF SEQ ID NOS: 29 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 23 LENGTH: 16
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Best Local Similarity 66.7
Matches 10; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 10; Conserva
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APPLICANT: Abbort Laboratories
APPLICANT: Abbort Lacy, Susan B.
APPLICANT: Abbort Emab
APPLICANT: Lacy, Susan B.
APPLICANT: Lacy, Susan B.
APPLICANT: Roguska, Michael B.
APPLICANT: Roguska, Michael B.
TITLE OF INVENTION: Antibodies To Erythropoietin Receptor TITLE OF INVENTION: And Uses Thereof
FILE REPRENCE: 73490281
CURRENT APPLICATION NUMBER: US/10/822,306A
CURRENT FILING DATE: 2004-04-12
PRIOR FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 16
         APPLICANT: Fung, Emma
APPLICANT: Belk, Johathan P.
APPLICANT: Relk, Johathan P.
APPLICANT: Relk, Michael
TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
TITLE OF INVENTION: And Uses Thereof
FILE REFERENCE: 7349USP1
CURRENT APPLICATION NUMBER: US/10/822,306A
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 10/821,497
PRIOR PILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 26
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.4%; Score 60; DB 5; Length 16; 66.7%; Pred. No. 0.012;
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US-10-822-306A-21
; Sequence 21, Application US/10822306A
; Publication No. US20050227289A1
; GENERAL INFORMATION:
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APPLICANT: Reilly, Edward B.
APPLICANT: Lacy, Susan E.
APPLICANT: Fung, Emma
APPLICANT: Relk, Johathan P.
APPLICANT: Roguska, Michael
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Matches 10; Conserv
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US-10-822-306A-23
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1 YISYDGTNNYKPSLKD 16
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; ORGANISM: Mus sp.
US-09-791-551-89
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; ORGANISM: Mus sp.
US-09-791-551-84
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US-09-791-551-84
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; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGES, TERESA L.
; APPLICANT: GCXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KB
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REPRENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR PLING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PATCHIN VET. 3.2
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APPLICANT: Berchtold, Peter
APPLICANT: Berchtold, Peter
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/9/424,840
FRIOR APPLICATION NUMBER: US/9/424,840
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US/9/424,840
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-12
PRIOR PAPLICATION NUMBER: DE 1975227.7
PRIOR PAPLICATION NUMBER: DE 1975227.7
PRIOR PILING DATE: 1997-10-6-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PAGE ID NOS: 128
SOFTWARE: PAGE ID NOS: 128
LENGTH: 16
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PRIOR FILING DATE: 1997-12-12
PRIOR PEDLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 110
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 112, Application US/1084424; Publication No. US20040202659A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                  Query Match 62.9%;
Best Local Similarity 66.7%;
Matches 10; Conservative
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Best Local Similarity 66.7
Matches 10; Conservative
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US-10-844-424-112
                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-844-424-110
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US-10-893-576-107
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; SEQ ID NO 107
; LENGTH: 16
; TYPE: PAT
; ORGANIEM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy chain
; OTHER INFORMATION: variable region CDR peptide
US-10-893-576-107
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| Publication No. US2003023584A1
| Publication No. US2003023584A1
| GENERAL INFORMATION:
| APPLICANT: HANNA, NABLL
| TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
| FILE REPRESENCE: 037003/0277869
| CURRENT APPLICATION NUMBER: US/09/791,551
| CURRENT PILING DATE: 2001-02-26
| PRIOR APPLICATION NUMBER: 60/185,390
| PRIOR PILING DATE: 2000-02-28
| PRIOR APPLICATION NUMBER: 60/233,625
| PRIOR APPLICATION NUMBER: 60/233,625
| PRIOR PILING DATE: 2000-09-18
| SOFTWARE: PATENTING OFFE: 2119
| SOFTWARE: PATENTING OFFE: 2119
| SOFTWARE: PATENTING OFFE: 2119
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; Bublication No. US20030235584A1
; Publication No. US20030235584A1
; GENERAL INPORMATION:
   APPLICANT: KLOETZER, WILLIAM S.
   APPLICANT: HANNA, NABIL
   TILE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
   FULE REPERENCE: 037003/037021
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT PILING DATE: 2001-02-26
; PRIOR FILING DATE: 2000-02-28
; PRIOR FILING DATE: 2000-02-8
; PRIOR FILING DATE: 2000-03-8
; PRIOR FILING DATE: 2000-03-8
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PATENTIN Ver. 2.1
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Best Local Similarity 50.0%; Pred. No. 0.11;
Matches 8; Conservative 6; Mismatches 2
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Best Local Similarity 60.0%; Pred. No. 0.076;
Matches 9; Conservative 2; Mismatches
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APPLICANT: Abbort Laboratories
APPLICANT: Reilly, Edward B.
APPLICANT: Reilly, Edward B.
APPLICANT: Pung, Susan B.
APPLICANT: Pung, Emma
APPLICANT: Pung, Emma
APPLICANT: Pung, Emma
APPLICANT: Roguska, Michaell
APPLICANT: Reguska, Michaell
APPLICANT: Reguska, Michaell
APPLICANT: Reguska, Michaell
APPLICANT: Roguska, Michaell
APPLICANT: Roguska, Michaell
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APPLICANT: Roguska, Michaell
APPLICANTON: And Uses Thereof
TITLE OF INVENTION: And Uses Thereof
TITLE OF INVENTION NUMBER: US/10/822,306A
CURRENT APPLICATION NUMBER: US/821,497
PRIOR APPLICATION NUMBER: 10/821,497
PRIOR PILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 19
ILBNGTH: 16
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TITLE OF INVENTION: Antibodies that bind alphaE Integrin
FILE REFERENCE: 1855.2025-000
CURRENT APPLICATION NUMBER: US/10/173,551
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 26
LENGTH: 16
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US-09-940-727B-53
Sequence 53, Application US/09940727B; Publication No. US20030077793A1
GENERAL INFORMATION:
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                                                                                                                                                                                                          RESULT 13
US-10-173-551-26
Sequence 26, Application US/10173551
Publication No. US20030232387A1
GENERAL INFORMATION:
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                                        2 ISYDGTNNYKPSLK 15
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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CRGANISM: Homo sapiens
US-10-173-551-26
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; ORGANISM: Homo sapiens
US-10-822-306A-19
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| Publication No. US20040022791A1
| Publication No. US20040022791A1
| GENERAL INFORMATION:
| APPLICANT: ASAT AG
| TITLE OF INVENTION: Inhibiting angiogenesis
| TITLE OF INVENTION: Inhibiting angiogenesis
| TITLE OF INVENTION: Inhibiting angiogenesis
| FILE REPERENCE: 23600PWO DRAS |
| CURRENT APPLICATION NUMBER: US/10/399,701 |
| FURRENT FILING DATE: 2003-04-21 |
| PRIOR APPLICATION NUMBER: 100 57 443.2 |
| NUMBER OF SEQ ID NOS: 12 |
| SEQ ID NO 5 |
| LENGTH: 16 |
| TYPE: PRT |
| ORGANISM: Artificial Sequence |
| PRIOR SETURE SEQUENCE |
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US-10-844-424-35
is Sequence 35, Application US/1084424
is Publication No. US20040202659A1
is GENERAL INFORMATION:
APPLICANT: Bearchcold, Peter
APPLICANT: Bearchcold, Peter
is APPLICANT: Bearchcold, Peter
is APPLICANT: Bearchcold, Peter
is APPLICANT: Bearchcold, Peter
is APPLICANT: Bearchcold, Peter
is APPLICANT: Bonner: 100564-40949
is TILE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
if TILE REFERENCE: 10056-40949
is CURRENT APPLICATION NUMBER: US/10/844,424
is PRIOR FILING DATE: 1999-12-03
is PRIOR PILING DATE: 1999-12-03
is PRIOR APPLICATION NUMBER: DE 19755227.7
is PRIOR APPLICATION NUMBER: DE 19755227.7
is PRIOR PILING DATE: 1997-12-12
is PRIOR FILING DATE: 1997-16-06
is NUMBER OF SEQ ID NOS: 128
is SQPTWARE: PatentIn version 3.1
is EQ ID NO 35: 1280
is ENGTH. 164
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Length 16;
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                                                                         4; Indels
Score 52; DB 3;
Pred. No. 0.23;
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64.3%; Pred. No. 0.34;
iive 2; Mismatches
Query Match 58.4%; Score 52; DB Best Local Similarity 60.0%; Pred. No. 0.23 Matches 9; Conservative 2; Mismatches
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Best Local Similarity 64.3
Matches 9; Conservative
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                                                                  Matches
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| APPLICANT: Landry, Donald W | TITLE OF INVENTION: ANTI-COCINE CATALYTIC ANTIBODY | TITLE REPERENCE: 0575/51400-B | CURRENT APPLICATION NUMBER: US/09/940,727B | CURRENT FILING DATE: 2002-09-04 | PRIOR APPLICATION NUMBER: 09/214,095 | PRIOR FILING DATE: 1997-06-25 | PRIOR PELING DATE: 1997-06-25 | PRIOR PELING DATE: 1997-06-25 | PRIOR FILING DATE: 1997-06-25 | PRIOR FILING DATE: 1997-06-25 | PRIOR FILING DATE: 1996-06-25 | PRIOR FILING DATE:
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Search completed: December 30, 2005, 14:43:48 Job time : 110 secs

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December 30, 2005, 14:25:45; Search time 8 Seconds (without alignments) 14.978 Million cell updates/sec
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1. /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4. /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5. /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
6. /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7. /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8. /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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89
                                                                                                  OM protein - protein search,
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Maximum DB seq length: 16
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 10, Appl	Sequence 24, Appl	314				226	61,	11,	15,	2261,	2266,	2323,	20,	38,	59,	274		286		16	22		Sequence 2947, Ap	Semience 3004. An
SUMMARIES		QI	US-11-012-353-10	US-11-009-939-24	US-11-054-515-3140	US-10-502-145-33	US-11-054-515-2799	US-10-507-662-5	US-11-054-515-2263	US-11-128-440-61	US-11-125-837-11	US-11-105-708-15	US-11-054-515-2261	US-11-054-515-2266	US-11-054-515-2323	US-11-055-163-20	US-10-503-575-38	US-10-999-866-59	US-11-054-515-2745	US-11-054-515-2792	US-11-054-515-2891	US-11-093-274-6	US-11-021-305-167	US-11-054-515-2221	US-11-054-515-2274	US-11-054-515-2947	11-054-515-3004
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		Score	89	45	31	29	26	25	25	25	24	24	23	23	23	22	21	21	21	21	21	21	21	20	20	20	20
	Result	No.	7	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 2307, Ap Sequence 2153, Ap Sequence 2157, Ap Sequence 2780, Ap Sequence 2783, Ap Sequence 183, App Sequence 6, Applisequence 2137, App Sequence 2143, App Sequence 2143, Ap Sequence 2143, Ap Sequence 2144, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2145, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Sequence 2115, Ap Ap Sequence 2115, Ap Ap Sequence 2115, Ap Ap Sequence 2115, Ap Ap Ap Sequence 2115, Ap Ap Ap Ap Ap Ap Ap Ap Ap Ap Ap Ap Ap	
16 7 US-11-054-515-2307 16 7 US-11-054-515-2153 16 7 US-11-054-515-2157 16 7 US-11-054-515-2780 16 7 US-11-054-515-2780 16 7 US-11-054-515-3090 16 6 US-10-054-515-3090 16 6 US-10-507-662-6 16 6 US-10-507-662-6 16 6 US-11-054-515-3137 16 7 US-11-054-515-2143 16 7 US-11-054-515-2145 16 7 US-11-054-515-214 16 7 US-11-054-515-214 16 7 US-11-054-515-2214 16 7 US-11-054-515-2214 16 7 US-11-054-515-2214 16 7 US-11-054-515-2215 17 US-11-054-515-2215 18 7 US-11-054-515-2215	US-11- US-11- US-11- US-11-
2	42 18 20.2 43 18 20.2 44 18 20.2 45 18 20.2

#### ALIGNMENTS

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US-11-01Z-353-10

Sequence 10. Application US/11012353

Sequence 10. Application US/205049730A1

GENERAL INFORMATION:

APPLICANT: GOETCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: HAEW, JEAN-FRANCIS

APPLICANT: HAEW, JEAN-FRANCIS

APPLICANT: HAEW, JEAN-FRANCIS

APPLICANT: HAEW, JEAN-FRANCIS

APPLICANT: HAEW, JEAN-FRANCIS

TITLE OF INVENTION: NOVEL ANTI-IOF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: NOVEL ANTI-IOF-IR AND USES THEREOF

TITLE OF INVENTION: NOVEL ANTI-IOF-IR AND USES THEREOF

TITLE OF INVENTION: NOVEL ANTI-IOF-IR AND USES THEREOF

TITLE OF INVENTION: NOVEL ANTI-IOF-IR

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2003-10-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-20

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; Pred. No. 2.3e-09;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
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; ORGANISM: Mus musculus
US-11-012-353-10
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Best Local Similarity 50.0
Matches 5; Conservative
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US-11-054-515-2799
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ORGANISM: Mus musculus
US-10-502-145-33
       1: | | |: : |
4 LNYDGSTDY 12
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Best Local Similarity
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## Publication No. US200502659981
| GENERAL INFORMATION:
| APPLICANT: Elson, Generalizing Antibodies and Methods of Use Thereof
| TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
| FILE REFERENCE: 23135-402
| CURRENT APPLICATION NUMBER: US/11/009,939
| CURRENT APPLICATION NUMBER: US/528,811
| PRIOR APPLICATION NUMBER: 60/528,812
| PRIOR PILING DATE: 2003-12-10
| PRIOR PLING DATE: 2003-12-10
| PRIOR APPLICATION NUMBER: 60/528,962
| PRIOR PILING DATE: 2003-12-10
| PRIOR PILING DATE: 2003-12-10
| PRIOR PILING DATE: 2003-12-10
| RIOR APPLICATION NUMBER: 60/528,962
| PRIOR PILING DATE: 2003-12-10
| PRIOR PILING DATE: 2003-12-10
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US-11-054-515-3140

i Sequence 3140, Application US/11054515

i Publication No. US2005025532A1

i GREERAL INPORMATION:

i APPLICAMT: Ruben et al.

i TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PF533P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2004-02-10

PRIOR PILING DATE: 2004-02-10

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2004-06-18

PRIOR PILING DATE: 2001-11-4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 7; Length 16; Pred. No. 0.053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
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; ORGANISM: Mus musculus
US-11-009-939-24
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US-11-054-515-3140
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Best Local Similarity
Matches 4; Conserva'
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US-10-502-145-33
; Sequence 33, Application US/10502145
; Sequence 33, Application US/10502145
; Publication Vo. US20050244406A1
; GENERAL INFORMATION;
; TITLE OF INVENTION; ALTL-C5AR antibodies and uses thereof
; TILE REFERENCE: RICE-032
; CURRENT APPLICATION; NUMBER: US/10/502,145
; CURRENT APPLICATION NUMBER: US/NO/19
; PRIOR APPLICATION NUMBER: USN 60/350,961
; RICH FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
: LENGTH: 16
                                                                                                                                                                                                                 Score 29; DB 6; Length 16;
Pred. No. 25;
2; Mismatches 3; Indels
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Pred. No. 80;
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Gaps

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ledbetter, Martha
APPLICANT: Brady, William A.

APPLICANT: Brady, William A.

APPLICANT: Brady, William A.

APPLICANT: Daw, Che-Leung
APPLICANT: Daw, Raj

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING

TITLE OF INVENTION: LYMPHOCYTE ACTIVATION

TITLE OF INVENTION: LYMPHOCYTE ACTIVATION

TITLE OF INVENTION: LYMPHOCYTE ACTIVATION

TITLE OF INVENTION: LYMPHOCYTE ACTIVATION

TITLE OF INVENTION: LYMPHOCYTE ACTIVATION

TITLE OF INVENTION: NUMBER: US/11/128,440

CURRENT PELLING DATE: 2003-08-21

PRIOR APPLICATION NUMBER: US 09/252,150

PRIOR PELLING DATE: 1998-02-18

PRIOR PELLING DATE: 1998-02-19

PRIOR APPLICATION NUMBER: (06/075,274

PRIOR APPLICATION NUMBER: 60/075,274

PRIOR APPLICATION NUMBER: 60/075,274

PRIOR APPLICATION NUMBER: 60/075,274

PRIOR APPLICATION NUMBER: 60/075,274

NUMBER OF SEQ ID NOS: 80

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 7; Length 16; Pred. No. 1.2e+02; 0; Mismatches 2; Indels
                                                                                                      Score 25; DB 7; Length 16;
Pred. No. 1.2e+02;
1; Mismatches 5; Indels
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Fublication No. US20050266003A1
GENERAL INFORMATION:
APPLICANT: Lin, Rong-Hwa
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-Jun
APPLICANT: Chen, Pei-Jun
APPLICANT: Chen, Pei-Jun
APPLICANT: Chen, Pei-Jun
APPLICANT: Chen, Pei-Jun
APPLICANT: Chen, Pei-Jun
APPLICANT: Chen, Pei-Jun
APPLICANT: Chen, Pei-Jun
APPLICANT: WORB-13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2005-05-10
FRIOR PRICH DATE: 2006-05-10
FRIOR PRICH DATE: 2006-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FASEUSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                 US-11-128-440-61
Sequence 61, Application US/11128440
Publication No. US20050261478A1
GENERAL INFORMATION:
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66.7%;
                                                                                                      Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                     3 YDTLTSYVPLL 13
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CRGANISM: Mus musculus
US-11-128-440-61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 YYDYDG 11
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Publication No. US2005025532A1
GENERAL INFORMATION:
IGENERAL INFORMATION:
INTILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF52783
CURRENT PELING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-02-11
PRIOR PILING DATE: 2004-06-18
PRIOR PILING DATE: 2004-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
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PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/270, 409
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
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NUMBER OF SEQ ID NOS: 3247
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US-10-507-662-5

Sequence 5, Application US/10507662

Publication No. US208c0255102A1

GENERAL INFORMATION:
APPLICANT: BIOGEN INC.

TITLE OF INVENIOUS ANTI-ALPHA-V BETA-6 ANTIBODIES

PILE REFERENCE: A136PCT

CURRENT FILING DATE: 2004-09-13

PRIOR PILING DATE: 2004-09-13

PRIOR PILING DATE: 2002-11-13

PRIOR PILING DATE: 2002-11-13

PRIOR PILING DATE: 2002-11-13

NUMBER OF SEQ ID NOS: 64

SEQ ID NOS: 64

LENGTHARE: PATENTIN VET: 2.1
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Pred. No. 1.2e+02;
2; Mismatches 6; Indels
        6; Indels
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.1%;
Best Local Similarity 42.9%;
Matches 6; Conservative
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     5; Conservative
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1 LDYDILTGYYPS 12
                                                              2 ISYDGTNNYKPS 13
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US-10-507-662-5
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LENGTH: 16
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        Matches
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US-11-054-515-2266

1 Sequence 2266, Application US/11054515

1 Publication No. US2005025532A1

2 GENERAL INFORMATION:

2 APPLICANT: Ruben et al.

3 TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

5 FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT APPLICATION NUMBER: G0/543,296

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2002-11-16

PRIOR FILING DATE: 2001-11-16

PRIOR PELING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/240,817

PRIOR APPLICATION NUMBER: 60/233,499

PRIOR FILING DATE: 2001-10-615

PRIOR PELING DATE: 2001-05-25

PRIOR PELING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR PELING DATE: 2001-05-25

PRIOR PELING DATE: 2001-03-21

PRIOR PELING DATE: 2001-03-21

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-01-17

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PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-16
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Pred. No. 2.6e+02;
1; Mismatches 4; Indels
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Best Local Similarity 44.4%;
Matches 4; Conservative
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CRGANISM: Homo sapiens
US-11-054-515-2261
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CORGANISM: Homo sapiens
US-11-054-515-2266
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APPLICANT: Van Epps, Dennis
APPLICANT: Van Epps, Dennis
APPLICANT: Wan Epps, Dennis
APPLICANT: Brooks, Peter
APPLICANT: Brooks, Peter
TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
FILE REFERENCE: 30797-704.501
CURRENT APPLICATION NUMBER: US/11/105,708
CURRENT APPLICATION NUMBER: 09/478,977
PRIOR APPLICATION NUMBER: 60/152,496
PRIOR PILING DATE: 1999-09-02
PRIOR FILING DATE: 1999-09-02
PRIOR FILING DATE: 1999-09-02
PRIOR PLILING DATE: 1999-09-02
PRIOR APPLICATION NUMBER: 60/114,878
PRIOR APPLICATION NUMBER: 60/114,878
PRIOR APPLICATION NUMBER: 60/114,877
PRIOR PLILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
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US-11-054-515-2261
US-11-054-515-2261
Sequence 2261, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2004-02-10
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-16
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                                                                                                                                           27.0%; Score 24; DB 7; Length 16; 40.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-11-105-708-15
Sequence 15, Application US/11105708
Publication No. US20050281821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 25
SOFWARE: Patentin version 3.2
SEQ ID NO 16
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pernasetti, Flavia
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Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                    Query Match
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                        6 GTNNYKPSLK 15
                                                                                                                                                                                                                                                                                                                        6 GGTSYNPKFK 15
             TYPE: PRT ORGANISM: Mus musculus
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ORGANISM: Artificial
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US-10-503-575-38

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Sequence 38, Application US/10503575

Publication No. US20050244823A1

SEQUENCE 38, Application No. US20050244823A1

APPLICANT: Drijfhout, Jan Wouter

APPLICANT: APPLICANT: Expanse Antonius

APPLICANT: Wan Veelen, Petrus Antonius

APPLICANT: Wan Veelen, Petrus Antonius

APPLICANT: Wan Veelen, Petrus Antonius

TITLE OF INVENTION: DETECTION THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS

TITLE OF INVENTION: DETECTION THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS

FILE REPERENCE: 2799/72843-PCT-US

CURRENT FILING DATE: 2004-08-04

PRIOR APPLICATION NUMBER: DFT/NL03/00077

PRIOR APPLICATION NUMBER: EP 02075456.0

PRIOR PILING DATE: 2002-04

NUMBER OF SEQ ID NOS: 340

SOFTWARE Patentin version 3.1

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; SEQ ID NO 20
1 LENGTH: 16
2 LYPE: PRT
3 ORGANIEM: Artificial Sequence
3 PEATURE:
4 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
5 OTHER INFORMATION: heavy chain peptide sequence
US-11-055-163-20
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 16;
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Best Local Similarity 37.5
Matches 3; Conservative
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; ORGANISM: Homo sapiens
US-10-503-575-38
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- protein search, using sw model OM protein December 30, 2005, 13:02:01; Search time 71.0968 Seconds (without alignments) 49.440 Million cell updates/sec Run on:

US-10-735-916A-12 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 YGRVFFDY 8 Scoring table: Sequence:

2443163 seqs, 439378781 residues Searched: 2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 21:* Database :

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2005s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		df			SUMMERTES	
ion i	Score	Query Match	Query Match Length	88	ID	Description
	47	100.0	8	7	ADJ76846	
7	47	100.0	80	σ	ADZ67016	_
٣	47	100.0	117	7	ADJ76903	•
4	47	100.0	117	7	ADJ76909	
ß	47	100.0	117	7	ADJ76917	Adj76917 Anti-IGF-
9	47	100.0	117	7	ADJ76913	Adj76913 Anti-IGF-
7	47	100.0	117	σ	ADZ67083	_
<b>c</b> o	47	100.0	117	9	ADZ67087	
σ	47	100.0	117	0	ADZ67073	Adz67073 Murine im
10	47	100.0	117	σ	ADZ67079	
11	47	100.0	127	7	ADJ76886	Adj76886 Anti-IGF-
12	47	100.0	127	σ	AD267056	
13	47	100.0	135	7	ADJ76911	
14	47	100.0	135	7	ADJ76919	
15	47	100.0	135	7	ADJ76915	Adj76915 Anti-IGF-
16	47	100.0	135	თ	ADZ67089	Adz67089 Human ant
17	47	100.0	135	σ	ADZ67081	Adz67081 Human ant
18	47	100.0	135	σ	ADZ67085	Adz67085 Human ant
19	38	80.9	138	7	ABO71408	_
20	37	78.7	221	9	ABM70706	
21	37	78.7	2920	80	ADG65227	
22	36	9.9/	410	m	AAY68969	Aay68969 Cps2T whi
23	35	74.5	233	7	ADH86117	Adh86117 Enterococ
24	35	74.5	390	7	AB084316	Abo84316 Pseudomon

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ABB54242 ABB71908 AAW62012 AAX2339 AAX2339 AAX73923 AAX73923 AAX73923 AAX3073 AAY3073 AAY3073 AAY3073 AAW62013 AAW62013 AAW62013 AAW62013 AAW62013 AAW62033 AAW63531	
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# ALIGNMENTS

RESULT 1

ADJ76846 standard; peptide; 8 AA.

ADJ76846;

(first entry) 06-MAY-2004 CDR sequence for anti-IGF-1R antibody.

cytostatic; antipsoriatic; antibody; insulin-like growth factor-l receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR. 

Mus musculus.

WO2003059951-A2.

24-JUL-2003

20-JAN-2003; 2003WO-FR000178

18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-0005753.

(FABR ) FABRE MEDICAMENT SA PIERRE.

Leger 0; Corvaia N, Goetsch L,

WPI; 2003-569653/53. N-PSDB; ADJ76845 New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Claim 1; SEQ ID NO 12; 164pp; French

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (BGFR) and/or with

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                         these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of ICRT and OFT EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplasm, prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetries; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsorlatic; psorlasis; dermatological disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
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hyperactivity of signal transduction pathways mediated by interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR00178.
11-JUL-2003; 2003FR-00008538.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                          Sequence 8 AA;
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(LEGE/)
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The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of

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comprising a light or heavy chain wings activity of the foreign.

Comprising a light or heavy chain waving at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino caids (ADZ670014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF1 R and/or EGFR, and/or connected with an overexpression and/or an abnormal charaction of IGF1 or IGF2 with IGF1R and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2 dependent and/or IGF2-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the
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specifically inhibiting tyrosine kinase activity of the receptor
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18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
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Disclosure; SEQ ID NO 75; 164pp; French

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 raceptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (II) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or the verexpression and/or abnormal activity of IGF-IR and/or pinkh overexpression pathways mediated by interaction of these receptors with their ligands. Especially they inhibit and/or proliferation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also by abnormal expression of IGF-IR and/or BGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insulin-like growth factor-1 receptor; IGP-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
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                                                                        New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                              Disclosure; SEQ ID NO 69; 164pp; French
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              Leger 0;
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18-JAN-2002; 2002FR-0000654.
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hes 8; Conservative
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                Corvaia N,
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              Goetsch L,
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                                       The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of transformation of tumor cells, so are useful against cancers of the proliferation of tumor cells, so are useful against cancers of the procease. Jung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriatis. A bare a lso used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
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18-JAN-2002; 2002FR-0000654.
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Best Local Similarity
Matches 8; Conserv
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prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psortais. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.

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100.0%; Score 47; DB 7; Length 117; 100.0%; Pred. No. 0.9;

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           treat diseases associated with overexpression and/or abnormal activity of fGP-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or proliferation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
activity of IGR-1R. Ab and its fragments are used to prevent or
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2002FR-00005753.
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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; meoplasm; prostete tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsorlatic; psoriasis; dermatological disease; immune disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
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                                                                                          Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.
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ADZ67083 standard; protein; 117 AA
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WD-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating cancer
                                                              (first entry)
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CORVAIA N.
LEGER O.
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (IGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit transformation of normal cells, so are useful against cancers of the

New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

(FABR ) FABRE MEDICAMENT SA PIERRE.

Leger 0;

Goetsch L, Corvaia N,

WPI; 2003-569653/53.

Disclosure; SEQ ID NO 79; 164pp; French

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cof an illness connected with an overexpression and/or an abnormal activation of a medicament intermed and or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a cativation of the IGF-IR and/or EGFR, and/or of the signal mediated by the interaction of IGFI or IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, appecially IGFI and/or IGF2.

C dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or
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preparation of a medicament intended for the prevention or treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD267087 standard; protein; 117 AA.
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; 2003WO-FR000178.
; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
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YGRVFFDY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YGRVFFDY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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The invention relates to a novel isolated anti-insulin-like growth factor of receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of an addicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with an overexpression and/or an abnormal of interaction of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of EGFR, where the administration of the medicament does not induce or only slightly receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral capendant and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/or EGF-dependent and/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (1), which is optionally labeled. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a novel isolated anti-insulin-like growth factor
                                                                                                                                                                                                                      Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.
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                                                                                                                                   Haeuw J,
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0; Mismatches
                                                                                                                                   Leger O, Duflos A,
                                                                                                                                                                                                                                                                                                                                              Example 13; SEQ ID NO 83; 125pp; English.
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                                                                                                                                      Corvaia N,
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CORVAIA N.
                 LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
                                                                                          BECK A.
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                                                                                                                                      Soetsch L,
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                                                                                       BECK/)
                                                            (HAEU/)
                        (LEGE/)
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IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.

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Gaps

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0; Indels

Score 47; DB 9; Pred. No. 0.9; ; Mismatches 0

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8; Conservative

Query Match Best Local Similarity

Best Loc Matches

Sequence 117 AA;

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1 YGRVFFDY

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100.0%; 100.08;

useful for treating cancer. GOET/) (DUFL/) (HAEU/) (BECK/) (CORV/) LEGE/) 

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Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genificurinary disease; osteosarcoma; musculloskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
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07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003WO-FR00178
11-JUL-2003; 2003FR-00008538.
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CORVAIA N.
LEGER O.
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                                                                                                                                                                                                                       Mus musculus.
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Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, WPI; 2005-321968/33

Example 13; SEQ ID NO 69; 125pp; English.

The invention relates to a novel isolated anti-insulin-like growth factor

I receptor (IGF-IR) antibody (I) or its functional fragment, being
capable of binding to human IGF-IR and, if necessary, capable of
specifically inhibiting troshne kinase activity of the receptor,
comprising a light or heavy chain having at least one complementary
determining region (CDR) consisting of one of two fully defined is amino
acids (ADS67006 and ADS67014). An antibody of the invention is useful in
the preparation of a medicament intended for the prevention or treatment
of an illness connected with an overexpression and/or an abnormal
activation of the transduction pathway of the signal mediated by the
interaction of the transduction pathway of the signal mediated by the
interaction of the transduction pathway of the signal mediated by the
interaction of the transduction pathway of the signal mediated by the
interaction of the transduction pathway of the signal mediated by the
interaction of the transformation of normal cells into cells with tumoral
creeptor. The antibody is useful for preparation of the insulin
receptor. The antibody is useful for preparation of the insulin
receptor. The antibody is useful for preparation of the insulin
considered for preparation of a medicament intended to inhibit the growth
and/or the proliferation of a medicament and/or EGP-dependent
consent intended for prevention or for the treatment of cancer,
the cancer is chosen from prostate cancer, osetosarcoma, lung cancer,
the cancer is chosen from prostate cancer, osetosarcoma, lung cancer,
the cancer is chosen from prostate cancer, osetosarcoma, lung cancer,
the cancer, endometrial cancer or colon cancer. (I) is useful in the
preparation of a medicament intended for the prevention or for the
preparation of a medicament intended for the prevention or for the prevention or or percaptessing of illnesses induced by an
overapression or an underexpression of the log-ill septenting from a biological sample in which the abnormal present or growth

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neoplasm; profette tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of specifically inhibiting tyrosine kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                                                               Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
                                                                                                                                                                               Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; SEQ ID NO 75; 125pp; English.
                                                                                     ADZ67079 standard; protein; 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2002FR-0000654.
; 2002FR-00005753.
; 2003WO-FR000178.
; 2003FR-00008538.
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                                                                                                                                                                                                                                                                                                         heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IR and specifically inhibit useful for treating cancer.
                                                                                                                                                (first entry)
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WPI; 2005-321968/33.
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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07-MAY-2002;
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                                                                                                                   ADZ67079;
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(HAEU/)
(BECK/)
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activation of the IGF-IR and/or EGFR, and/or connected with a activation of the IGF-IR and/or EGFR, and/or connected with a cativation of the IGF-IR and/or EGFR, and/or of the signal mediated by the interactivation of IGF1 or IGF2-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-C dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for preparation of a medicament intended to inhibit the growth and/or IGF2-dependent and/or EGF-dependent and/or IGF2-dependent and/or EGF-dependent of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer. (I) is useful in the preparation of a medicament intended for the specific targeting of a biologically active compound to the specific targeting of a biologically active compound to cells expressing or overexpressing to voerexpressing to voerexpressing to which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample in which the abnormal present.

CE Rand/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present
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07-MAY-2002; 2002FR-00005753.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 117 AA;
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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or-2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of transformation of summal calls to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate. Jung, breast, andometrium and colon, also osteosarcoma, and also for treating psoriaais. A bare a lso used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder; immunoglobulin; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.
New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 47; DB 7; Length 127; 100.0%; Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                       protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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'note= "leader peptide"
                                                 Disclosure; SEQ ID NO 52; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/note= "CDR3"
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2003FR-00008538
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                          Sequence 127 AA;
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18-JAN-2002;
07-MAY-2002;
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11-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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The invention relates to a novel isolated anti-insulin-like growth factor capable of capable of binding to human 10F-1R and, if necessary, capable of capable of binding to human 10F-1R and, if necessary, capable of specifically inhibiting tyroshie kinase activity of the receptor, capable of specifically inhibiting tyroshie kinase activity of the receptor, comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (ADSG7006 and ADSG7004). An antibody of the invention is useful in activation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a mediated by the interaction of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where continues secondary effects connected with inhibition of the Insulin receptor. The antibody is useful for preparation of a medicament intended to interacter, preferably IGF-dependent and/or IER2/neu-dependent cells with tumoral contended for preparation of a medicament intended to Inhibit the growth and/or the proliferation of a medicament intended to inhibit the growth and/or the proliferation of a medicament intended for prevention or for the treatment of cancer, where the cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of soriasis. (I) is useful in the preparation of a medicament intended for the prevention or for the present of preparation of a medicament intended for the presention of a medicament of psoriasis. (I) is useful in preparation of a medicament intended for prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically and/or EGFR receptor. (I) is useful in preparation of a medicament intended for the specific targeting of a biological will in the preparation of a medicament intended for t
                                                                                                                                                                                                                                                                                     Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor,
                                                                                                                                                                              Beck A;
                                                                                                                                                                              Haeuw J,
                                                                                                                                                                              Duflos A,
                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; SEQ ID NO 52; 125pp; English.
                                                                                                                                                                              Leger O,
                                                                                                                                                                                                                                                                                                                                                        useful for treating cancer.
                                                                                                                                                                              Soetsch L, Corvaia N,
                                                                                                                                                                                                                     WPI; 2005-321968/33.
                    GOETSCH L.
CORVAIA N.
LEGER O.
                                                                                  DUFLOS A. HAEUW J.
                                                                                                                                                                                                                                            N-PSDB; ADZ67055
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                                                                                    (DUFL/)
(HAEU/)
                         GOET/)
                                                                                                                                  BECK/)
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100.0%; Score 47; DB 9; Length 127; 100.0%; Pred. No. 0.97;
                           0; Indels
                           0; Mismatches
Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                     1 YGRVFFDY 8
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ADJ76911 standard; protein; 135 AA.
109 YGRVFFDY 116
                                                      RESULT 13
                                                                    ADJ76911
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ADJ76911

cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway;

Anti-IGF-1R related protein #27.

(first entry)

06-MAY-2004

**EEEKEKEKEK** 

ADJ76919;

ADJ76919 standard, protein, 135 AA.

ADJ76919

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The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or expiression and/or abnormal activity of theyeractivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
                                                                                         insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                        cytostatic; antipsoriatic; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Leger O;
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                                    Anti-IGF-1R related protein #23
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                                                                                                                                                                                                                                                                                                                               18-JAN-2002; 2002FR-00000653
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06-MAY-2004 (first entry)
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                                                                                                                                                                                    Homo sapiens.
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24-JUL-2003

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ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leger O;
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18-JAN-2002; 2002FR-00000654.
07-MAY-2002; 2002FR-00005753.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein sequence used to generate the Ab of the invention
                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 81; 164pp; French
                                                                                                                                         (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                 18-JAN-2002; 2002FR-0000653.
18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
                                20-JAN-2003; 2003WO-FR000178
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 30, 2005, 13:11:41; Search time 11.3548 Seconds (without alignments) 67.789 Million cell updates/sec Run on:

US-10-735-916A-12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 YGRVFFDY 8 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		æ				
Result No.	Score	Query Match	Length	DB	O.	Description
	35	74.5	90	7	AC1030	hypothetical prote
7	35	74.5	293	7	D90456	oxydoreductase, pr
m	35	74.5	384	7	AI1566	-
4	35	74.5	395	7	F86740	teichoic acid bios
Ŋ	35	74.5	682	N	C84295	UDP-sugar hydrolas
9	34	72.3	87	~	E81191	hypothetical prote
7	34	72.3	117		801822	
80	34	72.3			G69523	
σ	34	72.3			D69515	
10	34	72.3	297	~	C84509	
11	34	72.3			839866	_
12	34	72.3			T33531	hypothetical prote
13	34	72.3			A38560	nitrate transport
14	34	72.3		~	S16595	gene CARSR12 prote
15	34	72.3	739	•	A81430	
16	33	70.2		N	203077	Ig heavy chain V r
17	33	70.2		•	C69037	hypothetical prote
18	33	70.2	220	7	D71946	_
19	33	70.2		7	F64563	-
20	33	70.2		7	AB2109	hypothetical prote
21	33	70.2			F95289	conserved hypothet
22	33	70.2			T20302	hypothetical prote
23	33	70.2			CTINHP2	site-specific DNA-
24	33	70.2		~	S42379	hypothetical prote
25	33	70.2	m		JC6053	glycerol-3-phospha
26	33	70.2			AB3025	methionine gamma-1
27	33	70.2	427	N	G98259	methionine gamma-1
28	33	70.2	4		D97885	erved h
53	33	70.2	9	7	T28278	ORF MSV117 probabl

hypothetical prote ATP-dependent heli	ATP-dependent DNA probable ATP-depen	lipoxygenase (EC 1 ATP-dependent DNA	hypothetical prote	hypothetical prote	Ig heavy chain V r Ig heavy chain V r	Ig heavy chain V r Ig heavy chain V r	heavy	Ig heavy chain V r Ig heavy chain V r
T30621 H82751	AD3126 E98161	S74207 AE3166	C82931	T22668	PH1698 PH1713	PH1685 PH1712	PH1701	PH1718 PH1702
0.0	0 0	0 0	~ ~	N 64	0 0	04 0	1 (4	0 0
663	771	878	1084	1589	24	24	25	56 26
70.2	70.2	70.2	70.2	70.7	68.1 68.1	68.1	68.1	68.1 68.1
33	. e. e.	933	99	ກ ຕ ຕ ຕ	322	32	35	32
30	325	34.5	36	38	39 40	41	4.4	44 45

# ALIGNMENTS

hypothetical protein STY4564 [imported] - Salmonella enterica subsp. enterica serovar Typical protein STY4564 [imported] - Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: Accession: Ac1030 R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connetton, P.; Gronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Multhors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21834947; PMID:11677608

A,Status: preliminary A,Molecule type: DNA A,Recidues: 1-90 < PAR> A,Cross-references: UNIPARC:UP1000005A8A2; GB:AL513382; PIDN:CAD09340.1; PID:g16505340; C

A; Gene: STY4564 C, Genetics

ö Gaps ö 74.5%; Score 35; DB 2; Length 90; 85.7%; Pred. No. 6.3; tive 0; Mismatches 1; Indels Conservative Query Match Best Local Similarity Matches

8 GRVFFDY ~ g 8

RESULT 2

oxydoreductase, probable [imported] - Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C; Accession: D90456
R; She, Q; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to Genbank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: D90456

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-293 <KUR

A, Cross-references: UNIPROT: Q97V38; UNIPARC: UPI000064866; GB: AE006641; NID: 913816140; P C; Genetics:

Query Match

Length 293; DB 2; 74.5%; Score 35; ~

Accession: AI1566

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A; Accession: AI1566

A; Gene: lin1074 Query Match

ઠે 셤 RESULT 5 C84295

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Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniells, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liż A;Ttle: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pypothetical protein NMB0510 [imported] - Neisseria meningitidis (strain MC58 serogroup E C;Species: Neisseria meningitidis
C;Species: Nar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81191
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A,Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Fitle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibate: 31-Dec-1990 #sequence_revision (hybridoma 10B10S) - mouse (fragment)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiAccession: S01822
RiFOerster, I.; Gu, H.; Rajewsky, K.
EMBO J. 7, 3693-3703, 1988
A.Title: Germline antibody V regions as determinants of clonal persistence and malignant A; Reference number: S01822, MUID:89091115; PMID:3264787
A.Accession: S01822
A.Status: translation not shown
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-117 <FROE>
A.; Cross-references UNIPARC:UPI0000176B35; EMBL:X12388; NID:951924; PIDN:CAA30945.1; PID: C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9HPZO; UNIPARC:UPI0000638A1; GB:AE004437; NID:g10580911; P1
C;Genetics:
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A;Experimental source: serogroup B, strain MC58
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB
Pred. No. 48;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                  A; Accession: C84295
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-682 <STO>
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A; Residues: 1-87 <TET>
      C; Accession: C84295
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Best Local S
Matches 5
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C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86740
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malaxme, K.; Weissenbach, J.; Ehrli A;Dolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malaxme, K.; Weissenbach, J.; Ehrli A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Accession: F86740
                                                                                                                                                                                                                                                                                                                                                                                               Figlager, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schlueter, T.; Sinoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q92CU7; UNIPARC:UPI0000CC457; GB:AL592022; PIDN:CAC96305.1; C;Genetics:
                                                                                                                                                                                                                            RESULT 3
A11566
B. subtilis TagF protein (probable CDPglycerol glycerophosphotransferase) homolog lin107
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C;Genetics: A;Genetics: A;Gene: tagF
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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28;
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27;
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Pred. No. 28;
0; Mismatches
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   Pred. No. 20;
0; Mismatches
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Pred. No. 2
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75.0%;
   Similarity 75.0%;
6; Conservative
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75.0%;
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                                                                                                                                          159 YGNRFFDY 166
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                                                    1 YGRVFFDY
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C;Accession: C84509
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Noffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.v. Nature 402, 761-768, L999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MuID:20083487; PMID:10617197
A;Accession: C84509
A;Accuse type: DNA
A;Residues: 1-297 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Moraxella catarrhalis
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
R;Murphy, T:F; Kirkham, C.; Lesse, A.J.
Mol. Microbiol. 10, 87-97, 1993
Mol. Microbiol. 10, 87-97, 1993
A;Fitle: The major heat-modifiable outer membrane protein CD is highly conserved among 88
A;Reference number: 839866; MUID:95058186; PMID:7968522
A;Accession: 839866
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                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9SIT4; UNIPARC:UPI00000A248E; GB:AE002093; NID:g4558667; PII
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A;Cross-references: UNIPROT: Q9TZG7; UNIPARC: UPI000007C654; EMBL: AF098995; PIDN: AAC67482.
A;Experimental source: strain Bristol N2; clone F58E1
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33531
R;Mansley, P; Twyman, B.
R;Mansley, P; Twyman, B.
R;Mansley, P; Twyman, B.
R;Description: The sequence of C. elegans cosmid F58E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-453/Product: outer membrane protein CD #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.3%; Score 34; DB 2; Length 297; Best Local Similarity 100.0%; Pred. No. 33; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 72.3%; Score 34; DB 2; Length 453; Local Similarity 100.0%; Pred. No. 50; and 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: hypothetical protein containing F-box domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer membrane protein CD precursor - Moraxella catarrhalis
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 RVFFDY 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-453 < MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: At2g13630
A;Map position: 2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein AF2124 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Caccession: D69513
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J; Fleischmann, R.D.; Quackenbush, J. Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A62250; MuID:98049343; PMID:9389475
A;Accession: D69515
A;Accession: D69516
A;Residues: 1-142 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AP2191 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession. G69523
B;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Simith, H.O.; Wosse, C. R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A;Accession: G69523
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69523
A;Accession: G69523
A;Accession: G69523
A;Residues: 1-125 <a href="https://www.mcleic.acid.sequence.not.shown">https://www.mcleic.acid.sequence.not.shown; translation not shown
A;Residues: 1-125 <a href="https://www.mcleic.acid.sequence.not.shown">https://www.mcleic.acid.sequence.not.shown; translation not shown
A;Residues: 1-125 <a href="https://www.mcleic.acid.sequence.not.shown">https://www.mcleic.acid.sequence.not.shown</a>
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C84500
hypothetical protein At2g13630 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.3%; Score 34; DB 2; Length 125; 71.4%; Pred. No. 14; ive 2; Mismatches 0; Indels
                                                                                                         Length 117;
                                                                                                                                                                      Indels
                                                                                                                                                                      2;
                                                                                                  72.3%; Score 34; DB 2;
62.5%; Pred. No. 13;
cive 1; Mismatches
                                        F;11-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                        62.5%;
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Matches 6; Conservative
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Matches 5; Conservative
                                                                                                         Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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99 YGNYYFDY 106
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Gaps ô

2; Length 739; 1; Indels

Score 34; DB 2 Pred. No. 82; 0; Mismatches

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Riparkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
A.Title 403, 665-668, 2000
A.Title The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A,Rocession. A81430
A,Scession. A81430
A,Status. preliminary
A,Roiecule type: DNA
A,Roiecule type: DNA
A,Roidecule type: DNA
A,Roberimental source: serotype 02, strain NCTC 11168
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85.7%; Pred
0;
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Best Local Similarity 85.7
Matches 6, Conservative
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C;Genetics:
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C;Superfamily: beta-galactosidase bga
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Firaghothama, K.G.; Lawton, K.A.; Goldsbrough, P.B.; Woodson, W.R.
Plant Mol. Biol. 17, 61-71, 1991

A)Title: Characterization of an ethylene-regulated flower senescence-related gene from A; Reference number: S16595; MUID: 91329738; PMID: 1868223

A; Accession: S16595

A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                   nitrate transport protein crnA - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Species: Jane-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
C;Accession: A38560
R;Unkles, S.E.; Hawker, K.L.; Grieve, C.; Campbell, E.I.; Montague, P.; Kinghorn, J.R.
Proc. Natl. Acad. Sci. U.S.A. 88, 204-208, 1991
A;Title: crnA encodes a nitrate transporter in Aspergillus nidulans.
A;Reference number: A38560; MUID:91095428; PMID:1986367
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C;Species: Dianthus caryophyllus (clove pink)
C;Date: 13.Jan-1995 #sequence_revision 13.Jan-1995 #text_change 09.Jul-2004
C;Accession: S16595
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: A81430
                                                                                                                                                                      Gaps
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         A;Introns: 32/1; 104/1; 269/3; 424/3
C;Superfamily: Caenorhabditis elegans hypothetical protein T05A6.4
                                                                                                 Query Match 72.3%; Score 34; DB 2; Length 477; Best Local Similarity 100.0%; Pred. No. 53; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.3%; Score 34; DB 2; Length 483; Best Local Similarity 100.0%; Pred. No. 54; Matches 6; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 62.5
Matches 5; Conservative
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A; Residues: 1-731 < RAG>
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A;Residues: 1-483 <UNK>
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A81430
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S16595
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STRAIN=AvOP;
US DOE Joint Genome Institute (JGI-PGF);
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                                      December 30, 2005, 13:11:26; Search time 72 Seconds (without alignments) 78.392 Million cell updates/sec
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Q5tvq3
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                       2166443 segs, 705528306 residues
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Q97V38_SULSO
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Maximum Match 100%
Listing first 45 summaries
                            - protein search, using sw model
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Q720Y4_L
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1: uniprot_sprot:*
2: uniprot_trembl:*
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MEDLINE=228B2897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
MEDLINE=228B2897; PubMed=14500908; DOI=10.1073/pnas.193281800;
Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
Meyer F., Lederor H., Schuster S.C.,
Meyer F., Lederor H., Schuster S.C.,
Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
EMBL: BXSTAG19.249; UPP0118.
InterProc, IPR002549; UPP0118.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Wolinella.
NCBI_TaxID=844;
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ORFNames=AvinDRAFT 1630,
Azotobacter vinelandii Avop.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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04mjhs
05wdc6
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08cq19
008cq19
07mbv1
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Last sequence update)
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Last annotation update)
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Q4MJH5_BACCE
Q5WDC6_BACSK
Q6CQJ9_STAEP
Q8D518_V1BVU
Q7MBV1_V1BVY
Q9V1T9_DROME
Q9NFV5_DROME
Q4Z5SQ_PLABE
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Y2191 ARCFU
Y2124 ARCFU
Q5GTDI WOLTR
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Name=AMAA; OrderedLocusNames=WS1824;
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AC Q4IUN5;
DT 13-SEP-2005 (TEEMBLrel. 31,
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DT 13-SEP-2005 (TEEMBLrel. 31,
DT 13-SEP-2005 (TEEMBLrel. 31,
DE HYPOCHDELICAL PROCECH.
GN ORFWAMES-AVIDDRAFT 1630;
OS AZOCODACTER VINELANDIA AVOP.
OS BACTERIA; PROCEODACTERIA; GG
C PROUGMONDAGACEAC; AZOCODACTE
OX NCBI TAXID=322710;
RN | 11 | RP NUCLEOTIDE SEQUENCE.
RG STRAIN-AVOP;
RG US DOE JOINT GENOME INSTITUT
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13-SEP-2005 (TrEMBLrel. 31,
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Q7M880;
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Best Local Similarity
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SEQUENCE 345 AA
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NUCLEOTIDE SEQUENCE

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STRAIN=AvOP;

NUCLEOTIDE SEQUENCE

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"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003)
Rab. Biotechnol. 21:526-531(2003)
BMB1, BA070037;
BAB69170.1; -; Genomic_DNA.
GO; GO:0008171; F:O-methyltransferase activity; IEA.
GO; GO:000877; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
GO; GO:0016740; F:transferase activity; IEA.
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OSVLJG;
05VLJG;
01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
50 kDa protein.
Hevea brasiliensis (Para rubber tree).
Ebkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba
Sakaki Y., Hattori M., Omura S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=2147700; PIDMed=11572948; DOI=10.1073/pnas.211433198; MEDLINE=21477019; PubMed=11572948; DOI=10.1073/pnas.211433198; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakki Y., Hattori M.; Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Streptomycineae, Streptomycetaceae, Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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InterPro; IRR01077; O Met transf.
InterPro; IRR01051; SAM bind.
InterPro; IRR01091; Wing hix DNA bd.
Pfam; PF00891; Methyltransf 2; 1.
Complete protecome; Methyltransferase; Transferase.
SEQUENCE 331 AA; 36302 MW; A13B700B7F81AB5B CR
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      Mismatches
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1, Mismatches
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Q93HL7_STRAW PRELIMINARY;
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121 GKVFFDY 127
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US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                   Larimer F., Land M.;
"Annotation of the draft genome assembly of Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=plu3218;
photorbabdus luminescens (subsp. laumondii).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Pred. No. 11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOE Joint Genome Institute;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                  Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 149 AA; 16436 MW; B03FD0348CBACFDE CRC64;
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1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Complete genome, segment 11/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AAAU03000012; EAM04553.1; -; Genomic_DNA.
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EMBL; BXS71869; CAE15592.1; -; Genomic_DNA.
PhotoList; plu3218; -.
                                                                                                                                                                                                                                                                    US DOE Joint Genome Institute (JGI-ORNL);
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Pred. No.
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85.7%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Q7N273_PHOLL PRELIMINARY;

PHOLL

NUCLEOTIDE SEQUENCE. STRAIN=TT01;

RESULT 3
Q7N273 PH
DQ 7N273 PH
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NCBI_TaxID=141679;

Best Local Similarity

Complete proteome.

SEQUENCE Query Match

119 YGFVFFDY 126

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1 YGRVFFDY 8

preliminary data.

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Gaps

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NUCLEOTIDE SEQUENCE.

STRAIN=3D7,

A Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,

A Harris B., Lennard N., Hall N., Atkin R., Chillingworth C., Doggett J.,

B Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,

B Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,

B Berriman M., Barrell B.;

La Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

R BELL, AL844509; CAD52471.1; -; Genomic DNA.

R GO, GO:000384; F:catalytic activity; IEA.

R GO, GO:0005812; P:ubiquitin activating enzyme activity; IEA.

R GO, GO:0005512; P:ubiquitin activating enzyme activity; IEA.

B GO, GO:000512; P:ubiquitin cycle; IEA.

B InterPro; IPR000127; UBact_repeat.

DR InterPro; IPR00011; UBQ-activ_enz_E1.
                    NUCLEOTIDE SEQUENCE.
MEDLINE=20363099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                      Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata
Submitted (OCT-1999) to the RBBL/Genbank/DBJ databases.
EMBL; AP000606; BAB01195.1; -; Genomic DNR.
ERGURNCE 552 AA; 63036 MW; 740EA16CDEBB2447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PF13_0182.
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.7%; Score 37; DB 2; Length 552; 75.0%; Pred. No. 1.1e+02; 1ve 1; Mismatches 1; Indels
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Hypothetical protein.
SEQUENCE 1838 AA; 218523 MW; 460029B7943F3143 CRC64;
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Last annotation update)
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Pred. No. 3.8e+02;
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01-JUN-2002 (TrEMBLrel. 21, C)
01-JUN-2002 (TrEMBLrel. 21, Lic
01-OCT-2003 (TrEMBLrel. 25, Lic
Chey-like receiver domains.
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75.0%;
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QBIDZ6;
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Best Local Similarity 75.v.
6; Conservative
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283 WGRYFFDY 290
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 22, Last annotation update)
01-0CT-3002 (TrEMBLrel. 22, Last annotation update)
Emb|CAB77996.1.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Subrayota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons, rosids, eurosids; li, Brassicales, Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Major latex allergen Hev b 4 precursor.
Hevea brasiliensis (Para rubber tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Micrandreae;
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                                                                                                                                                      Kongsawadworakul P., Chrestin H.;
"Cloning and characterization of a cDNA encoding 50 kDa protein involved in latex coagulation.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY207386; AAP41849.1; -; mRNA.
GO; GO: 0003824; F: Catalytic activity; IRA.
InterPro; IPR001087; Lipase_GDSL.
Ffam; PP00657; Lipase_GDSL.
SEQUENCE 366 AA; 41163 MW; 006F1389B29DCBAD CRC64;
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"Hevea brasiliensis latex lecithinase homolog.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A4437086; AAR98518.1; -; mRNA.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL.
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OGLJBO;
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QET4PO;
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Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
J. Bacteriol. 185:2330-2337(2003).
EMBL; AL627282; CAD09340.1; -; Genomic_DNA.
EMBL; AL627282; CAD09340.1; -; Genomic_DNA.
Interpro; IPR010040; Plasmid_RAPRD.
Interpro; IRR010040; Plasmid_RAPRD.
ITGRPAMS; TIGR01690; plasmid_RAPRD.
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MEDLINE-21456156; PubMed=11572479;
Kawarabayasi Y., Hior Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
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Booth N.J., Bologna R.A.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY641981; AAT47192.1; -; Genomic_DNA.
InterPro; IPR010040; Plasmid RAQPRD.
IIGRPAMS; IIGR01690; plasmid_RAQPRD, 1.
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Enterobacteriaceae, Edwardsiella.
NCBI_TaxID=67780;
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SEQUENCE 113 AA; 12533 MW; 4F556CE8590CC469 CRC64;
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SEQUENCE 90 AA; 10309 MW; 133893BEF86FEDF0 CRC64;
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05-UIL-2004 (TrEMBLrel. 27, Created)
05-UIL-2004 (TrEMBLrel. 27, Last sequence update)
05-UIL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Edwardsiella ictaluri.
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QGGUD4 EDWIC PRELIMINARY;
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MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebalhia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., Mhite N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., Mhite N., Farrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica servovar Typhi CT18.";
Nature 413:848-852(2001).
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Enterobacteriaceae; Salmonella.
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STRAIN=TV2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
                                                              Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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0821KO 07C5G8;
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
10-MAR-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein STY4564.
OrderediocusNames=STY4564, t4262;
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            Name=CheY6; OrderedLocusNames=TTE1203;
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NUCLEOTIDE SEQUENCE.
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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1. Intracellular bacterial pathogen in humans."; Phosphodiester bonds at apurinic or apyrimidinic sites (AP sites) phosphodiester bonds at apurinic or apyrimidinic sites (AP sites).

1. FUNCTION: Endonuclease IV plays a role in DNA repair. It cleaves to produce new 5' ends that are base-free decayribose 5-phosphate residues. It preferentially attacks modified AP sites created by bloomycin and neocarzinostatin (By similarity).

2. CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-phosphooligonucleotide end-products.

3. C. I. COFACTOR: Binds 3 zinc ions (By similarity).

2. I. SIMILARITY: Belongs to the AP endonuclease 2 family.
                                     Oguchi A.,
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4FE-4S; Complete proteome; Electron transport; Hypothetical protein; Iron-sulfur; Metal-binding; Transport.
SEQUENCE 270 AA; 30000 MW; 4600F746DBBF1685 CRC64;
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29-MAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Name=nfconuclease IV (RC 3.1.21.2) (Endodeoxyribonuclease IV).
Name=nfc) OrderedLocusNames=MYPEI190;
Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Og
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
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Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                                                                                                                                          an aerobic thermoacidophilic
                                                                                                                                                                                                                                                                                                                GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0046872; F:mertal ion binding; IEA.
GO; GO:006118; P:electron transport; IEA.
INTERPRO; IPR001450; 4Fe4S Fe_S bd.
Pfam; PF00037; Fer4; 1.
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HSSP; P12638; 1QTW.
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                                                                                                                               "Complete genome sequence of an aerobic therm
Crenarchaeon, Sulfolobus tokodail strain7.";
DNA Res 8:123-140(2001).
BRBL; BA000023; BAB66929.1; -; Genomic_DNA.
HSSP; P11349; 1R27.
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InterPro; IPR001719; AP endnuclease2.
InterPro; IPR0101307; XyĪisom TIMbarrl.
Pfam; PF01261; AP endonuc 2; 1.
TIGRPAMs; TIGR00567; nfo; 1.
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nes 6; Conservative
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NUCLECTIDE SEQUENCE.

STRAIN=ATCC 35092 / DSM 1617 / P2;

NUCLECTIDE SEQUENCE.

MEDIINE=21332295; PubMed=11427726; DOI=10.1073/pnas.141222098;

She Q., Singh R.K., Confaionieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A heikamp-de Jong I., Jeftcher C.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gasaterland T.,

Charlebois R.L., Boolittle W.F., Duguet M., Wan der Oost J.,

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

REMBL, AE006873; AAK42907.1; -; Genomic_DNA.

RESP, P00214; 2PD2.
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PROSITE; PS00730; AP_NUCLEASE_F2_2; 1.
PROSITE; PS00731; AP_NUCLEASE_F2_3; 1.
Complete proteome; DNA damage; DNA repair; Endonuclease; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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4Fe-4S; Complete proteome; Blectron transport; Iron; Iron-sulfur;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 289;
                                                                                                                                       similarity).
2 (By similarity)
similarity).
                                                                                                       zinc 1 (By similarity).

116 Zinc 1 (By similarity).

152 Zinc 1 and 2 (By similarity).

186 Zinc 2 (By similarity).

189 Zinc 3 (By similarity).

230 Zinc 3 (By similarity).

231 Zinc 3 (By similarity).

232 Zinc 3 (By similarity).

235 Zinc 3 (By similarity).

235 Zinc 3 (By similarity).

235 Zinc 3 (By similarity).

245 Zinc 2 (By similarity).

255 Zinc 2 (By similarity).
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SEGUTENCE 293 AA; 32382 MW, C13A04963619EDAD CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             'Match 74.5%; Score 35; DB 1; I
Local Similarity 75.0%; Pred. No. 1.4e+02;
Les 6; Conservative 1; Mismatches 1;
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                                                                     Netal-binding, Nuclease; Zinc.
METAL 16 116 Zinc.
METAL 152 152 Zinc.
METAL 186 186 Zinc.
METAL 189 189 Zinc.
METAL 220 220 Zinc.
METAL 233 233 Zinc.
METAL 235 226 Zinc.
METAL 236 Zinc.
METAL 265 Zinc.
METAL 265 Zinc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxydoreductase, putative.
OrderedLocusNames=SSO2794;
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

X DubMed=15746427; DOI=10.1126/science.1107008;

X DubMed=15746427; DOI=10.1126/science.1107008;

X Abrat V., Lennard N., Partrick S., Crossman L.C., Blakely G.,

A Abrat V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,

A Barron A., Lord A., Norbertczak H., Ormond D., Price C.,

A Line A., Lord A., Norbertczak H., Ormond D., Price C.,

RA Rabbinowitsch B., Woodward J., Barrell B.G., Parkhill J.;

RX Extensive DNA inversions in the B. fragilis genome control variable R.

Extensive DNA inversions in the B. fragilis genome control variable R.

Science 307:1463-1465(2005).

B RMED; CRASC827; CAH09787.1; -; Genomic_DNA.

BRIL; CRASC827; CAH09787.1; -; Genomic_DNA.

BRIL; CRASC827; CAH09787.1; -; Genomic_DNA.

BRIL; RRO00165; HTHA AraC; 1.

BR RNINTS; PRO0015; HTHARAC; 1.

BR SMART; SM00342; HTH ARAC; 1.

BR PROSITE; PS00441; HTH ARAC; 1.

BR PROSITE; PS00441; HTH ARAC; 1.

RW Activator; Complete proteome; DNA-binding; Transcription;

Transcription regulation.

SEQUENCE 298 AA; 34641 MW; A08394D705F34AD1 CRC64;
                                                                                 Described by the precipitation of the project of the project of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the precipitation of the prec
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Matches
RESULT 15
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Search completed: December 30, 2005, 13:33:33 Job time: 75 secs

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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December 30, 2005, 13:14:26 ; Search time 17.9355 Seconds (without alignments) 36.877 Million cell updates/sec - protein search, using sw model OM protein Run on:

US-10-735-916A-12 1 YGRVFFDY Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

572060 seqs, 82675679 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Quer, Match	Query Match Length	DB	ar ar	Description
	38	80.9	138	7	US-09-252-991A-20154	1
7	35	74.	5 72	~	US-09-248-796A-21727	Sequence 21727, A
m	35	74.5		~	US-09-134-000C-4002	
4	35	74.	390	7	US-09-252-991A-33062	Sequence 33062, A
ហ	34	72.3		~	US-08-974-899-12	Sequence 12, Appl
9	34	72.		~	US-09-795-798-12	12,
7	34	72.3	3 17	-	US-08-306-871-41	Sequence 41, Appl
80	34	72.	3 17	-	US-08-569-959-41	43,
σ	34	72.3	3 26	٦	US-08-306-871-33	Sequence 33, Appl
10	34	72.3	3 26	٦	US-08-569-959-33	
11	34	72.	3 71	Н	US-08-306-871-28	
12	34	72.	3 71		US-08-569-959-28	28,
13	34	72.	3 92	~	US-09-270-767-61481	6148
14	34	72.	8	~	US-09-027-449-50	50,
15	34	72.	<u>«</u>	7	US-08-804-444A-50	Sequence 50, Appl
16	34	72.	m	~	US-09-026-985-50	20,
17	34	72.	<u>«</u>	~	US-09-121-952A-50	20,
. 18	34	72.	3 116	~	US-09-234-340A-50	50,
19	34	72.		~	US-09-355-014-50	Sequence 50, Appl
20	34	72.	<u> </u>	~	US-08-974-899-4	4,
21	34	72		7	US-08-974-899-5	Sequence 5, Appli
22	34	72.	<u>«</u>	7	US-08-974-899-24	Sequence 24, Appl
23	34	72.	<u>«</u>	~	US-09-795-798-4	Seguence 4, Appli
24	34	72.	<b>.</b>	~	US-09-795-798-5	'n
25	34	72	3 121	7	US-09-795-798-24	Sequence 24, Appl
26	34	72.	· ·	7	US-09-540-236-3221	Sequence 3221, Ap
27	34	72.	3 142	-	US-08-860-174A-7	Sequence 7, Appli

		sequence 20, Appl Sequence 15005, A Sequence 1, Appli	Sequence 7, Appli Sequence 2, Appli	Sequence 26, Appl Sequence 28, Appl	Sequence 10, Appl Sequence 11, Appl	Sequence 10, Appl Sequence 11, Appl	Sequence 91, Appl Sequence 91, Appl	Sequence 15, Appl
US-08-860-174A-12 US-08-860-174A-10	US-09-270-767-45943 US-09-902-540-12330	US-08-696-944-20 US-09-248-796A-15005 US-09-937-908-1	US-09-406-535-7 US-09-406-535-2	US-08-497-312-26 US-08-497-312-28	US-10-092-246-10 US-10-092-246-11	US-10-096-246A-10 US-10-096-246A-11	US-09-840-459-91 US-09-497-625A-91	US-08-454-899G-15
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### ALIGNMENTS

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Sequence 20154, Application US/09252991A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT;
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-20154
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Sequence 21727, Application US/09248796A Patent No. 6747137 98 YGRIFFRY 105 1 YGRVFFDY 8 US-09-248-796A-21727 ð 임

FRACELL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208

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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 62.5%;
Matches 5; Conservative 1
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TOPOLOGY: Linear
   RESULT 5
US-08-974-899-12
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Patent No. 6551795
GENERAL INFORMATION:
FRITLE OF INVENTION:
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT RELING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 33062
LENGTH: 390
LENGTH: 390
LENGTH: 390
LENGTH: 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.5%; Score 35; DB 2; Length 233; 62.5%; Pred. No. 64;
                                               Score 35; DB 2; Length 72;
Pred. No. 20;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa US-09-252-991A-33062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Enterococcus faecalis
                                                  74.5%;
71.4%;
; ORGANISM: Candida albicans
US-09-248-796A-21727
                                               Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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131 YGKISFDY 138
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11 YGRIFFE 17
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US-09-252-991A-33062
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US-09-134-000C-4002
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; Sequence 12, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCES: 24
; SORRESPONDENCES: Genentech, Inc.
STREET: 1 DNA WAY
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 12;
Pred. No. 5.1;
1; Mismatches 2; Indels
Sequence 12, Application US/08974899;
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Pardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfreatin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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ADDRESSES:
ADDRESSES:
1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: BM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,959
                                                          72.3%; Score 34; DB 1; Length 17; 100.0%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 17;
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Patent No. 5712118
GENERAL INFORMATION:
APPLICANT: Timothy F. Murphy
TILLE OF INVENTION: Vaccine For Branhamella catarrhalis
                                                                                                                                                                                                                                                                                                            US-08-569-959-41
; Sequence 41, Application US/08569959
; Patent No. 5725862
; GENERAL INFORMATION:
; APPLICANT: Timchy F. Murphy
; TITLE OF INVENTION:
Vaccine For Branhamella catarrhalis
; NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: CD amino acid positions 295-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/129,719
FILING DATE: September 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11520.0053
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 849-0349
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGAINSM: Branhamella catarrhalis
STRAIN: 25240
                                                            Query Match 72.3%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RVFFDY 14
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               JS-08-306-871-41
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1 Sequence 41, Application US/08306871

1 Patent No. 5712118

2 GENERAL INFORMATION:

3 GENERAL INFORMATION:

4 TITLE OF INVENTION:

5 VORRESPONDENCE ADDRESS:

5 CORRESPONDENCE ADDRESS:

5 CORRESPONDENCE ADDRESS:

6 CORRESPONDENCE ADDRESS:

7 TITLE OF INVENTION:

8 STREET: 1800 One MET Plaza

CORRESPONDENCE ADDRESS:

7 CORRESPONDENCE ADDRESS:

8 STREET: 1800 One MET Plaza

COUNTRY: United States

7 ZIP: 14203-2331

COMPUTER: READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MD storage

COMPUTER: IBM Compatible

9 COMPUTER: Nordperfect for Windows 5.1

CURRENT APPLICATION NUMBER: US/08/306,871

FILING DATE: 30-SEP-1994

PRIOR APPLICATION NUMBER: US 08/129,719

FILING DATE: 20-SEP-1994

PRIOR APPLICATION NUMBER: US 08/129,719

FILING DATE: 20-SEP-1994

NATORNEY/AGENT INFORMATION:

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud

NAME: Nelson, M. Bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.3%; Score 34; DB 2; Length 12; 62.5%; Pred. No. 5.1; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIPICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: «Unknown»
ATTORNEY,AGENT INPORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFRAX: 650/925-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: CD amino acid positions 295-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERCE/DOCKET NUMBER: 11520.0053
TELECOMMUNICATION:
TELEPHONE: (716) 856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Branhamella catarrhalis
STRAIN: 25240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
LENGTH: 17 residues
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5
Eaches 5; Conservative
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5 YGTTYFDY 12
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Sequence 28, Application US/08306871

Patent No. 571218

SEGUENCAL INFORMATION:

APPLICANT: Timothy F. Murphy
TITLE OF INVENTION:

APPLICANT: Timothy F. Murphy
TITLE OF INVENTION:

CORRESPONDENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSES: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One MkT Plaza
CITY: Buffalo

STREET: 1800 One MkT Plaza

CONTRY: United States

ZIP: 14203-2391

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
CONPUTER: IN COMPATIBLE

COMPUTER: Wordperfect for Windows 3.1

COMPUTER: Wordperfect for Windows 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,871

FILING DATE: September 29, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Nelson, M. Bud

RESTERBUEL/DOCKET NUMBER: 135,300

REFERENCE/DOCKET NUMBER: 1520.0053

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: CD amino acid positions 261-331 US-08-306-871-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD amino acid positions 286-311
FILING DATE: September 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11520.0053
TELECOMMUNICATION INFORMATION:
TELEFAX: (716) 866-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 residues
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Branhamella catarrhalis
STRAIN: 25240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Branhamella catarrhalis
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 71 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 RVFFDY 23
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STRAIN: 25240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: lir
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LOCATION:
US-08-569-959-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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       NUMBER OF SEQUENCES: 5-2
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1800 One MET Plaza
CITY: Buffalo
STREET: 1800 One MET Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM COMPATIS: DISKETTE: 1806 One MET Plaza
COMPUTER: Buf Compatible FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: Buf Compatible FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: 20-SEP-1994
COMPUTER: Buf Compatible FORM:
MEDIUM TYPE: 00-SEP-1994
PRICH APPLICATION NUMBER: 00-SEP-1994
PRICH APPLICATION NUMBER: 29, 1993
ATTORNEY/ AGENT INPCRMATION:
MAME: Nelson, M Buf 35, 300
FELENOME CARACTERICATION SEC 1000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5725862
GENERAL INFORMATION:
APPLICANT: Timothy F. Murphy
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,959
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/129,719
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Best Local Similarity 100.0
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US-08-569-959-33
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APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 116;
                                                                                                                                                                                                          Length 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 34; DB 2;
illarity 62.5%; Pred. No. 48;
Conservative 1; Mismatches 2
                                                                                                                                                                                                          Score 34; DB 2;
Pred. No. 38;
2; Mismatches
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 6217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61481
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-027-449-50
; Sequence 50, Application US/09027449
Patent No. 6025158
; GENERAL INFORMATION:
                                                                                                                                                ; ORGANISM: Drosophila melanogaster
US-09-270-767-61481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech, Inc
                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 116 amino acids TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650/952-9881
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APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
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                              DB 1; Length 71;
30;
                                                                                                                                                                                                                                                     Sequence 28, Application US/08569959
Patent No. 5725862
GENERAL INFORMATION:
APPLICANT: Tincthy F. Murphy
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Buffalo
STATE: New York
COUNTR: United States
ZIP: 14203-2331
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD amino acid positions 261-331
                              72.3%; Score 34; DB 100.0%; Pred. No. 30; ive 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/129,719
FILING DATE: September 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11520.0053
TELECOMMUNICATION INFORMATION:
TELECHONE: (716) 856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-270-767-61481
; Sequence 61481, Application US/09270767
; Patent No. 6703491
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 71 residues
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Best Local Similarity 100.
Matches 6; Conservative
                              Query Match 72.3
Best Local Similarity 100.
Matches 6; Conservative
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RVFFDY 48
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US-08-569-959-28
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US-08-569-959-28
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RESULT 15
US-00-804-444A-50
is Sequence 50. Application US/08804444A
is Patent No. 6117980
is GRUERAL INFORMATION:
is APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
is APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech. Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STREET: 1 DNA Way
CITY: South San Francisco
STREET: 1 DNA Way
CITY: South San Francisco
STREET: 3.5 inch, 1.44 Mb floppy disk
COUNTER: IBM PC compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1 DNA MAY
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TYPE: Amino Acid

TOPOLOGY: Linear

US-08-804-444A-50
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Search completed: December 30, 2005, 13:37:19 Job time: 17.9355 secs

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Sequence 69, Application US/10735916A
Publication No. US20050084906A1
GENERAL INPORMATION:
APPLICANT: GORTSCH, Liliane
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-735-916A-69
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2, Appli
28, Appl
42516, A
12, Appl
248530,
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                                                                                                                                         December 30, 2005, 13:33:42 ; Search time 59.4839 Seconds (without alignments) 56.194 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12,
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-735-916A-75
US-10-735-916A-79
US-10-735-916A-79
US-10-735-916A-52
US-10-735-916A-77
US-10-735-916A-77
US-10-735-916A-81
US-10-735-916A-85
US-10-735-916A-85
US-10-735-916A-85
US-10-735-916A-85
US-10-735-916A-85
US-10-735-916A-85
US-10-735-916A-85
US-10-735-916A-85
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US-11-097-143-42516
US-09-795-798-12
US-10-424-599-248530
US-09-795-798-4
US-09-795-798-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                           1867569 segs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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28 34 72.3 126 4 US-10-041-860-246 29 34 72.3 126 4 US-10-041-860-306 31 34 72.3 126 4 US-10-041-860-306 32 34 72.3 126 4 US-10-042-116-1908 32 34 72.3 218 4 US-10-282-1228-5140 33 34 72.3 218 4 US-10-282-1228-5140 34 72.3 303 4 US-10-739-930-754 35 34 72.3 362 4 US-10-739-930-754 36 34 72.3 362 4 US-10-739-930-754 37 34 72.3 453 4 US-10-425-115-3149 38 34 72.3 453 4 US-10-425-29-4 41 33 70.2 464 5 US-10-996-3195 42 33 70.2 18 5 US-10-996-315-349 43 33 70.2 220 4 US-10-42-599-115-44 33 70.2 220 4 US-10-42-599-115-44 33 70.2 220 4 US-10-42-599-115-44 33 70.2 220 4 US-10-335-977-6259 45 33 70.2 220 4 US-10-335-977-6259 45 BESULT 1 APPLICANT: CORVAILA, NATHABIE APPLICANT: CORVAILA, NATHABIE APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEGR., 011vier APPLICANT: HEURON NUMBER: FR 03/06 538 PRIOR PLING DATE: 2003-10-16 PRIOR PLING DATE: 2003-10-16 PRIOR PLING DATE: 2003-10-18 PRIOR PLING DATE: 2003-0-1-18 PRIOR PLING DATE: 2002-0-1-18 PRIOR PLING DATE: 2003-0-1-18 PRIOR PLING DATE: 2002-0-1-18 PRIOR PLING DATE: 2003-0-1-18 PRIOR PLING DATE: 2003-0-1-18 PRIOR PLING
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Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-10-735-916A-79
99 YGRVFFDY 106
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Sequence 75, Application US/10735916A

Publication No. US2050084906A1

GENERAL INFORMATION:
APPLICANT: GOSTSCH, Liliane
APPLICANT: GOSTVAIA, Nathalie
APPLICANT: DUFLOS, Alain
APPLICANT: BESEK, Alain
APPLICANT: BESEK, Alain
APPLICANT: BESEK, Alain
APPLICANT: BESEK, Alain
APPLICANT: BAEUM, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: FR 03/00 178
FRIOR APPLICATION NUMBER: FR 03/00 178
FRIOR PELLING DATE: 2003-07-11
FRIOR PELLING DATE: 2003-07-11
FRIOR PELLING DATE: 2002-01-18
FRIOR PELLING DATE: 2002-01-18
FRIOR PELLING DATE: 2002-01-18
FRIOR PELLING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
FRIOR PELLING DATE: 2002-01-18
FRIOR PELLING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
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DUFLOS, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
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APPLICANT:
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Gaps
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Sublication No. US20050084906A1
GENERAL INFORMATION:
APPLICANT: GORISCH, Liliane
APPLICANT: LEGEN, Olivier
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
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CURRENT PELICATION NUMBER: US/10/735,916A
CURRENT PILING DATE: 2003-12-16
PRIOR PELING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR PELING DATE: 2003-07-11
PRIOR PELING DATE: 2003-01-20
PRIOR PELING DATE: 2003-01-18
PRIOR PELING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR APPLICATION NUMBER: FR 02/00 654
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR APPLICATION NUMBER: FR 02/05 753
PRIOR PELING DATE: 2002-03-01
NUMBER: PR 02/05 753
SEQ ID NOS: 156
SEQ ID NOS: 156
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; ORGANISM: Homo sapiens
US-10-735-916A-81
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US-10-735-916A-77
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US-10-735-916A-85
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i Sequence 52, Application US/10735916A

i Sequence 52, Application US/10735916A

i Bedication No. US20050084906A1

i GENERAL INFORMATION:

APPLICANT: GOENSCH, Liliane

APPLICANT: GOENSCH, Liliane

APPLICANT: DIFLOS, Nathalie

APPLICANT: LEGER, Olivier

APPLICANT: HACUW, Jean-Francois

TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

FILE REFERENCE: 017753-183

CURRENT APPLICATION NUMBER: US/10/735, 916A

CURRENT FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-07-11

PRIOR FILING DATE: 2003-01-20

PRIOR FILING DATE: 2003-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-05-07

NUMBER OF SEQ ID NOS: 156

LEMCTH: 177-7
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GENERAL INCRNATION:
APPLICANT: CORVAIA, Nathalie
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-183
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILLING DATE: 2003-12-16
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                                                                                                                 100.0%; Score 47; DB 5; Length 117; 100.0%; Pred. No. 0.78;
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                                                                                                                                                                       0; Mismatches
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                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus
US-10-735-916A-52
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; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83
                                                                                                                                                                                                                        1 YGRVFFDY 8
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Best Local Similarity
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PRIOR FILING DATE: 2003-01-18

PRIOR FLIGHTON UNDER: RE 0.20

PRIOR FLIGHTON DATE: 2003-01-18

PRIOR FLIGHTON DATE: 2003-01-18

PRIOR FLIGHTON WORRER: RE 0.20 654

PRIOR FLIGHTON WORRER: RE 0.20 654

PRIOR FLIGHTON WORRER: RE 0.20 654

PRIOR FLIGHTON DATE: 2003-01-18

PRIOR FLIGHTON DATE: 2003-01-18

PRIOR FLIGHTON DATE: 2003-01-18

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PRIOR FLIGHTON DATE: 2003-01-18

PRIOR PLANT: 000-01-18

PRESENT: Read of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior o
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Sequence 122750, Application US/10437963

Sequence 122750, Application US/10437963

Sequence 122750, Application No. US2040123343A1

GENERAL INPORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Shou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bull and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

SEQ ID NO 122750

LENGTH: 264

LENGTH: 264

LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2564C.1.pep
US-10-437-963-122750
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75.0%;
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Best Local Similarity 75.0.
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Matches 6; Conservative
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ORGANISM: Oryza sativa
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121 YGKGFFDY 128
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US-10-156-761-10380
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US-10-424-599-232867
US-10-424-599-232867
Sequence 232867, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: 191ants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
UNMERO PS SEQ ID NOS: 285684
SEQ ID NO 222867
LENGTH: 101
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        APPLICANT: CHOKNALA, ACCURATE,
APPLICANT: LEGER, Olivier
APPLICANT: DUFLOS, Alain
APPLICANT: BECK, Alain
APPLICANT: BECK, Alain
APPLICANT: HAEUW, Jean-Francois
TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: NOWBER: US/10/735,916A
CURRENT APPLICATION NUMBER: US/10/735,916A
CURRENT FILING DATE: 2003-01-2-6
PRIOR APPLICATION NUMBER: FR 03/08 538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 02/00 653
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PACENTIN VET: 2.1
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_52303C.1.pep
US-10-424-599-232867
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OTHER INFORMATION: unsure at all Xaa locations
CORVAIA, Nathalie
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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78.7%; Score 37; DB 4; Length 264; 75.0%; Pred. No. 1.1e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genquence 10380, Application US/10156761
FUDLICATION NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WOSHIYUXI
APPLICANT: HATTORI, WOSHIYUXI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WOSHIYAKI
APPLICANT: HATTORI, WOSHIYAKI
APPLICANT: HATTORI, WOSHIYAKI
APPLICANT: HATTORI, WOSHIRA
CURRENT PILING DATE: 2002-05-29
RIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
RRIOR PILING DATE: 2001-05-30
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| Sequence 2, Application US/11083779
| Publication No. US20050227292A1
| GENERAL INFORMATION:
| APPLICANT: Malaysian Rubber Board
| APPLICANT: Sundersan Elumalai
| APPLICANT: Sundersan Elumalai
| APPLICANT: Yeang, Hoong Yeet
| TITLE OF INVENTION: AM ALLERGENIC PROTEIN COMPLEX OF NATURAL RUBBER LATEX
| FILE REFERENCE: SHP-PT086
| CURRENT APPLICATION NUMBER: US/11/083,779
| CURRENT PILING DATE: 2004-03-18
| PRIOR FILING DATE: 2004-03-18
| PRIOR FILING DATE: 2004-03-18
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 2
| LENGTH: 366
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Sequence 242 Application US/09767041

Patent No. US20020055168A1

SERVENCE INVENDATION:

APPLICANT: Smith, Hilda

TITLE REFERENCE: 2183-4726

CURRENT APPLICATION NUMBER: US/09/767,041

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1998-07-22

PRIOR PILING DATE: 1998-07-22

PRIOR PILING DATE: 1998-07-22

PRIOR PILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn version 3.0

SEQ ID NO 28

MANDEL 1410
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Hevea brasiliensis
US-11-083-779-2
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US-09-767-041-28
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US-09-767-041-28
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERRINCE: CLOOO728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/167,832
PRIOR PLING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PLING DATE: 1999-10-19
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
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PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOOTHWARE: BEALSERQ FOR WINGOWE VERSION 4.0
ILENGTH: 1425
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Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 1;
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US-11-097-143-42516
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Search completed: December 30, 2005, 14:15:03 Job time : 64.4839 secs

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77, Appl
81, Appl
12, Appl
4, Appli
5, Appli
54, Appli
50, Appli
50, Appli
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                                                                                                                                           December 30, 2005, 13:35:07 ; Search time 2.96774 Seconds (without alignments) 20.187 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12,
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-11-012-353-69

US-11-012-353-75

US-11-012-353-162

US-11-012-353-162

US-11-012-353-162

US-11-012-353-162

US-11-012-353-162

US-11-012-353-81

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US-11-012-353-69; Application US/11012353

RESULT 2

Sequence

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Query Match
Best Local Similarity 100.
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-11-012-353-79
                                  TYPE: PRT
ORGANISM: Homo sapiens
US-11-012-353-75
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LENGTH: 117
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US-11-012-353-75

Sequence 75. Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GOESCEN, LILIANE
APPLICANT: GOESCEN, LILIANE
APPLICANT: HARUW JEAN-FRANCOIS
APPLICANT: HARUW JEAN-FRANCOIS
APPLICANT: HEGER, OLIVIER
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: VS/11/012,353
CURRENT APPLICATION NUMBER: R 030636
FRIOR FILING DATE: 2003-12-16
FRIOR FILING DATE: 2003-01-20
FRIOR PRICK FILING DATE: 2003-01-20
FRIOR FILING DATE: 2003-01-20
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    Publication No. US20050249730A1
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Matches 8; Conservative
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US-11-012-353-79

Sequence 79, Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GOEDSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEDW, JEAN-FRANCOIS
APPLICANT: HAEDW, JEAN-FRANCOIS
APPLICANT: HAEDW, JEAN-FRANCOIS
APPLICANT: HAEDW, JEAN-FRANCOIS
APPLICANT: HAEDW, JEAN-FRANCOIS
APPLICANT: HAEDW, JEAN-FRANCOIS
APPLICANT: HAEDW, JEAN-FRANCOIS
APPLICANT: HAEDW, JEAN-FRANCOIS
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: NORBER: US/11/012,353
CURRENT PILING DATE: 2004-12-16
FRIOR APPLICATION NUMBER: 10/735-916
FRIOR PLICATION NUMBER: FR 0308538
FRIOR FILING DATE: 2003-07-11
FRIOR PLICATION NUMBER: FR 020553
FRIOR PLICATION NUMBER: FR 020553
FRIOR PLICATION NUMBER: FR 020553
FRIOR FILING DATE: 2002-01-18
FRIOR FILING DATE: 2002-01-18
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| Sequence 83, Application US/11012353
| Sequence 83, Application US/11012353
| Publication No. US20050249730A1
| GENERAL INFORMATION:
| APPLICANT: GOEYSCH, LILIANE
| APPLICANT: DUENCA, ALAIN
| APPLICANT: LEGER, OLIVIER
| APPLICANT: LEGER, OLIVIER
| APPLICANT: BECK, ALAIN
| APPLICANT: BECK, ALAIN
| TILLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
| TILLE OF INVENTION: RECEPPORS ANTIBODIES AND USES THEREOF
| FILE REFERENCE: 017753-198
                                                                                                Gaps
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100.0%; Score 47; DB 7; Length 117; 100.0%; Pred. No. 0.025;
                                                                                                0; Indels
                                                                                                     0; Mismatches
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US-11-01-353-77

Sequence 77, Application US/11012353

Publication No US20050249730A1

GENERAL INFORMATION:
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
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APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANTON NOVER ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: PR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-05-07
PRIOR FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CORTECL, LALLANDE
APPLICANT: CORTECL, LALLANDE
APPLICANT: CORTECL, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
APPLICANT: DUFLOS, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 01753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR PLING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PLING DATE: 2003-07-07
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2003-01-20
PRIOR PLING DATE: 2002-05-07
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
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100.0%; Score 47; DB 7; Length 127;

Best Local Similarity 100.0%; Pred. No. 0.026;

Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                              Sequence 52, Application US/11012353
Publication No. US20050249730A1
GENERAL INFORMATION:
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; Sequence 162, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOEYCAL, LILIANE
; APPLICANT: CORVAIA, NATTALIE
; APPLICANT: DIFLOS, ALAIN
; APPLICANT: DIFLOS, ALAIN
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: NECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: NECEPTORS ANTIBODIES AND USES THEREOF
; TITLE OF INVENTION: NUMBER: 10/735,916
; PRIOR APPLICATION NUMBER: PROSESS
; PRIOR PILING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2003-07-20
; PRIOR PILING DATE: 2003-01-20
; PRIOR PILING DATE: 2003-01-20
; PRIOR PILING DATE: 2002-01-18
; PRIOR FILING DATE: 2002-01-18
; SPRIOR FILING DATE: 2005-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 47; DB 7; Length 117; 100.0%; Pred. No. 0.025;
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CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR PLILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR FILING DATE: 2003-07-11
PRIOR PLILOATION NUMBER: FR 0308538
PRIOR PLICATION NUMBER: PCT/FR03/00178
PRIOR PLILOATION NUMBER: PCT/FR03/00178
PRIOR PLILOG DATE: 2003-07-11
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-01-18
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Best Local Similarity 100.
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-11-012-353-162
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ORGANISM: Homo sapiens
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99 YGRVFFDY 106
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US-11-012-353-81

Sequence 81. Application US/11012353

Publication No. US20050249730A1

GENERAL INFORMATION:
APPLICANT: GORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: LEGER, OLIVIER
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: BECK, ALAIN
APPLICANT: BCK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGP-IR AND/OR ANTI-INSULIN/IGP-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: UNMBER: US/11/012,353
CURRENT APPLICATION NUMBER: US/11/012,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                            100.0%; Score 47; DB 7; Length 135; 100.0%; Pred. No. 0.028;
                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR PILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR PILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PC7/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR PILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 020553
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION WUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PATENTIN Ver. 3.3
SEQ ID NO 77
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 85, Application US/11012353;
Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-81
                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-11-012-353-85
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LENGTH: 135
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| APPLICANT: IRREW, JENN-REMACIS
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| APPLICANT: IRREW, JENN-REMACIS
| TILLE REFRENCES: ALTHER DATE: A CONTINUED SIZE AND USES THERSOF |
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Indels

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NAME: Tan, Lee K
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Best Local Similarity 62.5
Matches 5; Conservative
5, Conservative
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                                                                            103 YGTTYFDY 110
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                                      1 YGRVFFDY
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Matches
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                                                                                                                                                                                                                                                            Score 34; DB 6; Length 12;
Pred. No. 0.74;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
                     REFERENCE/DOCKET NUMBER: P1014R1C1D1C1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-5ep-2003
CLASSIFICATION: cUrknown>
PRIOR APPLICATION NUMBER: (60/031971
RILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/974899
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 09/42045
APPLICATION NUMBER: 28-FEB-2001
                                                                                                                                                                       TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-10-665-658-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Prancisco
STATE: California
COUNTRY: USA
    REGISTRATION NUMBER: 39,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-4462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 121 amino acids
                                                       TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           LENGTH: 12 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELEFAX: 650/952-9881
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                               5 YGTTYFDY 12
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Best Local Similarity
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Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
                                                                                            Presta, Leonard G.

TILE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 135 inch, 1.44 Mb floppy disk
COMPUTER: 138 PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 19.5ep-2003
CILASSIFICATION NUMBER: 60/031971
APPLICATION NUMBER: 60/031971
APPLICATION NUMBER: 60/031971
APPLICATION NUMBER: 09/976798
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: 09/97798
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/97798
FILING DATE: 20-CCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FSB-2001
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P1014R1C1D1C1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-665-658-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 39,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/10665658 Publication No. US20050276801A1 GENERAL INFORMATION:
Sequence 5, Application US/10665658 Publication No. US20050276801A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 650/225-4462
                                                                           APPLICANT: Jardieu, Paula M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5
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COMPRESSES: Generated, Inc.

ADDRESSES: Generated, Inc.

ADDRESSES: Generated, Inc.

ADDRESSES: Generated, Inc.

STREET: Inv. Num way

CONTRY: South San Francisco

CONTRY: South San Francisco

CONTRY: South San Francisco

CONTRY: South San Francisco

CONTRY: South San Francisco

CONTRY: READABLE FORM:

MEDITATION TYPE: 3.5 inch, 1.4 wh floppy disk

COMPUTER IN FOR CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY: CONTRY:
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Query Match

Query Match

Best Local Similarity 62.5%; Pred. No. 5.7;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDX 8

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Db 103 YGTTYFDX 110

Search completed: December 30, 2005, 14:15:22
Job time : 2.96774 secs
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December 30, 2005, 15:35:45; Search time 182 Seconds (without alignments) 19:313 Million cell updates/sec
5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
                                                           sw model
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                                                         protein
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BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-735-916A-12 1 YGRVFFDY 8 Title: Perfect score: Scoring table: Sequence:

49824 Total number of hits satisfying chosen parameters:

2443163 seqs, 439378781 residues

Searched:

Minimum DB seq length: 8 Maximum DB seq length: 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* geneseqp2000s:* geneseqp2005s:* A Geneseq 21:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

δž	Query	Query Match Length DB	DB	QI	ion
	100.0	<b>0</b> 0 00	r 6	ADJ76846 ADZ67016	Adj76846 CDR seque Adz67016 Murine in
	59.6	89	N	AAR80018	Aar80018 Cytotoxic
	59.6	80	7	AAR84899	Aar84899 Epstein-B
	59.6	80	~	AAW40865	_
	59.6	80	~	AAY10595	
	59.6	æ	N	AAY10107	
	59.6	80	Ŋ	ABG80278	MHC
	59.6	æ	ß	ABG79790	
28	59.6	œ	æ	ADK68717	Adk68717 Epitope l
	59.6	σ.	æ	ADK69224	
	59.6	Φ	œ	ADJ84659	σ
	59.6	80	œ	ADQ11023	Adq11023 Cercopith
	59.6	<b>œ</b>	æ	ADQ10515	Adq10515 Cercopith
	59.6	80	œ	ADS80995	Ads80995 Tumour-as
	59.6	Φ	œ	ADS81503	Ads81503 Tumour-as
	55.3	æ	'n	ABP47168	Abp47168 Human BLy
	55.3	80	7	ADG97995	
	53.2	80	m	AAY77587	
	53.2	80	4	AAB78856	
	53.2	σ	Ŋ	ABG98099	Abg98099 Anti-neov
	53.2	60	ß	AAE28157	Aae28157 Murine 9F
	53.2	80	9	ABP74517	Abp74517 Human PSM
	53.2	80	7	ABR61876	Abr61876 Mouse MAb

10 00 === 10	Adz5851 VBGF rece Aea40143 TNF resis Aea38763 Humanized Aea38795 Humanized		Aea45972 Apolipopr Aau99851 Mouse AC1 Aac29925 Mouse ant Adj87910 Mouse AC1	Aaw29379 Somatosta Aay28181 Factor Xa Aam88001 Human pep	
	8 9 ADZ58521 8 9 AEA40143 8 9 AEA38763 8 9 AEA38795	000	8 9 AEA45972 8 5 AAU99851 8 7 AAO29925 8 8 ADJ87910	0.04	
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22 24 24 28	31 31 32	. w w w	38 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0444	4 4 4 6 4 6

## ALIGNMENTS

sequence for anti-IGF-1R antibody. ADJ76846 standard; peptide; 8 AA. (first entry) 06-MAY-2004 ADJ76846; CDR ADJ76846 

cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity; or epidermal growth factor receptor; EGFR; signal transduction pathway; ligand; tumor; cancer; osteosarcoma; complementarity determining region; CDR.

Mus musculus

WO2003059951-A2.

24-JUL-2003

20-JAN-2003; 2003WO-FR000178.

18-JAN-2002; 2002FR-0000653. 18-JAN-2002; 2002FR-0000654. 07-MAY-2002; 2002FR-00005753.

(FABR ) FABRE MEDICAMENT SA PIERRE.

Leger O; Corvaia N, Goetsch L,

WPI; 2003-569653/53. N-PSDB; ADJ76845. New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.

Claim 1; SEQ ID NO 12; 164pp; French.

The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-IR) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-IR. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with

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             these receptors with their ligands. Especially they inhibit transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents an CDR sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody (I) or its functional fragment, being capable of binding to human IGF-IR and, if necessary, capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic; neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma; musculoskeletal disease; respiratory disease; lung tumor; endocrine disease; gynecology and obstetrics; breast tumor; endometroid carcinoma; gastrointestinal disease; colon tumor; antipsoriatic; psoriasis; dermatological disease; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated anti-insulin-like growth factor I receptor (IGF-IR) antibody or its functional fragment, being capable of binding human IGF-IR and specifically inhibiting tyrosine kinase activity of receptor, useful for treating cancer.
hyperactivity of signal transduction pathways mediated by interaction of
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:12
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                                                                                                                                                                               100.0%; Score 47; DB 7; Length 8; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duflos A,
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                                                                                                                                                                                                                                                                                                                                                                  ADZ67016 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2002; 2002FR-0000654.
07-MAY-2002; 2002FR-00005753.
20-JAN-2003; 2003MO-FR000178.
11-JUL-2003; 2003FR-00008538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-2003; 2003US-00735916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002FR-00000653
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                                                                                                                                                                                                                8; Conservative
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CORVAIA N.
LEGER O.
DUFLOS A.
HAEUW J.
                                                                                                                                                                                               Local Similarity
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                                                                                                                                                  Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8-JAN-2002;
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Matches
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ADZ67016
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comprising a light or heavy chain having at least one complementary determining region (CDR) consisting of one of two fully defined 16 amino acids (AD267006 and AD267014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of the preparation of a medicament intended for the prevention or treatment of activation of the IGF-IR and/or Connected with a noverexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a horeration of the IGF-IR and/or of EGFR, and/or of EGFR, where the administration of the ransduction pathway of the signal mediated by the induces secondary effects connected with inhibition of the insulin creeptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of nor of normal colls with tumoral character, preferably IGF-dependent, especially IGF-dependent and/or IGFI and/or IGF2-dependent and/or EGFR dependent and/or IGFI and/or IGFI-dependent and/or IGFI-dependent and/or IGFI-dependent and/or IGFI-dependent and/or IGFI-dependent and/or IGFI-dependent calls. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of postiasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to treatment of postiasis. (I) is useful in preparation of a medicament intended for invitro diagnosis of illnesses induced by an overexpressing the IGF-IR and/or EGFR receptor is useful in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the contact is used in the exemplification of the invention.
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specifically inhibiting tyrosine kinase activity of the receptor.
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HALL INST MEDICAL RES WALTER & ELIZA.
BIOTECH AUSTRALIA PTY LTD.
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Best Local Similarity
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24-APR-1996
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and at least one cytotoxic

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Query Match
Best Local Similarity
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                                                                                                New cytotoxic T-cell epitopes of Epstein-Barr virus have been isolated and purified (AAR80017-R80028). Variants of these epitopes have also been identified (AAR80019-R80038). The epitopes are small, stable peptides whose manufacture does not involve use of any infectious material. The epitopes may be used as components of subunit vaccines to induce cytotoxic T lymphocytes in a subject. The vaccines are partic, useful against viral infections where CD8+ cytotoxic T lymphocytes are protective. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for induction of cytotoxic T cells - comprising CTL epitope and cone antigen, in a water in oil formulation.
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                   Suhribier
                                                      - useful in
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                   Burrows JM,
                                                      New cytotoxic T-cell epitope(s) of Epstein Barr virus unit vaccines to induce cytotoxic T cells.
                                                                                                                                                                                                                                                                                                                                                                                    virus derived cytotoxic T cell epitope.
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                    Kerr BM,
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                     Khanna R,
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                                                                                  Claim 1; Page 15; 23pp; English
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HALL INST MEDICAL
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                     Burrows SR,
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                                     WPI; 1995-336817/43.
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Best Local Similarity
Matches 4; Conserv
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  CSL LTD
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25-APR-1996
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                     Moss DJ,
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(BIOT-)
(CSLC-)
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AAR84899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus type 4; Epstein-Barr virus; EBV; cytotoxic;
T-cell epitope; nuclear antigen; human leukocyte antigen; HLA; vaccine;
tetanus toxoid; diphtheria toxoid; Bordetella pertussis;
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individual will mount an anamnestic response, and at least one cytotoxi T cell (CTL) epitope can be used to induce CD8+ CTL cells in a vaccine, where the CTL epitope is known. The antigen is a diphtheria toxoid, a pertussis or poliovirus antigen, a helper epitope or esp. a tetanus toxoid, and the CTL epitope is 1 of the Epstein-Barr virus derived peptides AAR84898-910. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                         Length 8;
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Pred. No. 2e+06;
1; Mismatches
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UNIV MELBOURNE.
HALL INST MEDICAL RES WALTER & BLIZA
BIOTECH AUSTRALIA PTY LTD.
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ilarity 80.0%;
Conservative
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Matches 4; Conserv
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Length 8;

Score 28; DB 2; Pred. No. 2e+06;

59.6%;

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Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
                                                                                                                                                                                      T cell epitope/MHC ligand SEQ ID NO:37.
                                              AAY10107 standard; peptide; 8 AA.
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                        Human herpesvirus 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-1997;
10-DEC-1997;
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                                                                                                                                       12-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuendig TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1999,
                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                            AAY10107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The method comprises: (a) delivering an antigan to the mammal at a level to induce an immunological CTL response in the mammal; and (b) maintaining the level of the antigan in the mammal's lymphatic system to maintain the immunologic CTL response. The method can be used for the delivery of e.g. a differentiation antigen, a tumour-specific multilineage antigen, an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene antigen, or a viral antigen. They can be used for the treatment of antigen, or a viral antigen. They can be used for the treatment of antigen, or a viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes contain the milieu of the lymphoid organ, and it sustains stimulation that is necessary to keep CTL active, cytotoxic and recirculating through the body. AAX10071 to AAX10639 represent examples of peptide antigens
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
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  Indels
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                      HLA Class I motif peptide SEQ ID NO:525.
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                                                                                                                                                                                                              AAY10595 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                        (first entry)
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human herpesvirus 4.
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4 IFFDY 8
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10-DEC-1997;
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The present invention describes a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The method comprises: (a) delivering an antigen to the mammal The a level to induce an immunological CTL response in the mammal; and (b) maintaining the level of the antigen in the mammal is lymphatic system to maintain the immunologic CTL response. The method can be used for the delivery of e.g. a differentiation antigen, a tumour-specific multilineage antigen, an oncogene antigen, a mutated tumour-suppressor gene entigen, or a viral antigen. They can be used for the treatment of antigen, or a viral antigen. They can be used for the treatment of cleases such as cancer, e.g. malignant melanoma or infectious disease, c.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes place in the milieu of the lymphoid organ, and it sustains stimulation that is necessary to keep CTL active, cytotoxic and recirculating through the body. AAY10071 to AAY10639 represent examples of peptide antigens
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1; Mismatches
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                                                                                                                                                                 (CTLI-) CTL IMMUNOTHERAPIES CORP.
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                                                              97CA-02209815.
97US-00988320.
98WO-US014289
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                                                                                                                                                                                                                               Simard JJL;
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Best Local Similarity
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15-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal comprising administering directly to the lymphatic system of the mammal: (a) an antigen in the form of a polypeptide; (b) a vector comprising a nucleic acid encoding the antigen; or (c) a non-peptide antigen. The nucleic acid encoding the antigen, or (c) a non-peptide antigen. The retrieval is particularly useful for treating a mammal having a malignant tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious clasease (e.g. heparlis, acquired immune deficiency syndrome (AIDS), malaria, measles or tuberculosis), or in an animal having a cats, mice, predisposition to these diseases. The mammal may be dogs, cats, mice, cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-ABG8031 represent viral epitopes on major histocompatibility complex (MHC) class I molecules, used in the method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducing or sustaining immunological cytotoxic T lymphocyte response in a mammal, useful for treating a mammal with malignant tumor or infectious disease, by directly administering an antigen to the lymphatic system of
                                                                  Major histocompatibility complex; MHC; MHC class I molecule; virus; epicope; cytotoxic T lymphocyte response; CTL response; lymphatic system; antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia; lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis; acquired immune deficiency syndrome; AIDS.
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                                   MHC class I molecule, viral epitope #526.
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                                                                                                                                                                                                                                                                                         22-JAN-2002; 2002WO-US002033.
                                                                                                                                                                                                                                                                                                                             02-FEB-2001; 2001US-00776232.
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 15-NOV-2002
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15-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal comprising administering directly to the lymphatic system of the mammal: (a) an antigen in the form of a polypeptide; (b) a vector comprising a nucleic acid encoding the antigen; or (c) a non-peptide antigen. The method is useful for inducing and/or sustaining CTL response in a mammal. This is particularly useful for treating a mammal having a malignant
antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia; lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis; acquired immune deficiency syndrome; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tunour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS), malaria, messles or tuberculosis), or in an animal having a predisposition to these diseases. The mammal may be dogs, cats, mice, cattle, sheep, pigs, goats, rabbits, or preferably humans, ABG79753-ABG80191 represent viral epitopes on major histocompatibility complex (MHC) class I molecules, used in the method of the invention. (Updated 6-4NG-2003 to correct OS field.)
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80.0%; Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 18; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK68717 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CTL1-) CTL IMMUNOTHERAPIES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                   Cercopithecine herpesvirus 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-2001; 2001US-00776232.
                                                                                                                                                                                                                                                                                                                                                                   22-JAN-2002; 2002WO-US002033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simard JJL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-657506/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
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4 IFFDY (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003228634-A1
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                                                                                                                                                                                                                           WO200262368-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-2004
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07-NOV-2002; 2002US-00292413. 07-NOV-2001; 2001US-0336968P.

US2003228634-A1.

11-DEC-2003

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This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the substrate permits processing by a proteasome; contacting the substrate with a composition including the proteasome; and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, the development of compounds with a cytostatic, antibacterial, addition, the invention may allow development of a vaccine. The invention is useful for identifying a polypeptide suitable for epitope liberation, where the epitope is a housekeeping epitope. The compositions comprising the identified housekeeping epitopes are useful in vitro in vaccine the identified housekeeping epitopes are useful in vitro in vaccine corrupts, bacterium, protozoan or fungus. CTL epicopes are identified based on the knowledge that such epitopes are; in fact, produced by the control knowledge that such epitopes are, in fact, produced by the chousekeeping proteasome system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic CTL responses against housekeeping proteasome expressing target cells in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epitope liberation; substrate; proteasome; cytostatic; antibacterial; protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system.
                                                                                                                                                                                                                                                                             Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.6%; Score 28; DB 8; Length 8; 80.0%; Pred. No. 2e+06; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                          Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epitope liberation-related peptide #587.
                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 80; 67pp; English.
                                                                                                                                                                                                          Qin Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK69224 standard; peptide; 8 AA.
                                    07-NOV-2002; 2002US-00292413
                                                                         07-NOV-2001; 2001US-0336968P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                        Simard JJL, Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 80.0
                                                                                                             (SIMA/) SIMARD J J L.
                                                                                                                                DIAMOND D C.
                                                                                                                                                                                                                                        WPI; 2004-167209/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VFFDY 8
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4 IFFDY 8
                                                                                                                                                QIU Z.
LEI X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8 AA;
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11-DEC-2003
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                                                                                                                              (DIAM/) (QIUZ/) (LEIX/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ADK69224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest, providing substrate polypeptide sequence including the epitope, wherein the substrate permits processing by a proteasome; contacting the substrate bermits processing by a proteasome; contacting the substrate by encessing of the substrate by proteasome; and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, protozoacide or fungicide activity acting as T-cell activators. In caddition, the invention may allow development of a vaccine. The invention is useful for identifying a polypeptide suitable for epitope liberation, where the epitope is a housekeeping epitope. The compositions comprising contentified housekeeping epitopes are useful in vitro in vaccine development or in the generation or expansion of cytotoxic T lymphocyte (CT) to be used in adoptive immunotherapy. The invention is also useful for activating T-cells against neoplastic cells, and cells infected with virus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the housekeeping proteasome system. Once identified, these epitopes, embodied con the knowledge that such epitopes are, in fact, produced by the conservations. The present sequence is that of a peptide which is related to the method of the invention.
                                                                                                                                                                                                                                                                                                                      Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipopeptide, lipid moiety, T helper cell epitope, Th epitope, cytotoxic T cell epitope; CTL epitope; immune response; immunisation; influenza; hepatitis C virus; Listeria monocytogenes; vaccine; cancer; cytostatic; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 8; Length 8; Pred. No. 2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.6%; Sco. 80.0%; Pred. No. 20.
                                                                                                                                                                                                                                                  Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 22; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTL epitope peptide SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ84659 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                  Qiu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                  Diamond DC,
                                                                                                                                             (SIMA/) SIMARD J J L.
(DIAM/) DIAMOND D C.
(QIUZ/) QIU Z.
(LEIX/) LEI X.
                                                                                                                                                                                                                                                                                      WPI; 2004-167209/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VFFDY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8 AA;
                                                                                                                                                                                                                                                Simard JJL,
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Unidentified

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                    The present invention describes a lipopeptide comprising a polypeptide conjugated to one or more lipid moieties, where the polypeptide comprises a mainto acid sequence that comprises; (a) the amino acid sequence of a T helper cell (Th) epitope and the amino acid sequence of a cytotoxic T cell (TL) epitope, where the amino acid sequences are different; and (b) one or more internal lysine analogue residues for covalent attachment of each of the lipid moieties via the epsilon-amino group or terminal side-chain group of the lysine or lysine or lysine con analogue. Each of the one or more lipid moieties is covalently attached to a terminal side-chain group of the one or more internal lysine cenidues or to a terminal side-chain group of the one or more internal lysine con analogue residues. Also described: (1) producing a lipopeptides; (2) a composition comprising the lipopeptide and an excipient or diluent; (3) eliciting an immune response in a subject; (4) immunising a subject against influenza or hepatitis C virus or Listeria monocytogenes is from a nifluenza virus or hepatitis C virus or Listeria monocytogenes an influenza virus or hepatitis C virus or Listeria monocytogenes and a nifluenza virus or hepatitis C virus or Listeria monocytogenes protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                       New lipopeptide comprising a polypeptide comprising an amino acid sequence of a T helper cell and cytotoxic T cell epitope, useful for preparing a composition for treating or preventing cancer, or hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (6) treating or preventing cancer; and (7) a vaccine against cancer comprising the lipopeptide, where the CTL epitope is a tumour-specific CTL epitope. The lipopeptide has cytostatic and virucide activities, and can be used in vaccine. The lipopeptide is useful for preparing a composition for treating or preventing cancer, or hepatitis C virus or influenza virus. The present sequence is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunostimulant; cytostatic; vaccine; tumour-associated antigen SSX-2; SSX-2 antigen; epitope cluster; MHC receptor peptide binding cleft;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 8; Length 8;
Pred. No. 2e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecine herpesvirus 15 T-cell epitope segid 588.
                                                                                                                                                      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 117; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ11023 standard; peptide; 8 AA.
                                                                                                 12-AUG-2003; 2003WO-AU001019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.08;
                                                                                                                           12-AUG-2002; 2002US-0403328P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                   influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention.
  Human herpesvirus 4.
                                                                                                                                                                                                           WPI; 2004-238736/22
                                                                                                                                                                                  Jackson D, Zeng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VFFDY 8
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                                         WO2004014957-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-2004
                                                                     19-FEB-2004
                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ11023;
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                                                                                                                                                                                                                                                                                   virus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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The invention describes an isolated nucleic acid (I) comprising a reading frame comprising a first sequence, where the first sequence encodes one or more segments of tumour-associated antigen SSX-2, which comprises a sequence of 188 amino acids (SEQ ID NO: 40), where the first sequence does not encode the complete SSX-2 antigen, and where each segment comprises an epitope cluster, the cluster comprising or encoding at least two amino acid sequences having a known or predicted affinity for a same WHC receptor peptide binding cleft. Also described are: an isolated polypeptide comprising the amino acid sequence encoded in the reading comprising and an immunopantic composition comprising (I) or the polypeptide of [1]. (I) is a nucleic acid encoding a tumour-associated antigen SSX-2 comprising a fully defined sequence of 188 amino acids (SEQ ID NO: 40). The nucleic acid, the encoded antigen, and composition are useful in an uncleic acid, the encoded antigen, and composition are useful in control of an immune response and in treating cancer. Expression cassettes are used in vaccine vectors. This is the amino acid sequence of a T-cell epitope MHC lighting with methods, therapies and compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunostimulant; cytostatic; vaccine; tumour-associated antigen SSX-2; SSX-2 antigen; epitope cluster; MHC receptor peptide binding cleft; immunospanic composition; immuno response; cancer; vaccine vector; epitope liberation; human leukocyte antigen; HLA A2-specific CTL; cytotoxic T lymphocyte; T-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid encoding tumor-associated antigen SSX-2, useful in inducing an immune response and in treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
immunogenic composition; immune response; cancer; vaccine vector; epitope liberation; human leukocyte antigen; HLA A2-specific CTL; cytotoxic I lymphocyte; I-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecine herpesvirus 15 T-cell epitope segid 80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 8;
Pred. No. 2e+06;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 588; 260pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ10515 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qiu Z,
                                                                                                                                                          Cercopithecine herpesvirus 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2001; 2001US-0336968P. 07-NOV-2002; 2002US-00292413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.6%;
                                                                                                                                                                                                                                                                                                                                                                     10-FEB-2004; 2004US-00777053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SIMA/) SIMARD J J L.
(DIAM/) DIAMOND D C.
(QIUZ/) QIU Z.
(LEIX/) LEI X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-517003/49.
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Best Local Similarity
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frame comprising a first sequence, where the first sequence encodes one or more segments of tumour-associated antigen SSx-2, which comprises a sequence of 188 amino acids (SK-10 NO: 40), where the first sequence does not encode the complete SK-2 antigen, and where each sequence comprises an epitope cluster, the cluster comprising or encoding at least two amino acids sequences having a known or predicted affinity for a same MHC receptor peptide binding cleft. Also described are: an isolated polypeptide comprising the amino acid sequence encoded in the reading frame; and an immunogenic composition comprising (I) or the polypeptide of (1). (1) is a nucleic acid encoding at tumour-associated antigen SSx-2 comprising a fully defined sequence of 188 amino acids (SEQ ID NO: 40). The nucleic acid, the encoded antigen, and composition are useful in chucing an immune response and in treating cancer. Expression casesties are used in vaccine vectors. This is the amino acid sequence of a T-cell epitope MHC ligand associated with methods, therapies and compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated nucleic acid (I) comprising a reading
                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid encoding tumor-associated antigen SSX-2, useful in inducing an immune response and in treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour-associated antigen; NY-ESO; epitope cluster; major histocompatibility complex; MHC receptor peptide binding cleft; immunogenic composition; vaccine; sarcoma; fibro sarcoma; osteogenic sarcoma; breast cancer; ovarian cancer; prostate cancer; chronic lenkaemia; Hodgkin's disease; non-Hodgkin's disease; multiple myeloma; Waldenstrom's macroglobulinaemia; epitope.
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                                                                                                                                                                                                                                                                                                                                    Lei X;
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                      Cercopithecine herpesvirus 15
                                                                                                                                      10-FEB-2004; 2004US-00777053
                                                                                                                                                                         07-NOV-2001; 2001US-0336968P
07-NOV-2002; 2002US-00292413
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                                                                                                                                                                                                                                (SIMA/) SIMARD J J L.
(DIAM/) DIAMOND D C.
(QIUZ/) QIU Z.
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(LEIX/) LEI X.
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KW tumou
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KW major
KW immun
KW osteo
KW multi:
XX
OS Cerco
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The invention describes an isolated nucleic acid (1) comprising a reading frame comprising a first sequence, where the first sequence encodes one or more segments of tunour-associated antigen NY-ESO having a fully defined sequence of 180 amino acids (S1) as given in the specification, where the first sequence does not encode the complete NY-ESO antigen, and where each segment comprises an epitope cluster; the cluster comprising or encoding at least two amino acid sequences having a known or predicted affinity for a same major histocompatibility complex (MHC) receptor affinity for a same major histocompatibility complex (MHC) receptor comprising the amino acid sequence encoded in the zeading frame of (S1); and an immunogenic composition comprising (I) or (II). The following are disclosed: epitope clusters identified in the tumour-associated antigen NY-ESO; expression cassettes for use in vaccine vectors; vectors including house-keeping epitope; and activating T-cell using the vector. (I) is useful in designing recombinant vaccines against tumours such as human sarcoma, fibro sarcoma, osteogenic sarcoma, breast cancer, ovarian cancer, prostate cancer, chronic leukaemia, Hodgkin's disease, non-salorate ancer, chronic leukaemia, protozoa or fungi. (I) cancer, prostate ancer, chronic leukaemia, protozoa or fungi. (I) cancers or manufacture a recombinant vaccine economically and rapidly, by a simple process. The vaccine is highly safe as it consists of only a fragment of the antigen rather than the whole protein. This is the amino caid sequence of a tumour-associated antigen epitope useful in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid comprising reading frame having first sequence that encodes segments of tumor-associated antigen NY-ESO, usef in designing recombinant vaccines against tumors such as fibro sarcoma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 80; 259pp; English
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                                                                                                                                                                                                                                                                                                                        Lei X;
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                                                                                                      30-APR-2004; 2004US-00837217.
                                                                                                                                                 07-NOV-2001; 2001US-0336968P. 07-NOV-2002; 2002US-00292413.
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(DIAM/) DIAMOND D C.
(QIUZ/) QIU Z.
(LEIX/) LEI X.
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Best Local Similarity
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                      US2004203051-A1.
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                                                              14-0CT-2004
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

model using sw - protein search, OM protein

Run on:

December 30, 2005, 15:45:25; Search time 36 Seconds (without alignments) 21.382 Million cell updates/sec

US-10-735-916A-12 Title: Perfect score:

1 YGRVFFDY 8 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

149 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 8 Maximum DB seq length: 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database

PIR 80:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	telomeric and tetr	**	inulinase (EC 3.2.	cytochrome oxidase	cholecystokinin -		Ig H chain V-D-J r	unidentified 6.5/3	leucokinin VIII -	blood cell protein	158K exoantigen -	neuropeptide calla	Ig heavy chain CRD	ဌ			hypothetical prote	cardioacceleratory	Ig heavy chain V r	м	c			Na+-transporting A	glucose-6-phosphat	calliFMRFamide 8 -		ochrome-c	MHC class I histoc
QI	PC4373	PT0311	PT0030	T13818	PQ0012	A43001	PH1618	PQ0701	JS0318	868325	B33099	E47393	PT0279	B27867	A61467	A25836	T48890	866646	PH1407	S16324	PT0298	B45800	PH0803	866296	S11078	H41978	D47393	865381	A59028
DB	0	~	~	~	~	~	~	~	7	7	~	~	~	N	N	~	~	N	7	N	~	N	N	N	N	~	~	7	7
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* Query Match	31	29	8	29	7	27	27	27	7	27	5	25	ď	7	~	~	N	21	19	ä	Ä	Ä	ä	ä	Ä	Ä	ä	ř	ä
Score	15	14	14	14	13	13	13	13	13	13	12	12	11	11	11	11	11	10	6	o,	Ø	σ	Q	σ,	σ,	Q	6	O	0
Result No.	-	N	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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A44960 A58620 S11545	\$55310 \$10596 \$08995 A49823	A28004 S15422 A58641 S70727	501433 PT0724 S19288 A21440
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31	1 W W W W	788 80 40 10	4 4 4 4 4 1 4 6 4 7

## ALIGNMENTS

telomeric and tetraplex DNA binding protein qTBP42 III - rat (fragment)

Cispecies: Rattus norvegicus (Norvey rat)
Cipate: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
Cipate: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
Cipate: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
Cipate: Residence norman-Shomer, P.; Fry, M.
Risarig, G.; Weisman-Shomer, P.; Fry, M.
A; Reference number: Res. Commun. 237, 617-623, 1997
A; Reference number: PC4371; MUID:97445086; PMID:9299414
A; Reference number: PC4373
A; Reference number: PC4373
A; Residues: 1-8 < SAR>

A;Gross-references: UNIPROT:Q7M012; UNIPARC:UPI000017CA04 C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular F;1-4/Domain: RNP1 #status predicted <RNP>

Gaps ö Score 15; DB 2; Length 8; Pred. No. 2.8e+05; 2; Mismatches 2; Indels y Match 31.9%; Local Similarity 33.3%; nes 2; Conservative Query Match Best Loc Matches

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ø : | : | 2 FGFILF 7 1 YGRVFF 셤 ଚ

Ig heavy chain CRD3 region (clone 6-100) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-5p-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: Pr0311
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Fitle: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Fitle: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: Pr0222; MUD:91108337; PMID:1899102
A;Reference number: Pr0222; MUD:91108337; PMID:1899102
A;References: UNIPARC:UPI000017C20F
A;Residues: 1-8 < YAM>
A;Residues: 1-8 < YAM>
A;Residues: 1-8 < YAM>
C;Keywords: heterotetramer; immunoglobulin

Gaps 4, Query Match 29.8%; Score 14; DB 2; Length 8; Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels

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1 YGRVFFDY Š 셤

4 YG----DY 7

Query Match 29.8 Best Local Similarity 66.7 Matches 2; Conservative

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PHIG18
IG H chain V-D-J region (clone B-less 33) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHIG18
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PHI580; MUID: 93301609; PMID: 8315387
A;Accession: PHI618
A;Accession: PHI618
A;Molecula type: DNA
A;Residues: 1-8 <LEV>
A;Cross-references : UNIPARC: UPI000017C6A7
A;Cross-references in UNIPARC: Upi00017C6A7
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NyAlternate names: Corn. (tammar wallaby)
Species: Macropus eugeni (tammar wallaby)
C;Date: 30-oct-1992 #sequence_revision 30-oct-1992 #text_change 09-Jul-2004
C;Date: 30-oct-1992 #sequence_revision 30-oct-1992 #text_change 09-Jul-2004
C;Date: 30-oct-1992 #sequence_revision 30-oct-1992 #text_change 09-Jul-2004
C;Accession: A.43001; PQ0012
A;Title: Cholecystckinin octapeptide purified from brains of Australian marsupials.
A;Title: Cholecystckinin octapeptide purified from brains of Australian marsupials.
A;Title: Cholecystckinin octapeptide purified subsidered arsupials.
A;Residues: 1-8 <ANN>
A;Residues: 1-8 <ANN>
A;Cross-references: UNIPROT:P30369; UNIPARC:UPI000002CDD4
C;Superfamily: gastrin
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C;Superfamily: gastrin
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: PQ0701
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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F;8/Modified site: amidated carboxyl end (Phe) #status predicted
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                                                                27.7%; Score 13; DB 2; Length 8; 100.0%; Pred. No. 2.8e+05; ive 0; Mismatches 0; Indels
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    tammar wallaby

                                                                    Query Match 27.7
Best Local Similarity 100.
Matches 2; Conservative
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Matches 2; Conservative
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N;Alternate names: CCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13818
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Myol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI A;Reference number: Z17775; MUID:97398704; PMID:9254918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DEL>
A;Residues: UNIPROT:021079; UNIPARC:UPI000016D463; EMBL:Y09527; NID:g2340019; PI
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PO01012
PO01012
Cholecystokinin - southeastern quol1
NiAlternate names: CCK
CiSpecies: Dasyurus viverrinus (southeastern quol1)
CiDate: 07-56p-1990 #sequence_revision 07-5ep-1990 #text_change 09-Jul-2004
CiAccession: P00102
R;Pan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A;File: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: P00012; MUID:88234141; PMID:3375140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                 NyAlternate names: inulase
C;Species: Aspergillus ficuum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: PT0030
R;Ettalibi, M.; Baratti, J.C.
Agric. Biol. Chem. 54, 61-68, 1990
A;Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.
A;Reference number: PT0030; MUID:90344234; PMID:1368526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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C, Superfamily: gastrin
C; Keyworfs: amidated carboxyl end, hormone; neuropeptide; sulfoprotein
F; 2/Binding site: sulfate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Reaidues: 1-8 <ETT>
A;Cross-references: UNIPROT:O7M4U4; UNIPARC:UPI000017B3B3
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.8%; Score 14; DB 2; Length 8; 66.7%; Pred. No. 2.8e+05; tive 1; Mismatches 0; Indel8
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                                                                        inulinase (BC 3.2.1.7) - Aspergillus ficuum (fragment)
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3; Conservative

Matches

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Query Match Best Local Similarity

A; Molecule type: protein A; Residues: 1-8 < FAN>

A;Note: COI C;Keywords: mitochondrion

A; Genome: mitochondrion

Genetics:

Gaps

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Query Match

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C; Accession: E47393
R; Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A. Pritle: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequence A; Reference number: A47393; MUID:93211980; PMID:8460157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 355-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0279
158K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Calliphora vomitoria
C.Date: 16-Peb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.5%; Score 12; DB 2; Length 8; 33.3%; Pred. No. 2.8e+05; rative 2; Mismatches 0; Indels
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A; Note: sequence extracted from NCBI backbone (NCBIP:128482)
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A;Residues: 1-8 <DUV>
A;Cross-references: UNIPROT:P41841; UNIPARC:UPI000002EABS
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.5%; Score 12; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
                                                                                      CiAccesion: B3309
RiNichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Reference number: A33098
A;Reference number: A33098
A;Reference number: A33098
A;Reference: Preliminary
A;Rolecule type: protein
A;Residues: 1-8 eMIC>
A;Residues: 1-8 eMIC>
A;Cross-references: UNIPARC:UPI000017B5DF
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C, Keywords: heterotetramer; immunoglobulin
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Matches 2; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-8 <YAM>
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4 YDF 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leucokinin VIII - Madeira cockroach
[CiSpecies: Leucophaea maderae (Madeira cockroach)
[CjSpecies: Leucophaea maderae (Madeira cockroach)
[CjSpecies: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
[CjAccession: JS0318
[RjHolman, G.M.; Cook, B.J.; Nachman, R.J.
[RjHolman, G.M.; Cook, B.J.; Nachman, R.J.
[AjTitle: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P19990; UNIPARC:UP1000012E29F
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            끕
           Theor. Appl. Genet. 86, 935-942, 1993

A; Title: A rice protein library; a data-file of rice proteins separated by two-dimension A; Reference number: P00696

A; Reference number: P00701

A; Status: proliminary

A; Nolecule type: protein

A; Residues: 1-8 < KCM>
A; Cross-references: UNIPROT: Q7MIU0; UNIPARC: UPI000017B129
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blood cell protein A8 - Ascidia ceratodes (fragment)

blood cell protein A8 - Ascidia ceratodes

blood cell protein A8 - Ascidia ceratodes

c; Species: Ascidia ceratodes

c; Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

c; Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

c; Arcession: 568325

Arch. Biochem. Biophys. 324, 228-240, 1995

Arch. Biochem. Biophys. 324, 5-trihydroxyphenylalanine-containing polypeptides from the Reference number: 568325; MUID:96132650; PMID:8554314
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F;2,3,4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental
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27.7%; Score 13; DB 2; Length 8;
Best Local Similarity 28.6%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                     27.7%; Score 13; DB 2; Length 8; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels
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Matches 2; Conservative
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Best Local Similarity
2; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: JS0318
A, Molecule type: protein
A, Residues: 1-8 <HOL>
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RESULT 11 B33099

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homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Os-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C;Accession: B27867
R;Saari, G.; Bienz, M.
BMBO J. 6, 1775-1779, 1987
A;Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.
A;Reference number: A91072
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A;Cross-references: FlyBase:FBgn0003944
C;Keywords: DNA binding; nucleus; transcription regulation
                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 1-8 <SAA>
A,Crost-references: UNIPROT:P83949; UNIPARC:UPI000016BDEE
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1; Conserv
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A61467

A61467

Benalbumin - Adelie penguin (fragment)

C;Species: Pygoscelis adelie (Adelie penguin)

C;Species: Pygoscelis adelie (Adelie penguin)

C;Date: 07-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004

C;Accession: A61467

R;Oauga, D.T.; Aminlari, M.; H6, C.Y.K.; Allison, R.G.; Feeney, R.E.

J. Protein Chem. 2, 43-62, 1983

A;Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparisons

A;Reference number: A61467

A;Residues: 1-8 coSus

A;Residues: 1-8 coSus

A;Residues: 1-8 coSus

C;Cross-references: UNIPROT:Q7LZ18; UNIPARC:UP1000017C04A

C;Comment: Penalbumin is a major protein component of egg whites from penguins but not fine C;Reywords: egg white; glycoprotein

Gaps ;. 0 1; Indels 23.4%; Score 11; DB 2; Length 8; 25.0%; Pred. No. 2.8e+05; Live 2; Mismatches 1; Indels 1; Conservative Best Local Similarity Matches 1; Conserva Query Match

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1 GSIY 4 2 GRVF 5 셤

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Search completed: December 30, 2005, 15:56:00 Job time : 37 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 30, 2005, 15:36:05; Search time 224 Seconds (without alignments) 25.197 Million cell updates/sec Run on:

US-10-735-916A-12 Perfect score: Title:

1 YGRVFFDY 8 **BLOSUM62** Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

2166443 segs, 705528306 residues Searched:

707 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 8 Maximum DB seq length: 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q66x60 isodon phar Q4x617 plasmodium O13591 saccharomyc Q56759 xanthobacte Q7m032 rattus norv Q80h91 newcastle d Q7m044 aspergillus Q40530 nicotiana t Q99nx9 hydrochoeru Q94cd02 terranatos P68125 dasyurus vi P68126 marchpus eu P19990 leucophaea Q35792 saccharomyc Q6bcz9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9uuh9 homo sapien Q9ulh0 oryza sattv Q66111 assechorocc Q85406 coxiella bu G5yda4 oncorhynchu Q5yda4 oncorhynchu Q5yda4 in myrmotherul Q68111 myrmotherul Q68111 myrmotherul Q68111 myrmotherul Q68111 alliphora P81156 cydia pomon Q10582 bothrops ja
SUMMARIES	QEEXEG 91AMI QAX617_PLACH 01591_YEAST 056759_XANAU Q7M032_RAT 080191_9PAZA Q7M012_SART Q40530_TOBAC Q99X93_HYDHY Q40530_TOBAC Q99X93_HYDHY Q5TD02_SARG ALL16_CARMA CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU CCKN_MACEU G9UM100_CRYSA Q9UM100_CRYSA Q6BLP1_9PASS Q6BLP1_9PASS Q6BLP1_9PASS ALL1C_CCKN ALL1C_CCKN ALL1C_CCKN ALL1C_CCKN ALL1C_CCKN ALL1C_CCKN ALL1C_CCKN ALL1C_CCKN ALL1C_CCKN ALL1C_CCKN
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ORMY_ORCLI 015899_BABOV QBMC218_QUIIN QBMC20_9NYRT Q7X139_9STAAP Q7X145_STAAP Q9XQ47_9ENTR Q9LFNB_CHICK Q6JFNB_CHICK Q6JFNB_CHICK Q6SE42_DROSI Q9TWH6_9ANNE Q28866_MEGNO Q6R4QB_UBBU
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## ALIGNMENTS

L We	QGEX60_9LAMI PRELIMINARY; PRT; 8 AA.		(TrEMBLrel. 28,	(TrEMBLrel. 28,	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	Ribosomal protein (Fragment).	:= <b>r</b> ps16;	Isodon pharicus.	Chloroplast.	Viridiplantae, Streptophyta, Embryophyta, Tracheog	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Isodon.	NCBI_TaxID=204134;			Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Willis F.,	il M.P., Savolainen V.;	Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.	EMBL; AJ505344; CAD45467.1; -; Genomic_DNA.	GO:0009507; C:chloroplast; IEA.	GO; GO:0003735; F:structural constituent of ribosome; 1EA.	Chloroplast; Ribosomal protein.	-1	8	JENCE 8 AA; 881 MW; 175059C732C8/8// CKC64;	Query Match 38.3%; Score 18; DB 2; Length 8; Beet Loral Similarity 57.1%; Pred. No. 2.2e+06;	ative 0	2 GRVFFDX 8	2 GGVLFIY 8
RESULT 1	OEEX60	O6EX60;	25-OCT-	25-0CT-	25-0CT-	Ribosom	Name=rps16	Isodon	Chlorop	Eukaryo	Spermat	lamiids	NCBI_Ta	Ξ	NUCLEOT	Paton A	Powell	Submitt	EMBL; A	9	9 9	Chlorop	NON TER	NON TER	SEQUENC	Query Match	Matches		
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13-SEP-2005 (TrEMBLrel. 31, Created)
17 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
17 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
18 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
19 Hypothetical protein.
19 Plasmodium chabaudi.
10 RRNames=PQ46559.00.0;
10 Plasmodium chabaudi.
10 RNCLETTAXID=5825;
11 RNCLECTIDE SEQUENCE.
11 RAIL N., Karas M., Raine J.D., Carlton J.M., Kooij T.W.A.,
11 Hall N., Farras M., Planssen C.S., Pain A., Christophides G.K.,
12 Annes K., Rutherford K., Harris B., Harris D., Churcher C., 8 AA. PRT; RESULT 2
04X617 PLACH
1D 04X617_PLACH PRELIMINARY;
AC 04X617,
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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STRAIN=6310;
MEDIINE=9517313; PubMed=7868610;
Van der Ploeg J., Willemsen M., van Hall G., Janssen D.B.;
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Obermaier B., Piravandi E., Rinke M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z71612; CAA96271.2; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 8 AA; 1098 MW; B24B4B5449D2D2C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
ORF YNL337w (Fregment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA; 1005 MW; 5CA441E449C9C720 CRC64;
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Q56759_
01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-DEC-2001 (TYEMBLrel. 19, Last annotation update)
Name-dalls;
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60.0%; Pred. No. 2.2e+06;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                             preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
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013591;
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2 VVFNY 6
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MEDLINE-97445086; PubMed=9299414; DOI=10.1006/bbrc.1997.7198; Sarig G., Weisman-Shomer P., Fry M.; Sarig G., Weisman-Shomer P., Fry M.; "Telomeric and tetraplex DNA binding properties of QTBP42: A homologue of the CArG box binding protein CBF-A."; Blochem. Blophys. Res. Commun. 237:617-623(1997). PIR: PC4373; PC4373.
"Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to activation and mobilization of the haloacetate dehalogenase gene by insertion element IS1247.";
J. Bacteriol. 177:1348-1356(1995).
EMBL; X84038; GAAS8857.1; -; Genomic_DNA.
NON_TER 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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"Evaluation of the molecular basis of pathogenicity of the variant Newcastle disease viruses termed 'pigeon PMV-1 viruses'.";
Arch. Virol. 134:403-411(1994).
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Paramyxoviridae; Paramyxovirinae; Avulavirus.
NCBI_TaxID=11176;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Telomeric and tetraplex DNA binding protein qTBF42 III
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Last annotation update)
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MEDLINE=94175786; PubMed=8129624;
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Q80H91;
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Matches 2; Conservative
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Q7M032;
01-MAR-2004 (TrEMBLrel. 2
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MEDLINE=90344234; PubMed=1368526;
Ettailbi M., Baratti J.C.;
"Molecular and kinetic properties of Aspergillus ficuum inulinases.";
Agric. Biol. Chem. 54:61-68(1990).
PIR; PT0030; PT0030.
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Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
VCBI_TaxID=5058;
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MEDLINE=87089808; PubMed=3540612;
Herman L.M.F., Montagu M.C.V., Depicker A.G.;
Harman L.M.F., Montagu M.C.V., Depicker A.G.;
Harman L.M.F., Montagu M.C.V., Depicker A.G.;
Mol. Cell. Biol. 6:4486-4492(1986).

EMBL; M14685; AAA34090.1; -; Genomic DNA.

SEQUENCE 8 AA; 1109 MW; E257205BI9C9C9C6 CRC64;
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Q40530;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
N.tabacum P20 with a leader peptide.
Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Inulinase (EC 3.2.1.7) (Fragment).
Aspergillus ficuum.
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                         8 AA; 929 MW; 33D4087AA337205B CRC64;
                                                                            31.9%; Score 15; DB 2; L. L. L. 100.0%; Pred. No. 2.2e+06; Conservative 0; Mismatches 0;
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8 AA; 1102 MW;
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Q7m4U4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hrbek T., Larson A.;
"The evolution of diapause in the killifish family Rivulidae
"The evolution of diapause in the killifish family Rivulidae
Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
biogeographic perspective.";
Evolution 53:1200-1216 (1999).
                                                                                                                                                                    Hydrochoerus hydrochaeris (Capybara) (Carpincho).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Hystricognathi; Hydrochaeridae; Hydrochaeris.
                                                                                                                                                                                                                                                                                                                                                                                                                                O'Brien 8.J.;
"Molecular phylogenetics and the origins of placental mammals.";
Nature 409:614-618(2001).
EMBL; AY011342; AAG47377.1; -; Genomic_DNA.
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MEDLINE-21082082; PubMed-11214319; DOI-10.1038/35054550;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14; DB 2; Length 8; Pred. No. 2.2e+06; 1; Mismatches 0; Indels
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SEQUENCE 8 AA; 1084 MW; F0C9D3640DD44056 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
Terranatos dolichopterus.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA; 1071 MW; 1356D686DB19C9C3 CRC64;
                                               01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 2.2e+06;
0; Mismatches 1;
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8 AA
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GO; GO:0005739; C:mitochondrion; IEA.
  PRT;
                                                                                                                                   Amyloid beta protein (Fragment).
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Best Local Similarity 75.0%;
Matches 3; Conservative
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Best Local Similarity 66.7%;
Matches 2; Conservative
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Q9TD02;
Q99NX9 HYDHY PRELIMINARY;
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Peptides 9:429-431(1988).
-!- FUNCTION: This peptide hormone induces gall bladder contraction and the release of pancreatic enzymes in the gut. Its function the brain is not clear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88234141; PubMed=3375140; DOI=10.1016/0196-9781(88)90280-X; Fan Z.W., Eng J., Shaw G., Yalow R.S.; "Cholecystokinin octapeptide purified from brains of Australian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Dasyuromorphia, Dasyuridae, Dasyurus.
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                                                                                                                                                                                                                                                                                                      "Isolation and identification of multiple neuropeptides of the
                                                                                                                                                                                                                                                                                                                 allatostatin superfamily in the shore crab Carcinus maenas.";

Eur. J. Blochem. 250:727-734(1997).

-!- FUNCTION: May act as a neurotransmitter or neuromodulator.

-!- SUBCELLUIAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the allatostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
                                                                                                                                                                                                                                    TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                    Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Plecyemata, Brachyura,
Eubrachyura, Portunoidea, Portunidae, Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.7%; Score 13; DB 1; Length 8; 100.0%; Pred. No. 2.2e+06;
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                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCKN_DASVI STANDARD; PRT; 8 AA. P68125; P30369; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 01-APR-1993 (Rel. 45, Last annotation update) Cholecystokinin (CCK).
                                  8 A.
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Les 2; Conservative
                                STANDARD;
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ALL16 CAM
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P81819;
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SEQUENCE
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-1- FUNCTION: This peptide hormone induces gall bladder contraction and the release of pancreatic enzymes in the gut. Its function in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macropus eugenii (Tammar wallaby).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
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PIR; PQ0012; PQ0012.
InterPro; IPR001651; Gastrin.
InterPro; PS00259; GASTRIN; 1.
Amidation; Direct protein sequencing; Hormone; Sulfation.

2 2 Sulfotyrosine.
Phenylalanine amide.
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InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Amidation; Direct protein sequencing; Hormone; Sulfation.
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Pred. No. 2.2e+06;
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MEDLINE=B069885; PubMed=6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;
Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;
"Assembly of the mitochondrial membrane system. Structure and
nucleotide sequence of the gene coding for subunit 1 of yeast
cycohrome oxidase.";
J. Biol. Chem. 255:11927-11941(1980).
EMBL; V00694; CAA24063.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae."; Comp. Biochem. Physiol. 886:31-34 (1987).
- I- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach protodeum (hindgut).
- I- SUBCELDUAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Leucokinin-8 (Leucokinin VIII) (L-VIII)
Leucophaea maderae (Madeira cockroach)
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopeeroidea; Dictyoptera; Blattaria; Blaberoidea;
Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.7%; Score 13; DB 2; Length 8; 100.0%; Pred. No. 2.2e+06;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Mondation; Direct protein sequencing; Neuropeptide.
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SEQUENCE 8 AA; 902 WW; 736365AB59CAADD8 CRC64;
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Saccharomyces cerevisiae (Baker's yeast).
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Q35792;
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Score 28; DB 1; Length 8; Pred. No. 4.6e+05; 1; Mismatches 0; Indels

Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-09-920-195A-19
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Pred. No. 4.6e+05;
1; Mismatches 0;
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US-09-920-195A-19
IS-09-920-195A-19
Sequence 19, Application US/09920195A
PREED NO. 6703024
GENERAL INFORMATION:
APPLICANT: KHANNA, RAJIV
APPLICANT: KHANNA, RAJIV
APPLICANT: MISKO, IHOR S.
APPLICANT: MISKO, IHOR S.
APPLICANT: BURROWS, SCOTT R.
TILE APPLICANT: BURROWS, SCOTT R.
TILE REFERENCE: FERC:004USC1
CURRENT APPLICATION NUMBER: 09/194,450
FRIOR PILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 19
                                                                                                                                                                          APPLICANT: KHANNA, RAJIV
APPLICANT: KHANNA, RAJIV
APPLICANT: KERR, BEVERLEY M.
APPLICANT: MISKO, IHOR S.
APPLICANT: MOSS, DENIS J.
APPLICANT: BURROWS, SCOTT R.
TITLE OF INVENTION: EBV CTL EPITOPES
FILE REPERENCE: PERC:00818C2
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 09/920,175
PRIOR APPLICATION NUMBER: 09/194,450
PRIOR PILING DATE: 1998-11-23
PRIOR PILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                             Sequence 19, Application US/09920174 Patent No. 6699477
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
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IFFDY 8
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US-09-920-174-19
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Score 28; DB 2; Length 8; Pred. No. 4.6e+05;

59.6%;

Query Match Best Local Similarity

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Gaps
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APPLICANT: Sinth, Andrew John Stuart
APPLICANT: Sinth, Andrew John Hammond
APPLICANT: Sinth, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SECURESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

RILNG DATE: 05-DEC-1994

CLASSIFICATION OF A35

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 910549.4

FILING DATE: 15-MAY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB91/01134

FILING DATE: 10-UL-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 15-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 15-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/150,002

PRIOR APPLICATION DATA:

APPLICATION DATA:

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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
RELECOMMUNICATION INFORMATION:
TELEPONE: 312-47-6300
INFORMATION FOR SEQ ID NO: 423:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                                                  Sequence 423, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
4; Conservative
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STATE: Illinois
COUNTRY: USA
                                                                          4 VEFDY 8
                                                                                                                                   : | | | | 4 IFFDY 8
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Gaps

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Materinous, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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COUNTY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Audrey L. Bartnicki
STREBT: Marshall, Gerstein & Borun
6300 Saars Tower, 233 South Wacker Drive
                                                                                                   Length 8;
                                                                                             Query Match 53.2%; Score 25; DB 1; Le Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bartnicki, Audrey L.
REGISTRATION WUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/350,260
PILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1993
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 14-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear SEQ ID NO: 423: US-09-104-337A-423
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 422, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
HAPPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-474-6300 INFORMATION FOR SEQ ID NO: 423: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 600
; STRANDEDNESS: sin;
; TOPOLOGY: linear
US-08-350-260A-486
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US-09-104-337A-423
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: USA
ADDRESSEE: Days Gars Tower, 233 South Wacker Drive CITY: Chicago CITY: Chicago CITY: Chicago CITY: Chicago CITY: Chicago CITY: Chicago COUNTRY: USA
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                           Score 25; DB 1; Length 8; Pred. No. 4.6e+05; 1; Mismatches 1; Indels
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RR: 28111/32372
                                                                                                                                                                                                                                                                                                                                                                                                     Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                     Sequence 486, Application US/08350260A Patent No. 5962255 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 486:
                                 53.2%;
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        Query Match
Best Local Similarity 66./
                                                                                                                                       RVFFDY 8
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3 RKYFDY 8
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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TYPE: PRT
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  Matches
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Nissim, Ahuva
Johnson, Kevin Stuart
Johnson, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BA PC compatible
COMPUTER: Patchin Release #1.0, Version #1.25 (BPO)
SOFTWARE: Patchin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
PRILOR DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 910549.4
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB92/00605
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 34-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAY-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 18-MAY-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 18-MAY-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 18-MAY-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 18-MAY-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 18-MAY-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 18-MAY-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 18-MAY-1994
APPLICATION NUMBER: US 08/150,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSER: Audrey L. Bartnicki
STREET: Marshall, Gestein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%; Score 25; DB 2; Length 8; 100.0%; Pred. No. 4.6e+05;
                             Length 8;
                   Score 25; DB 2; I
Pred. No. 4.6e+05;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bartnicki, Audrey L.
REGISTATION WÜMBER: 40,499
REFRENCE/DOCKET HÜMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 486:
US-09-104-337A-486
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                   ; Sequence 486, Application US/09104337A; Patent No. 6492160; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: USA
Query Match
Best Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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3 RKYFDY 8
                                                                                                                    3 RVFFDY
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Gaps
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Sequence 380, Application US/08350260A
Sequence 380, Application US/08350260A
GENERAL INFORMATION:
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Wilsim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCES: 602
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: Giol Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 2; Length 8;
Pred. No. 4.6e+05;
0; Mismatches 3; Indels
Indels
..
0
0; Mismatches
                                                                                                                                                                                                                               APPLICANT: A)-00-01d, Fahad
APPLICANT: A1-Obeidd, Fahad
APPLICANT: Ostrem, James A.
APPLICANT: Safar, Pavel
APPLICANT: Sterandova, Alena
APPLICANT: Sterandova, Alena
APPLICANT: Sterandova, Alena
APPLICANT: Sterandova, Alena
APPLICANT: Walser, Armin
TITLE OF INVENTION: Factor Xa Inhibitors
TITLE REFERENCE: P-SE343
CURRENT APPLICATION NUMBER: US/09/211,715
CURRENT FILING DATE: 1994-04-26
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 206
LENGTH: 8
LENGTH: 8
                                                                                                                                                                                       Sequence 206, Application US/09211715 Patent No. 6759384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: synthetic construct FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.9%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YGRVFFDY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                 5 FFDY
                                          5 FFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-350-260A-380
                                                                                                                                                                       US-09-211-715-206
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US-08-350-260A-487

Sequence 487, Application US/08350260A

Sequence 487, Application US/08350260A

Sequence 487, Application US/08350260A

Sequence 487, Application:
APPLICANT: Winter, Gregory Paul
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva

APPLICANT: Smith, Andrew John Hammond

TITLE OF INVENTION: Methods for producing members of specific

TITLE OF INVENTION: binding pairs

NUMBER OF SEQUENCES: 602

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
FILING DATE: 15-MAY-1991
RRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 10-JUJ-1991
RPIOR APPLICATION DATA:
APPLICATION NUMBER: CT/0891/01134
FILING DATE: 10-JUJ-1991
RPIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/0892/00083
FILING DATE: 15-MAY-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAY-1994
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 11-MAR-1994
ATPORNEY/AGENT INFORMATION:
NAME: Clough, DAVIG W
REGISTRATION NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
NAME: CLOUGH, DAVIG W
REGISTRATION NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
NAME: CLOUGH, DAVIG W
REGISTRATION NUMBER: 381.07
REPERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 391:
CENTIFY CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22; DB 1; Length 8;
Pred. No. 4.6e+05;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50...
A; Conservative
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US-08-350-260A-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YGRVFFDY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YKSLSFDY
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; Sequence 391, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
    APPLICANT: Williams, Andrew David
    APPLICANT: Williams, Samuel Cameron
    APPLICANT: Nisein, Ahuva
    APPLICANT: Nisein, Ahuva
    APPLICANT: Smith, Andrew John Hammond
    TITLE OF INVENTION: Methods for producing members of specific
    TITLE OF INVENTION: Methods for producing members of specific
    TITLE OF INVENTION: Methods for producing members of specific
    NUMBER OF SEQUENCES: 602
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                    PatentIn Release #1.0, Version #1.25 (BPO)
                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
CLASSIFICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIGH BATA:
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIGH BATE:
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIGH BATE:
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIGH BATE:
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIGH BATE:
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIGH BATE:
ATTORNEY/AGENT INFORMATION:
TELEBOHONE: 312-474-6300
INFORMATION FOR SEQ 1D NO: 380:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SECUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserva
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RTSFDY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-350-260A-380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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Gaps

; 0

Length 8;

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GENERAL INFORMATION:
APPLICANT: SHIRAKAMA, KAMON
APPLICANT: MATUSUE, TOMOKAZU
APPLICANT: MATUSUE, TOMOKAZU
APPLICANT: MATUSUE, TOMOKAZU
APPLICANT: CO. MAN SUNG
APPLICANT: CO. MAN SUNG
APPLICANT: CO. MAN SUNG
APPLICANT: CO. MAN SUNG
TITLE OF INVENTION: MATINILIANO
TITLE OF INVENTION: MATINILIANO
TITLE OF INVENTION: MATINILIANO
TITLE OF INVENTION: MATHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
STREET: PO BOX 747
STREET: PO BOX 747
STREET: VA
CONTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
MEDIUM TYPE: FIOPPY disk
MEDIUM TYPE: FIOPPY disk
MEDIUM TYPE: FIOPPY disk
MEDIUM TYPE: FIOPPY disk
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Pred. No. 4.6e+05;
1; Mismatches 0; Indels
COUNTRY: USA
ZIP: 22040-0147
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUNERHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REPRENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION NUMBER: 1110-160
TELECOMMUNICATION NUMBER: 1110-160
TELECOMMUNICATION NUMBER: 1110-160
TELECOMMUNICATION NUMBER: 20,977
REPRENCE (703) 205-8000
TELERAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TUNDE: AMINO acids
TELENGTH: A amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1110-160
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ATTORNEY/AGENT INFORMATION:
NAME: WIMPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPERBYCE/DOCKET NUMBER: 117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.8%;
ilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3, Conserva
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US-08-649-100-23
i Sequence 23, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: NAGUEZ, MAXIMILIANO
TITLE OF INVENTION: ATTI-FAS LIGAND ANTIBODY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
COTTY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
         ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25 (BPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 0.-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 910549.4
FILING DATE: 15-MAY-1991
RPIOR APPLICATION DATA:
APPLICATION NUMBER: GB 910549.4
FILING DATE: 15-MAY-1991
RPIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-UUL-1991
RPIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
PRIOR APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1993
RPIOR DATE: 15-MAY-1994
RPIOR APPLICATION NUMBER: US 08/150,002
PRIOR DATE: 14-SEP-1994
APPLICATION NUMBER: US 08/150,002
PRIOR DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 487:
SEQUENCE CHARACTERISTICS:
"THE PROPAGET FREE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: THE SECONDERS: T
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Best Local Similarity 75.0
Matches 3; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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5 YFDY 8
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      COUNTRY:
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Gaps

Gaps

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Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
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ZIP: G6606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 34-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 13-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 13-MAR-1994
APPLICATION NUMBER: US 08/307,619
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ADDRESSE: Audrey L. Bartnicki
STREET: Marshall, Gestein & Borun
STREET: Marshall, Geste Tower, 233 South Wacker Drive
                                                                                                        Length 8;
                                                                                                 Score 22; DB 2;
Pred. No. 4.6e+05;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGLETRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 391:
  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 380: US-09-104-337A-380
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                      Sequence 391, Application US/09104337A Patent No. 6492160 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 391:
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STRANDEDNESS: single
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                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
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COUNTRY: USA
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Nissim, Ahuva
Ohnson, Kevin Stuart
Smith, Andrew John Hammond
INVENTION: Methods for producing members of specific binding pairs
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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Audrey L. Bartnicki
STREET: Marshall, Gestein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                        Score 22; DB 2; Length 8; Pred. No. 4.6e+05;
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REGISTATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/06605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 380, Application US/09104337A Patent No. 6492160 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                         Query Match
Best Local Similarity 75.v.
      SEQUENCE CHARACTERISTICS LENGTH: 8 amino acids
                          LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                          MOLECULE TYPE: peptide US-08-649-100-39
                                                                                                                                                                                                                                                                                        :|||
5 YFDY 8
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US-09-104-337A-380
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US-09-104-337A-391

0; Gaps Query Match 46.8%; Score 22; DB 2; Length 8; Best Local Similarity 50.0%; Pred. No. 4.6e+05; Matches 4; Conservative 1; Mismatches 3; Indels

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Ω 8

Search completed: December 30, 2005, 15:56:51 Job time : 45 secs

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APPLICANT: KHANNA, RAJIV
APPLICANT: KERR, BEVERLEY M.
APPLICANT: MISKO, IHOR S.
RESULT 2
US-09-920-174-19
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Sequence 80, Appl
Sequence 80, Appl
Sequence 80, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 3179, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 11, Appl
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401, App
8, Appli
8, Appli
195, App
62, Appl
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Sequence 19, Appl
                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                              December 30, 2005, 15:56:06; Search time 160 Seconds (without alignments) 20.891 Million cell updates/sec
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Sequence 1
Sequence 6
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
?: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
:: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
?: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
?: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-777-053-80
US-10-777-053-88
US-10-837-217-80
US-10-837-217-588
US-10-752-380-19
US-09-880-748-3179
US-10-293-418-3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-094-699-56
US-10-160-232-17
US-10-117-937-401
US-10-117-937-401
US-10-117-937-401
US-11-067-064-401
US-11-067-064-401
US-11-067-064-401
US-10-47-25-8
US-10-496-628-8
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3-09-972-656-62
3-09-802-083-9
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                    1867569 segs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                              using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                   US-10-735-916A-12
                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                                              protein search,
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i Sequence 12, Application US/10735916A

j Sequence 12, Application US/10735916A

j Publication No. US2050084906A1

j GENERAL INFORMATION:

j APPLICANT: GORNALION:

j APPLICANT: GORNAL, Nathalie

j APPLICANT: DEGER, Olivier

j APPLICANT: HAEUW, Jean-Francois

APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j APPLICANT: HAEUW, Jean-Francois

j PRIOR FILING DATE: 2003-10-16

j PRIOR FILING DATE: 2003-01-11

j PRIOR FILING DATE: 2002-01-18

j PRIOR FILING DATE: 2002-01-18

j PRIOR FILING DATE: 2002-01-18

j PRIOR FILING DATE: 2002-01-18

j PRIOR FILING DATE: 2002-01-18

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US-10-601-953-601

US-10-322-266-473

US-11-010-797-9

US-11-102-403-41

US-10-190-082-523

US-10-190-082-523

US-10-190-082-582

US-09-974-879-581

US-09-974-879-582

US-09-818-683-582

US-09-818-683-582

US-09-818-683-582

US-10-499-566-60

US-10-499-566-16

US-10-239-656-16

US-10-239-656-16
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US-08-424-550B-308
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; ORGANISM: Mus musculus
US-10-735-916A-12
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Best Local Similarity
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1 YGRVFFDY
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Sequence 588, Application US/1077053

Sequence 588, Application US/1077053

Publication No. US20040132088A1

SEXERAL INFORMATION:

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

TITLE OF INVENTION: EXRESSION VECTORS ENCODING EPITOPES OF

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TITLE OF INVENTION: EXRESSION VECTORS ENCODING EPITOPES OF

TITLE OF INVENTION: EXRESSION VECTORS ENCODING EPITOPES OF

TITLE OF INVENTION: EXPENSION VECTORS ENCODING EPITOPES OF

TITLE OF INVENTION NUMBER: 10/292,413

PRIOR PILING DATE: 2002-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

SEQ ID NOS: 979

SEQ ID NO 588

LENGTH: B
APPLICANT: Qiu, Zhiyong
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REFERENCE: MANNK.0221
CURRENT APPLICATION NUMBER: US/10/777,053
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 10/292,413
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SOFTWARE: PASLESEQ for Windows Version 4.0
ENGTH: 8
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Publication No. US20040203051A1
GENERAL INFORMATION:
APPLICANT: Simmard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Qiu, Zhiyong
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 4; Length 8; Pred. No. 1.7e+06; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.6%; Score 28; DB 4; Length 8; 80.0%; Pred. No. 1.7e+06; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT CRGANISM: Epstein-Barr Virus (EBNA) US-10-777-053-588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.6%;
                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-777-053-80
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Best Local Similarity 80.0-
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4 IFFDY 8
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US-10-777-053-588
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US-10-837-217-80
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US-09-920-174-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-09-920-195A-19
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US-09-920-195A-19
i Sequence 19, Application US/09920195A
j Publication No. US20030175300A1
GENERAL INFORMATION:
APPLICANT: KHANNA, RAJIV
APPLICANT: KHANNA, RAJIV
APPLICANT: MISKO, IHOR S.
APPLICANT: MOSS, DENIS J.
APPLICANT: BURROWS, SCOTT R.
TITLE OF INVENTION: EBV CTL EPITOPES
FILE REPERENCE: FBRC:008USC.
CURRENT APPLICATION NUMBER: US/09/920,195A
CURRENT PELING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 19
LENGTH: 8
  APPLICANT: MOSS, DENIS J.
APPLICANT: BURROWS, SCOTT R.
TITLE OF UNVENTION: EBV CTL EPITOPES
FILE REFERENCE: FERC: 000 USC2
CURRENT APPLICATION NUMBER: US/09/920,174
CURRENT PILING DATE: 2001-08-01
PRIOR PILING DATE: 2001-08-01
PRIOR PILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PALENT NET: 1998-11-23
NUMBER OF SEQ ID NOS: 50
LENGTH: 8
LENGTH: 8
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APPLICANT: Simard, John J. L.; APPLICANT: Diamond, David C.
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Matches 4; Conservative
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Matches 4, Conservative
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US-10-777-053-80
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CURRENT FILING DATE:
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US-10-293-418-3179
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Sequence 588, Application US/10837217

Publication No. US20040203051A1

GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Lei, Xiang-Dong
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
TITLE OF INVENTION: US-10-627
CURRENT APPLICATION NUMBER: US/10/837,217
CURRENT FILING DATE: 2004-04-30
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 979

SEQ ID NO 588
LENGTH: 8
LENGTH: 8
LENGTH: 8
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FILE REFERENCE MANNK. O22CZ
CURRENT APPLICATION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
CURRENT APPLICATION NUMBER: US/10/837,217
CURRENT PILING DATE: 2004-04-30
FRIOR APPLICATION NUMBER: 10/292,413
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
SOFTWARE: PASTEGO for Windows Version 4.0
SEQ ID NO 80
SEQ ID NO 80
LENGTH: 8
TWARE: LENGTH: 8
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Pred. No. 1.7e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.6%; Score 28; DB 4; Length 8; 80.0%; Pred. No. 1.7e+06;
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APPLICANT: KHANNA, RAJIV
APPLICANT: KERR, BEVERLEY M.
APPLICANT: MISKO, IHOR S.
APPLICANT: MOSS, DENIS J.
TITLE OF INVENTION SBV CTL EPITOPES
TITLE OF INVENTION: EBV CTL EPITOPES
TITLE REPERRENCE: FERC:008
CURRENT APPLICATION NUMBER: US/10/752,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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US-10-837-217-588
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US-10-752-380-19
; Sequence 19, Application US/10752380
; Publication No. US2005008498A1
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-837-217-80
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Matches 4; Conserv
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Matches 4; Conserv
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4 IFFDY 8
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Sequence 3179, Application US/09880748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICATY: RUbben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 3179
                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3179, Application US/10293418
Publication No. US2003022396A1
Publication No. US20030223996A1
Publication No. US20030223996A1
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
CURRENT APPLICATION UNDER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR PPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
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80.0%; Pred. No. 1.7e+06;
iive 1; Mismatches 0;
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PRIOR APPLICATION NUMBER: US/09/194,450
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 19
LENGTH: 8
                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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US-09-880-748-3179
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Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-160-232-17
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US-10-044-896-12

Sequence 12, Application US/10044896

Sequence 12, Application US/10044896

Sequence 12, Application US/2003166228A1

GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan

APPLICANT: Stewart, Timothy

APPLICANT: Stewart, Timothy

APPLICANT: STEWART, MANI-INTERFERON-ALPHA ANTIBODIES

FILE REFERENCE: GENENT: 074A

CURRENT APPLICATION NUMBER: US/10/044,896

CURRENT FILING DATE: 2002-109

PRIOR APPLICATION NUMBER: 60/270775

PRIOR APPLICATION NUMBER: 201-02-109

SPRIOR FILING DATE: 2001-02-109

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0

| FRANCETION 101
                              CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/315,051
PRIOR FILING DATE: 1998-07-20
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 17
LENGTH: 8
             CURRENT APPLICATION NUMBER: US/10/160,232
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Sequence 401, Application US/10117937

Publication No. US20030220239A1

GENERAL INFORMATION:

APPLICANT: CTL IMMUNO THERAPIES CORP.

APPLICANT: SIMARD, John, J.L.

APPLICANT: LIU, Liping

APPLICANT: LIU, Liping

APPLICANT: XIAOND

TILE OF INVERTION: EPITOPE SEQUENCES

FILE REFERENCE: CTLIMM.027A
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Best Local Similarity 100.
Matches 4; Conservative
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ORGANISM: Homo sapiens
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Publication No. US20030088075A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HTO, MIKITO
APPLICANT: HAMAI, NOBUO
APPLICANT: NAKAMDA, YOKO
APPLICANT: NAKAMDA, YOKO
APPLICANT: NAKAMDA, WASABUMI
ITILE OF INVENTION: AMAILHHUYA, MASABUMI
FILE REFERENCE: 249-107
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Sequence 56, Application US/10094699

Publication No. US20030046714A1

GENERAL INFORMATION:

APPLICANT: SIMARD, John, J.L.

APPLICANT: DIAWOND, David, C.

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: CANCER

FILE REFERENCE: CTLIMM.015A

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 60/274,063

PRIOR FILING DATE: 2001-03-07

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 4; Length 8; Pred. No. 1.7e+06; 1; Mismatches 0; Indels
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-17
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
SEQ ID NOS: 3247
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Best Local Similarity 66.7
Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-10-293-418-3179
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; ORGANISM: Homo sapien
US-10-094-699-56
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US-10-160-232-17
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US-10-855-013-31

i Sequence 31, Application US/10855013

j Sequence 31, Application US/10855013

j GENERAL INFORMATION:
    APPLICANT'S BIOGEN, Inc. et al.
    TITLE OF INVENTION: ANTIBODIES AGAINST MONOCYTE CHEMOTACTIC PROTEINS
    FILE REFERENCE: BGN-006PC
    CURRENT FILING DATE: 2004-05-27
    PRIOR APPLICATION NUMBER: US 60/343391
    PRIOR FILING DATE: 2001-11-30
    PRIOR PELING DATE: 2001-11-30
    PRIOR PELING DATE: 2002-05-24
    PRIOR PELING DATE: 2002-08-01
    NUMBER OF SEQ ID NOS: 34
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 31
    LENGTH: BANCH ANDIBLE CORD WINDOWS OF SEQ ID NO 31
    LENGTH: BANCH ANDIBLE CORD WINDOWS OF SEQ ID NO 31
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                                                                                                                                                                                                                                                                                                                                                                                       53.2%; Score 25; DB 4; Length 8; 80.0%; Pred. No. 1.7e+06; live 1; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 401
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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; ORGANISM: Mus musculus
US-10-855-013-31
                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-937-401
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4.993 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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length: 8
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Maximum DB seq
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Query Match 53.2%;
Best Local Similarity 57.1%;
Matches 4; Conservative
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Matches 4; Conservative
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GENERAL INFORMATION:

APPLICATION:
APPLICATION:
ALTICLE OF INVENTION:
FILE REPRENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT APPLICATION NUMBER: 00/443,296
FRIOR FILING DATE: 2004-06-18
FRIOR FILING DATE: 2004-06-18
FRIOR FILING DATE: 2004-06-18
FRIOR FILING DATE: 2001-11-16
FRIOR PLICATION NUMBER: 00/331,469
FRIOR FILING DATE: 2001-11-16
FRIOR FILING DATE: 2001-11-16
FRIOR FILING DATE: 2001-06-15
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FRIOR FILING DATE: 2001-03-21
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FRIOR FILING DATE: 2001-03-21
FRIOR FILING DATE: 2001-03-16
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US-11-073-347-56
i Sequence 56, Application US/11073347
i Publication No. US20050260234A1
i GENERAL INFORMATION:
i APPLICANT: SIMARD, John J. L.
i APPLICANT: SIMARD, John J. L.
i TITLE OF INVENTION: ANTI-NECVASCULATURE PREPARATIONS FOR
ITILE OF INVENTION: CANCER
ITILE OF INVENTION: CANCER
IFILE REFERENCE: MANNK.015C1
CURRENT APPLICATION NUMBER: US/11/073,347
CURRENT FILING DATE: 2005-03-04
i PRIOR PILING DATE: 2002-07
i PRIOR PILING DATE: 2001-07
i PRIOR PILING DATE: 2001-07
i PRIOR PILING DATE: 2001-07
i RIGHT PILING DATE: 2001-07
i RIGHT PILING DATE: 2001-07
i RIGHT PILING DATE: 2001-07
i RIGHT PILING DATE: 2001-07
i RUMBER OF SEQ ID NOS: 159
i SOFTWARE: FastSEQ for Windows Version 4.0
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1; Mismatches 0
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Best Local Similarity 66.
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-11-054-515-3179
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ORGANISM: Homo sapien
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                                                                     APPLICANT: ADAMS, CAMELLIA W.
APPLICANT: FERRARA, NAPOLEONE
APPLICANT: FISTRARA, NAPOLEONE
APPLICANT: FILVAROPE, ELLEN H.
APPLICANT: PRESTA, LEONARD G.
APPLICANT: TEADA, MAX L.
TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
FILE REFERENCE: P1954R1US
FILLS REFERENCE: P1954R1US
CURRENT APPLICATION NUMBER: US/11/096,046
CURRENT FILING DATE: 2005-03-31
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JUS-11-15-747-37

JUS-11-152-747-37

JUS-11-152-747-37

JUDICATION NO. USZO050251881A1

JUDICATION NO. USZO050251881A1

JUDICANT: E. I. du Pont de Nemours, Inc.

APPLICANT: T. du Pont de Nemours, Inc.

APPLICANT: Tao, Luan

TITLE OF INVENTION: CAROTENOID KETOLASE GENE

FILE REFERENCE: CL-1849 US NA

CURRENT APPLICATION NUMBER: US/11/152,747

CURRENT APPLICATION NUMBER: 3005-06-14

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 47

SOFTWARE: MICROSOft Office 97

LENGTH: 8

LENGTH: 8

FILENGTH: 8

FILENGTH: 8

FILENGTH: 8

FILENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial sequence FATURE: ORGANISM: Artificial sequence ORGANISM: PRATURE: OTHER INFORMATION: sequence is synthesized US-11-096-046-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-11-127-677-112
; Sequence 112, Application US/11127677
Sequence 23, Application US/11096046 Publication No. US20050276802A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Deinococcus radiodurans
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Publication No. US20050272107A1

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US-11-016-706-77
; Sequence 77, Application US/11016706
; Publication No. US/0050244334A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 50.0°
....nes 3; Conservative
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NAME/KEY: MOD_RES
LOCATION: (8)
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APPLICANT: LAKE, THOMAS P.
APPLICANT: LAKE, THOMAS P.
APPLICANT: LAKE, THOMAS P.
APPLICANT: SANDERS, VIRCINIA J.
APPLICANT: SANDERS, VIRCINIA J.
APPLICANT: SNOW, ALAN D.
TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
CURRENT APPLICATION NUMBER: US/11/016,706
CURRENT FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PARENTIN VET: 3.2
SEQ ID NO 76
LENGTH: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Derived protein sequence of intracellular Dab
US-11-127-677-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.8%; Score 22; DB 7; Length 8; 66.7%; Pred. No. 4.4e+04; ive 0; Mismatches 2; Indels
GENERAL INCORRATION:
APPLICANT: Rebibits, Terence H
APPLICANT: Rebibits, Terence H
APPLICANT: Rebibits, Terence H
APPLICANT: Tanaka, Tomoyuki
TITLE OF INVENTION: Intracellular antibodies
FILE REPERRECE: 18396/2462
CURRENT APPLICATION NUMBER: US/11/127,677
CURRENT PILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: PCT/GB03/04942
PRIOR FILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-15
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Version 3.1
SEQ ID NO 112
LENGTH: 8
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; OTHER INFORMATION: Tyr or not present US-11-016-706-76
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; Sequence 76, Application US/11016706

; Publication No. US20050244334A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial sequence
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Matches 3; Conservative
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: LAKE, THOMAS P.

APPLICANT: LAKE, THOMAS P.

APPLICANT: LAKE, THOMAS P.

APPLICANT: LAKE, THOMAS P.

APPLICANT: LAKE, THOMAS P.

APPLICANT: SANDERS, VIRGINIA J.

APPLICANT: SNOW, ALAN D.

TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS

TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS

TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS

TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS

TITLE OF INVENTION: OWNBER: US/11/016,706

CURRENT APPLICATION NUMBER: 09/962,955

PRIOR FILING DATE: 2001-09-22

PRIOR FILING DATE: 2001-09-22

PRIOR FILING DATE: 1997-10-08

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PATENTIN VEY: 3.2

SEQ ID NO 77
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j Publication No. Us2005025532A1
general INFORMATION:
general INFORMATION:
j APPLICANT: Ruben et al.
general INFORMATION:
j TITLE OF INVERTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF23P3
cURRENT APPLICATION NUMBER: US/11/054,515
j CURRENT APPLICATION NUMBER: 06/543,296
pRIOR APPLICATION NUMBER: 60/543,296
pRIOR PILING DATE: 2004-02-10
pRIOR FILING DATE: 2004-06-18
j PRIOR FILING DATE: 2004-06-18
j PRIOR FILING DATE: 2001-11-14
pRIOR FILING DATE: 2001-11-16
j PRIOR APPLICATION NUMBER: 60/340,817
pRIOR PRILING DATE: 2001-11-16
j PRIOR PILING DATE: 2001-12-19
j PRIOR PILING DATE: 2001-05-25
j PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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US-11-093-274-7
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Publication No. US2005025532A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TILLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PE523P3

CURRENT APPLICATION NUMBER: US/11/054,515

FRICE REPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2004-00-11

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR APPLICATION NUMBER: 60/543,418

PRIOR APPLICATION NUMBER: 60/31,469

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-21

PRIOR PRILOR DATE: 2001-03-21

PRIOR PRILOR DATE: 2001-03-16

PRIOR PRILOR DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2000-03-16

RIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 3092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3111
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.4%; Score 19; DB 7; Length 8; Best Local Similarity 100.0%; Pred. No. 4.4e+04; Matches 3; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.4e+04;
:ive 0; Mismatches 0;
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US-11-054-515-3141
A: Sequence 3141, Application US/11054515
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-11-054-515-3092
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US-11-054-515-3111
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US-11-054-515-3111
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATION:
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APPLICATION:
AALIDOGUES THAT Immunospecifically Bind BLyS
FILE REFERENCE: PF523P3
FILE REFERENCE: PF523P3
FILE REPERENCE: PF523P3
CURRENT PELING DATE: 2005-02-10
FRIOR APPLICATION NUMBER: 60/580,347
FRIOR APPLICATION NUMBER: 60/580,347
FRIOR PELING DATE: 2004-06-18
FRIOR FILING DATE: 2002-11-14
FRIOR FILING DATE: 2002-11-14
FRIOR FILING DATE: 2001-11-16
FRIOR FILING DATE: 2001-11-16
FRIOR FILING DATE: 2001-12-19
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-03-16
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FRIOR FILING DATE: 2001-03-17
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Publication No. US20050266008A1

GRUBRAL INFORMATION.

APPLICANT: Cardarelli, Josephine M.

APPLICANT: Cardarelli, Josephine M.

APPLICANT: Cutter, Beth

APPLICANT: Stinivasan, Mohan

TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES

FILE REFERENCE: 04280/120101-US1

CURRENT FILING DATE: 2005-02-28

PRIOR FILING DATE: 2005-03-29

FRICH APPLICATION NUMBER: 60/557,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
40.4%; Score 19; DB 7; I
Best Local Similarity 60.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 1;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 8
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-11-093-274-7
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Best Local Similarity
Matches 3; Conserval
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Query Match
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4 VFIEY 8
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APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT PILING DATE: 1999-10-0.2
FRIOR APPLICATION NUMBER: US 08/412,863
FRIOR PILING DATE: 1993-03-05
FRIOR PILING DATE: 1993-03-05
FRIOR FILING DATE: 1993-06-06
FRIOR FILING DATE: 1993-06-06
FRIOR FILING DATE: 1993-08-06
FRIOR FILING DATE: 1993-08-06
FRIOR FILING DATE: 1993-08-06
FRIOR FILING DATE: 1993-1-29
FRIOR APPLICATION NUMBER: US 08/159,184
FRIOR APPLICATION NUMBER: US 08/159,339
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                                                                                                                                                                                                                                APPLICANT: Quralishi, Omar APPLICANT: Quralishi, Omar APPLICANT: Bridon, Dominique P.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN TITLE OF INVENTION: CONNUGANES
FILE REFERENCE: 500862003700
CURRENT APPLICATION NUMBER: US 11/112,277
CURRENT FILING DATE: 2006-04-22
PRIOR APPLICATION NUMBER: US 60/565,228
PRIOR PILING DATE: 204-04-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: RastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 7; Length 8; Pred. No. 4.4e+04; 1; Mismatches 2; Indels
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. OTHER INFORMATION: Xaa is Lys linked to MPA
US-11-112-277-3
                                                                                                                                     ; Sequence 3, Application US/11112277
; Publication No. US20050267293A1
; RENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 420, Application US/11045024, Publication No. US20050271676A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Southwood, Scott
Livingston, Brian
Chesnut, Robert
Baker, Denise Marie
Celis, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: K5 Analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.4%;
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APPLICANT: Sidney, John
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Best Local Similarity 50.0
Matches 3; Conservative
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2 RKLYDY 7
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2 WGRAF 6
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APPLICANT: Sidney,John
APPLICANT: Sidney,John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Colis, Robert
APPLICANT: Calis, Bateban
APPLICANT: Calis, Rateban
APPLICANT: Raiph
APPLICANT: Rpimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01.28
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                                                                                                                                                                                                                                                                                                                                Length 8;
                                                                                                                                                                                                                                                                                                                                Score 19; DB 7; 1
Pred. No. 4.4e+04;
1; Mismatches 1;
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PRIOR APPLICATION NUMBER: US 09/412,863

PRIOR FILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1993-06-04

PRIOR PILING DATE: 1993-06-04

PRIOR PILING DATE: 1993-06-06

PRIOR PILING DATE: 1993-06-06

PRIOR PILING DATE: 1993-10-29

PRIOR PILING DATE: 1993-11-29

PRIOR PILING DATE: 1994-12-01

NUMBER OF SEQ ID NOS: 14528

SOFTWARE: PARLER PARLERS FOR WINDOWS VERSION 4.0

SEQ ID NO 3592
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR AFLING DATE: 1994-03-04
PRIOR PILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 420
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ORGANISM: HUMAN IMMUNOBEFICIENCY VIRUS
                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3592, Application US/11045024 Publication No. US20050271676A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0%;
Matches 3; Conservative
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Search completed: December 30, 2005, 16:06:47 Job time : 12 secs

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